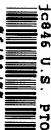


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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: "*Corynebacterium Glutamicum Genes Encoding Proteins Involved in Genetic Stability, Gene Expression, and Protein Secretion and Folding*"

Enclosed are:

- ☒ 69 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 9 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 19 pages of Table 4;
- ☒ 117 pages of Appendix A;
- ☒ 38 pages of Appendix B;
- ☒ 788 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
- ☒ A pre-paid acknowledgment postcard.

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**CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN GENETIC STABILITY, GENE EXPRESSION, AND PROTEIN
SECRETION AND FOLDING**

5 **Related Applications**

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/143752, filed July 14, 1999, and U.S. Provisional Patent Application Serial No. 60/151671, filed August 8, 1999. This application also claims priority to prior filed
10 German Patent Application No. 19931412.8, filed July 8, 1999, and German Patent Application No. 19932928.1, filed July 14, 1999. The entire contents of all of the aforementioned applications are expressly incorporated herein by this reference.

Background of the Invention

15 Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic
20 compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have
25 been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

30 The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for
35 transformation. These novel nucleic acid molecules encode proteins, referred to herein as stability, gene expression, or protein secretion/folding (SES) proteins.

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5 *C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SES nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the SES nucleic acids of the invention, or modification of the sequence of the SES nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

10 The SES nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

15 The SES nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

25 e.g. e.g. The SES proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the repair or recombination of DNA, transposition of genetic material, expression of genes (i.e., involved in transcription or translation), protein folding, or protein secretion in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey et al., U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata et al., *J. Bacteriol.* 159: 306-311 (1984); and Santamaria et al., *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or

efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

- There are a number of mechanisms by which the alteration of an SES protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, modulation of proteins involved directly in transcription or translation (e.g., polymerases or ribosomes) such that they are increased in number or in activity should increase global cellular transcription or translation (or rates of these processes). This increased cellular gene expression should include those proteins involved in fine chemical biosynthesis, so an increase in yield, production, or efficiency of production of one or more desired compounds may occur. Modifications to the transcriptional/translational protein machinery of *C. glutamicum* such that the regulation of these proteins is altered may also permit increased expression of genes involved in the production of fine chemicals. Modulation of the activity or number of proteins involved in polypeptide folding may permit an increase in the overall production of correctly folded molecules in the cell, thereby increasing the possibility that desired proteins (e.g., fine chemical biosynthetic proteins) are able to function properly. Further, by mutating proteins involved in secretion from *C. glutamicum* such that they are increased in number or activity, it may be possible to increase the secretion of a fine chemical (e.g., an enzyme) from cells in fermentor culture, where it may be readily recovered.
- Genetic modification of the SES molecules of the invention may also result in indirect modulation of production of one or more fine chemicals. For example, by increasing the number or activity of a DNA repair or recombination protein of the invention, one may increase the ability of the cell to detect and repair DNA damage. This should effectively increase the ability of the cell to maintain a mutated gene within its genome, thereby increasing the likelihood that a transgene engineered into *C. glutamicum* (e.g., encoding a protein which will increase biosynthesis of a fine chemical) will not be lost during culture of the microorganism. Conversely, by decreasing the number or activity of one or more DNA repair or recombination proteins, it may be possible to increase the genetic instability of the organism. Such manipulations should improve the ability of the organism to be modified by mutagenesis without the introduced mutation being corrected. The same holds true for proteins involved in transposition or rearrangement of genetic elements in *C. glutamicum* (e.g., transposons). By mutagenizing these proteins such that they are either increased or decreased in number or activity, it is possible to simultaneously increase or decrease the genetic stability of the microorganism. This has a profound impact on the ability of any other mutation to be introduced into *C. glutamicum*, and on the ability of introduced

mutations to be retained. Transposons also offer a convenient mechanism by which mutagenesis of *C. glutamicum* may be performed; duplication of desired genes (e.g., fine chemical biosynthetic genes) is readily accomplished by transposon mutagenesis, as is disruption of undesired genes (e.g., genes encoding proteins involved in degradation of desired fine chemicals).

By modulating one or more proteins (e.g. sigma factors) involved in the regulation of transcription or translation in response to particular environmental conditions, it may be possible to prevent the cell from slowing or stopping protein synthesis under unfavorable environmental conditions, such as those found in large-scale fermentor culture. This should lead to increased gene expression, which in turn may permit increased biosynthesis of desired fine chemicals under such conditions. Mutagenesis of proteins involved in protein secretion systems may result in modulated secretion rates. Many such secreted proteins have functions critical for cell viability (e.g., cell surface proteases or receptors). An alteration of a secretory pathway such that these proteins are more readily transported to their extracellular location may improve the overall viability of the cell, and thus result in greater numbers of *C. glutamicum* cells capable of producing fine chemicals during large-scale culture. Further, the secretion apparatus (e.g., the sec system) is also known to be involved in the insertion of integral membrane proteins (e.g., pores, channels, or transporters) into the membrane. Thus, the modulation of activity of proteins involved in protein secretion from *C. glutamicum* may affect the ability of the cell to excrete waste products or to import necessary metabolites. If the activity of these secretory proteins is increased, then the ability of the cell to produce fine chemicals may be similarly increased. If the activity of these secretory proteins is decreased, then there may be insufficient nutrients available to support overproduction of desired compounds, or waste products may interfere with such biosynthesis.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SES proteins, which are capable of, for example, participating in the repair or recombination of DNA, transposition of genetic material, expression of genes (i.e., the processes of transcription or translation), protein folding, or protein secretion in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SES protein are referred to herein as SES nucleic acid molecules. In a preferred embodiment, an SES protein participates in improving or decreasing genetic stability in *C. glutamicum*, in the expression of genes (i.e., in transcription or translation) or protein folding in this organism, or in protein secretion from *C. glutamicum*. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SES protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SES-
5 encoding nucleic acid (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at
10 least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred SES proteins of the
15 present invention also preferably possess at least one of the SES activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, e.g.,
20 sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an SES activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (i.e., the processes of transcription or translation), in protein folding, or in protein secretion in
25 *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (e.g., an entire amino acid sequence selected from those sequences set forth in Appendix B). In
30 another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an SES fusion protein) which includes
35 a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (i.e.,

the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table I, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

5 In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SES
10 protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SES protein by culturing the host cell in a suitable medium. The SES protein
15 can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SES gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SES sequence as a transgene. In another embodiment, an endogenous SES gene within the genome of the microorganism has been altered, e.g., functionally disrupted, by homologous recombination with an altered SES gene. In another embodiment, an endogenous or introduced SES gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SES protein. In still another embodiment, one or more of the regulatory regions (e.g., a promoter, repressor, or inducer) of an SES gene in a microorganism has been altered (e.g., by deletion, truncation, inversion, or point mutation) such that the expression of the SES gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SES protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SES protein or portion thereof can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SES protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*.

The invention also provides an isolated preparation of an SES protein. In preferred embodiments, the SES protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated SES protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SES protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of SES proteins also have one or more of the SES bioactivities described herein.

The SES polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SES polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SES protein alone. In other preferred embodiments, this fusion protein participates in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*,

the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

- 5 In another aspect, the invention provides methods for screening molecules which modulate the activity of an SES protein, either by interacting with the protein itself or a substrate or binding partner of the SES protein, or by modulating the transcription or translation of an SES nucleic acid molecule of the invention.

- Another aspect of the invention pertains to a method for producing a fine
10 chemical. This method involves the culturing of a cell containing a vector directing the expression of an SES nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SES nucleic acid. In another preferred embodiment, this method
15 further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

- Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates SES protein activity or SES nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* processes involved in genetic stability, gene expression, protein folding, or protein secretion such that the yield, production, or efficiency of production of a desired fine
25 chemical by this microorganism is improved. The agent which modulates SES protein activity can be an agent which stimulates SES protein activity or SES nucleic acid expression. Examples of agents which stimulate SES protein activity or SES nucleic acid expression include small molecules, active SES proteins, and nucleic acids encoding SES proteins that have been introduced into the cell. Examples of agents
30 which inhibit SES activity or expression include small molecules and antisense SES nucleic acid molecules.

- Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SES gene into a cell, either maintained on a separate plasmid or integrated into the genome of
35 the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be

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modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

5

Detailed Description of the Invention

The present invention provides SES nucleic acid and protein molecules which are involved in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein
10 folding, or in protein secretion in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of activity of a protein involved in secretion of a fine chemical (*e.g.*, an enzyme) has a direct impact on the yield, production, and/or efficiency of production of
15 a fine chemical from the modified *C. glutamicum*), or an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the activity or number of copies of a *C. glutamicum* DNA repair protein results in alterations in the ability of the microorganism to maintain the introduced mutation, which in turn may impact the
20 production of one or more fine chemicals from such a strain). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an
25 organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related
30 compounds, p. 561-612, in Biotechnology vol. 6, Rehm et al., eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial
35 Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological

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Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term “amino acid” is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann’s Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. *Biochemistry*, 3rd edition, pages 578-590 (1988)). The ‘essential’ amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 ‘nonessential’ amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) *Amino acids –*

technical production and use, p. 466-502 in Rehm *et al.* (eds.) *Biotechnology* vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transfer of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways,

see Stryer, L. *Biochemistry*, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

5 *B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses*

 Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active
10 substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry,
15 "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to
20 occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

25 The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and
30 Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

 Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate
35 (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxa-

5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate

- 5 biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the
- 10 precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantotheine (and its derivatives) and coenzyme A.

- Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been
- 15 identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives
- 20 of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

- Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and
- 25 porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD
- 30 (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

- The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
- 35 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (i.e., AMP) or as coenzymes (i.e., FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (e.g. Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kunitake, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm et al., eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*,

Wiley; New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto et al., (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Genetic Stability; Protein Synthesis and Protein Secretion in *C. glutamicum*

The production of a desired compound from a cell such as *C. glutamicum* is the culmination of a large number of separate yet interrelated processes, each of which is critical to the overall production and release of the compound from the cell. In engineering a cell to overproduce one or more fine chemicals, consideration must be given to each of these processes to ensure that the biochemical machinery of the cell will be compatible with such genetic manipulation. Cellular mechanisms of particular importance include the stability of the altered gene(s) upon introduction into the cell, the ability of the mutated gene to be properly transcribed and translated (including issues of codon usage), and the ability of the mutant protein product to be appropriately folded and/or secreted.

A. Bacterial Repair and Recombination Systems

Cells are constantly exposed to nucleic acid-damaging agents, such as UV irradiation, oxygen radicals, and alkylation. Further, even the action of DNA polymerases is not error-free. Cells must maintain a balance between genetic stability (which ensures that genes necessary for vital cellular functions are not damaged during normal growth and metabolism) and genetic variability (which permits cells to adapt to a changing environment). Therefore, there exist separate, but interrelated pathways of DNA repair and DNA recombination in most cells. The former serves to stringently correct errors in DNA molecules by either directly reversing the damage or excising the damaged region and replacing it with the correct sequence. The latter recombination system also repairs nucleic acid molecules, but only those lesions that result in damage to both strands of DNA such that neither strand is able to serve as a template to correct the other. Recombination repair and the SOS response may readily lead to inversions, deletions, or other genetic rearrangements within or around the region of the damage, which in turn promotes a certain degree of genomic instability which may contribute to the ability of the cell to adapt to changing environments or stresses.

High-fidelity repair mechanisms include direct reversal of DNA damage and excision of damage and resynthesis using the information encoded on the opposite DNA strand. Direct reversal of damage requires an enzyme having an activity opposite of that which originally damaged the DNA. For example, inappropriate methylation of DNA may be corrected by the action of DNA repair methyltransferases, and nucleotide dimers created by UV irradiation may be fixed by the activity of deoxyribodipyrimidine photolyase, which, in the presence of light, cleaves the dimer back to its constituent nucleotides (see Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York, and references therein).

Precise repair of more extensive damage requires specialized repair mechanisms. These include the mismatch repair and excision repair systems. Damage to a single base may be corrected by a series of cleavage reactions, where first the sugar-base bond is cut, followed by cleavage of the DNA backbone at the site of damage and removal of the damaged base itself. Finally, DNA polymerase and DNA ligase act to fill in and seal the gap using the second DNA strand as a template. More significant DNA damage which results in altered conformation of the double helix is corrected by the ABC system, in which helicase II, DNA polymerase I, UvrA, UvrB, and UvrC proteins combine to nick the double helix at the site of damage, to unwind the damaged region in an ATP-dependent fashion, to excise the damaged region, and to fill in the missing region using the other strand as a template. Lastly, DNA ligase seals the nick. Specific repair systems also exist for G-T mismatches (involving the Vsr protein) and for small

deletion/insertion errors resulting in mispairing of the two strands (involving the methylation-directed pathway).

There also exist low-fidelity repair systems which are generally used to correct very extensive DNA damage in bacteria. Double-strand repair and recombination occurs in the presence of a lesion which affects both strands of DNA. In this situation, it is impossible to repair the damage utilizing the other strand as the template. Thus, this repair system involves a double-crossover event between the area of the lesion and another copy of the region on a homologous DNA molecule. This is possible because bacteria divide so rapidly that a second copy of genomic DNA is usually available before actual cell division occurs. This crossover event may readily lead to inversions, duplications, deletions, insertions and other genetic rearrangements, and thus increases the overall genetic instability of the organism.

The SOS response is activated when sufficient damage is present in the DNA that DNA polymerase III stalls and cannot continue replication. Under these circumstances, single-stranded DNA is present. The RecA protein is activated by binding to single-stranded DNA, and this activated form results in the activation of the LexA repressor, thereby lifting the transcriptional block of more than 20 genes, including UvrA, UvrB, UvrC, helicase II, DNA pol III, UmuC, and UmuD. The combined activities of these enzymes results in sufficient filling of the gap region that DNA pol III is able to resume replication. However, these gaps have been filled in with bases which should not be present; thus, this type of repair results in error-prone repair, contributing to overall genetic instability in the cell.

B. Transposons

The aforementioned systems, whether high or low fidelity, exist to repair DNA damage. In certain circumstances, this repair may accidentally incorporate additional genetic rearrangements. Many bacterial cells also have mechanisms specifically designed to cause such genetic rearrangements. Particularly well-known examples of such mechanisms are the transposons.

Transposons are genetic elements which are able to move from one site to another either within a chromosome or between a piece of extrachromosomal DNA (e.g., a plasmid) and a chromosome. Transposition may occur in multiple ways; for example, the transposable element may be cut out from the donor site and integrated into the target site (nonreplicative transposition), or the transposable element may alternately be duplicated from the donor site to the target site, yielding two copies of the element (replicative transposition). There is generally no sequence relationship between the donor and target sites.

There are a variety of results possible from such a transposition event. The integration of a transposable element into a gene disrupts the gene, usually abrogating its function entirely. An integration event that occurs in the DNA surrounding a gene may not perturb the coding sequence itself, but can have a profound effect on the regulation of the gene and thus, on its expression. Recombination events between two copies of a transposable element found in different portions of the genome may result in deletions, duplications, inversions, transpositions, or amplifications of segments of the genome. It is also possible for different replicons to fuse.

The simplest transposon-like genetic elements are termed insertion (IS) elements. IS elements contain a nucleotide region of varying length (though usually less than 1500 bases) lacking any coding regions, surrounded by inverted repeats at either end. Thus, since the IS element does not encode any proteins whose activity may be detected, the presence of an IS element is generally only observed due to a loss of function of one or more genes in which the IS element is inserted.

Transposons are mobile genetic elements which, unlike IS elements, contain nucleic acid sequences bounded by repeats which may encode one or more proteins. It is not unusual for these repeat regions to consist of IS elements. The proteins encoded by the transposon are typically transposases (proteins which catalyze the movement of the transposon from one site to another) and antibiotic resistance genes. The mechanisms and regulation of transposable elements are well known in the art and are have been described at least in, for example, Lengeler *et al.* (1999) *Biology of Prokaryotes*, Thieme Verlag: Stuttgart, p. 375-361; Neidhardt *et al.* (1996) *Escherichia coli* and *Salmonella*, ASM Press: Washington, D.C.; Sonenshein, A.L. et al., eds. (1993), *Bacillus subtilis*, ASM Press: Washington, D.C.; Voet, D. and Voet, J.G. (1992) *Biochemie*, VCH: Weinheim, p. 985-990; Brock, T.D., and Madigan, M.T. (1991) *Biology of Microorganisms*, 6th ed., Prentice Hall: New York, p. 267-269; and Kleckner, N. (1990) "Regulation of transposition in bacteria", *Annu. Rev. Biochem.* 61: 297-327.

C. Transcription

Gene expression in bacteria is regulated mainly at the level of transcription. The transcriptional apparatus consists of a number of proteins that can be divided into two groups: RNA polymerase (the processive DNA-transcribing enzyme) and sigma factors (which regulate gene transcription by directing RNA polymerase to specific promoter-DNA sequences which these factors recognize). The combination of RNA polymerase and sigma factors creates the RNA polymerase holoenzyme, an activated complex. Gram positive bacteria such as *Corynebacteria* contain only one type of RNA-polymerase, but a variety of different sigma factors specific for different promoters,

growth phases, environmental conditions, substrates, oxygen levels, transport processes, and the like, which permits adaptability of the organism to different environmental and metabolic conditions.

Promoters are specific DNA sequences that serve as docking sites for the RNA polymerase holoenzyme. Many promoter elements possess conserved sequence elements that may be recognized through homology searches; alternately, promoter regions for a particular gene may be identified using standard techniques such as primer extension. Many promoter regions from gram-positive bacteria are known (see, e.g., Sonenshein, A.L., Hoch, J.A., and Losick, R., eds. (1993) *Bacillus subtilis*, ASM Press: Washington, D.C.).

Promoter transcriptional control is influenced by several mechanisms of repression or activation. Specific regulatory proteins which bind promoters have the ability to block (repressors) or to assist (activators) the binding of the RNA holoenzyme, and thus to regulate transcription. The binding of these repressor and activator molecules in turn is regulated by their interactions with other molecules, such as proteins or other metabolic compounds. Transcription may alternately be regulated by factors influencing processes such as elongation or termination (see, e.g., Sonenshein, A.L., Hoch, J.A., and Losick, R., eds. (1993) *Bacillus subtilis*, ASM Press: Washington, D.C.). The ability to regulate transcription of genes in response to a variety of environmental or metabolic cues affords cells the ability to tightly control when a gene may be expressed and or how much of a gene product may be present in the cell at one time. This in turn prevents unnecessary expenditure of energy or unnecessary utilization of possibly scarce intermediate compounds or cofactors.

25 *D. Translation and tRNA-Aminoacyl Synthetases*

Translation is the process by which a polypeptide is synthesized from amino acids according to the information contained within an mRNA molecule. The main components of this process are ribosomes and specific initiation or elongation factors, such as IF1-3, EF-G, and EFTu (see, e.g., Sonenshein, A.L., Hoch, J.A., Losick, R., eds. (1993) *Bacillus subtilis*, ASM Press: Washington, D.C.).

Each codon of the mRNA molecule encodes a particular amino acid. The conversion from mRNA to amino acid is effected by transfer RNA (tRNA) molecules. These molecules consist of a single strand of RNA (between 60 and 100 bases), which exists in an L-shaped three dimensional structure having protruding areas, or 'arms'. One such arm forms base pairs with a particular codon sequence on the mRNA molecule. A second arm interacts specifically with a particular amino acid (the one encoded by the codon). Other arms of the tRNA include the variable arm, the T ψ C arm

(which bears thimidylylate and pseudouridylylate modifications), and the D arm (which bears a dihydrouridine modification). The function of these latter structures remains unknown, but their conservation between tRNA molecules suggests a role in protein synthesis.

- 5 In order for the nucleic acid-based tRNA molecule to associate with the correct amino acid, a family of enzymes, termed the aminoacyl-tRNA synthetases, must act. There exist many different of these enzymes, each of which is specific for a particular tRNA and a particular amino acid. These enzymes link the 3' hydroxyl of the terminal tRNA adenosine ribose moiety to the amino acid in a two step reaction. First, the enzyme is activated by reaction with ATP and the amino acid to result in an aminoacyl-tRNA synthetase-aminoacyl adenylate complex. Second, the aminoacyl group is transferred from the enzyme to the target tRNA where it remains in the high-energy state. Binding of the tRNA molecule to its cognate codon on the mRNA molecule then brings the high-energy amino acid attached to the tRNA into contact with the ribosome.
- 10 Within the ribosome, the amino-acid charged tRNA (aminoacyl-tRNA) occupies one binding site (the A site) adjacent to a second site (the P site) containing a tRNA molecule whose amino acid arm is attached to the nascent polypeptide chain (peptidyl-tRNA). The activated amino acid on the aminoacyl-tRNA is sufficiently reactive that a peptide bond spontaneously forms between this amino acid and the next amino acid on the nascent polypeptide chain. Hydrolysis of GTP provides the energy for the transfer of the now-polypeptide chain-loaded tRNA from the A site to the P site of the ribosome, and the process repeats until a stop codon is reached.

- There are a number of different steps at which translation may be regulated. These include the binding of the ribosome to mRNA, the presence of mRNA secondary structure, codon usage, or the abundance of particular tRNAs. Also, special regulation mechanisms such as attenuation may act at the level of translation. For an in-depth review of many of these mechanisms, see, e.g., Vellanoweth, R.L. (1993) "Translation and its Regulation" in: *Bacillus subtilis* and other Gram Positive Bacteria, Sonenshein, A.L. et al., eds., ASM Press: Washington D.C., p. 699-711, and references cited therein.

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E. Protein Folding and Secretion

- Synthesis of proteins by the ribosome results in polypeptide chains, which must take on a three-dimensional form before the protein can function normally. This three-dimensional structure is achieved by a process of folding. Polypeptide chains are flexible, and (in principle) move readily and freely in solution until they attain a conformation which results in a stable three-dimensional structure. However, it is sometimes difficult for proteins to fold correctly, either due to environmental conditions
- 35

(e.g., high temperature, where the extra kinetic energy present in the system makes it more difficult for the polypeptide to settle in the energy well of a stable structure) or due to the nature of the protein itself (e.g., the hydrophobic regions in nearby polypeptides have a tendency to aggregate and thereby sequester themselves from aqueous solution).

- 5 Proteinaceous factors have been identified that are able to catalyze, chaperone, or otherwise assist in the folding of proteins being synthesized either co- or posttranslationally. Members of these protein folding molecules are the prolyl-peptidyl isomerases (e.g., trigger factor, cyclophilin, and FKBP homologs), and proteins of the heat shock protein group (e.g., DnaK, DnaJ, GroEL, small heat shock proteins, HtpG and members of the Clp family (e.g., ClpA, ClpB, ClpW, ClpP, and ClpX)). Many of these proteins are essential for the viability of cells: in addition to their functions in protein folding, translocation, and processing, they frequently serve as key targets for the overall regulation of protein synthesis (see, e.g., Bukau, B., (1993) *Molecular Microbiology* 9(4): 671-680; Bukau, B., and Horwich, A.L. (1998) *Cell* 92(3):351-366; 10 Hestekamp, T., Bukau, C. (1996) *FEBS Lett.* 389(1):32-34; Yaron, A., Naider, F. (1993) *Critical Reviews in Biochemistry and Molecular Biology* 28(1):31-81; Scheibel, R., Buchner, J. (1998) *Biochemical Pharmacology* 56(6):675-682; Ellis, R.J., Hartl, F.U. (1996) *FASEB Journal* 10(1): 20-26; Wawrzynow, A. et al. (1996) *Molecular Microbiology* 21(5): 895-899; Ewalt, K.L., et al. (1997) *Cell* 90(3): 491-500).
- 15 20 Chaperones identified thus far function in one of two ways: they either bind and stabilize polypeptides, or they provide an environment in which folding may occur without interference. The former group, including, e.g., DnaK, DnaJ, and the heat shock proteins, bind directly to the nascent or misfolded polypeptide, frequently with concomitant ATP hydrolysis. The association of the chaperone prevents the polypeptide 25 from aggregating with other polypeptides, and can force such aggregates to dissipate if they have already formed. After interaction with a second chaperone, GrpE (which permits an ADP-ATP exchange to occur), the polypeptide is released in a molten globule state and is permitted to fold. If misfolding occurs, the chaperones again associate with the misfolded protein, forcing it to return to an unfolded state. This cycle 30 may be repeated until the protein is correctly folded. Unlike the first type of chaperones, which simply bind to the polypeptide, the second group (e.g. GroEL/ES) not only bind to the polypeptide, but also completely surround it such that it is protected from the surrounding environment. The GroEL/ES complex is composed of 2 stacked 14-member rings having a hydrophobic interior surface, and a 7-membered ring 'cap'. The 35 polypeptide is drawn into the channel in the center of this complex in an ATP-dependent reaction where it is able to fold without interference from other polypeptides. Incorrectly folded proteins are not released from the complex.

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An important step in protein folding is the creation of disulfide bonds. These bonds, either within a subunit or between subunits of a protein, are critical for protein stability. Disulfide bonds form readily in aqueous solution, and incorrect disulfide bond formation is difficult to reverse without the aid of a reducing environment. To assist in this process of correct disulfide bond formation, thiol-containing molecules, such as glutathione or thioredoxin, and their respective oxidation/reduction systems are found in the cytosol of most cells (Loferer, H., Hennecke, H. (1994) *Trends in Biochemical Sciences* 19(4): 169-171).

There are times, however, when folding of nascent polypeptide chains is not desirable, such as when these polypeptides are to be secreted. The folding process generally results in the hydrophobic regions of the protein being in the center of the protein, away from aqueous solution, and the hydrophilic regions being presented at the outer surfaces of the protein. This conformational arrangement, while creating greater stability for the protein, makes it difficult for the protein to be translocated across membranes, since the hydrophobic core of the membrane is inherently incompatible with the hydrophilic exterior of the protein. Thus, proteins synthesized by the cell which must be secreted to the exterior of the cell (e.g., cell surface enzymes and membrane receptors) or which must be inserted into the membrane itself (e.g., transporter proteins and channel proteins) are generally secreted or inserted prior to folding. The same chaperones which prevent aggregation of nascent polypeptide chains also prevent folding of polypeptides until they are disengaged. Thus, these proteins may 'escort' nascent polypeptide chains to an appropriate cellular location where they either are removed, thereby permitting folding, or they transfer the polypeptide to a transport system which will either secrete the polypeptide or aid its insertion into a membrane.

A specialized protein machinery has evolved that specifically detects, binds, transports, and processes proteins bearing specific prosequences (these sequences are later removed from the protein by cleavage). This machinery consists of a number of proteins which are collectively termed the sec (type II secretion) system (for review, see Gilbert, M. *et al.* (1995) *Critical Reviews in Biotechnology* 15(1): 13-39 and references therein; Freudl, R. (1992) *Journal of Biotechnology* 23(3): 231-240 and references therein; Neidhardt, F.C. *et al.* (1996) *E. coli* and *Salmonella* ASM Press: Washington, D.C., p. 967-978; Binet, R. *et al.* (1997) *Gene* 192(1): 7-11; and Rapoport, T.A. (1986) *Critical Reviews in Biochemistry* 20(1): 73-137, and references therein). The sec system is composed of chaperones (e.g., SecA and SecB), integral membrane proteins, also called translocases (e.g., SecY, SecE, and SecG), and signal peptidases (e.g., LepB). The nascent polypeptide having a prosequence directing secretion is bound by SecB, which delivers it to SecA at the inner surface of the cell membrane. Sec A binds to the

prosequence and, upon ATP hydrolysis, inserts into the membrane and forces a portion of the polypeptide through the membrane as well. The remainder of the polypeptide is guided through the membrane by a complex of translocases, such as SecY, SecE, and SecG. Finally, the signal peptidase cleaves off the prosequence and the polypeptide is
5 free on the extracellular side of the membrane, where it spontaneously folds.

Sec-independent secretion mechanisms are also known. For example, the signal recognition particle-dependent pathway involves the binding of a signal recognition particle (SRP) protein to the nascent polypeptide as it is being synthesized, forcing the ribosome to stall. A receptor for SRP at the inner surface of the membrane then binds
10 the ribosome-polypeptide-SRP complex. Hydrolysis of GTP provides the energy necessary to transfer the complex to the sec translocase complex, where the nascent polypeptide is guided across the membrane as it is synthesized by the ribosome. Other secretion mechanisms specific to only a few proteins are also known to exist.

15 III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SES nucleic acid and protein molecules, which participate in *C. glutamicum* DNA repair or recombination, in the transposition or other rearrangement of *C. glutamicum* DNA, in *C. glutamicum* gene expression (e.g., the
20 processes of transcription or translation), or in protein folding or protein secretion from this microorganism. In one embodiment, the SES molecules participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (i.e., the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*. In a preferred embodiment, the activity of the SES
25 molecules of the present invention with regard to DNA repair or recombination, transposition of DNA, gene expression, protein folding or protein secretion has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SES molecules of the invention are modulated in activity, such that the *C. glutamicum* cellular processes in which the SES molecules participate
30 (e.g., DNA repair or recombination, transposition of DNA, gene expression, protein folding, or protein secretion) are also altered in activity, resulting either directly or indirectly in a modulation of the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SES protein" or "SES polypeptide" includes proteins which
35 participate in a number of cellular processes related to *C. glutamicum* genetic stability, gene expression, protein folding, or protein secretion. For example, an SES protein may be involved in *C. glutamicum* DNA repair or recombination mechanisms, in

rearrangements of *C. glutamicum* genetic material (such as those mediated by transposons), in transcription or translation of genes in this microorganism, in the mediation of *C. glutamicum* protein folding (such as the activity of chaperones) or in secretion of proteins from *C. glutamicum* cells (e.g., the sec system). Examples of SES

5 proteins include those encoded by the SES genes set forth in Table 1 and Appendix A. The terms "SES gene" or "SES nucleic acid sequence" include nucleic acid sequences encoding an SES protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SES genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the

10 concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield"

15 is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms

20 "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation

25 products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation

30 pathways in the cell related to this compound. The term "DNA repair" is art-recognized and includes cellular mechanisms whereby errors in DNA (due either to damage, such as, but not limited to, ultraviolet radiation, methylases, low-fidelity replication, or mutagens) are excised and corrected. The term "recombination" or "DNA recombination" is art-recognized and includes cellular mechanisms whereby extensive

35 DNA damage affecting both strands of a DNA molecule is corrected by homologous recombination with another, undamaged copy of the DNA molecule within the same cell. Such repairs are generally low-fidelity, and may result in genetic rearrangements.

- The term "transposon" is art-recognized and includes a DNA element which is able to insert randomly throughout the genome of an organism, and which may result in the disruption of genes or their regulatory regions, or in duplications, inversions, deletions, and other genetic rearrangements. The term "protein folding" is art-recognized and
- 5 includes the movement of a polypeptide chain through multiple three-dimensional configurations until the stable, active, three-dimensional configuration is attained. The formation of disulfide bonds and the sequestration of hydrophobic regions from the surrounding aqueous solution provide some of the driving forces for this folding process, and correct folding may be enhanced by the activity of chaperones. The terms
- 10 "secretion" or "protein secretion" is art-recognized and includes the movement of proteins from the interior of the cell to the exterior of the cell, in a mechanism whereby a system of secretion permits their transit across the cellular membrane to the exterior of the cell.

- In another embodiment, the SES molecules of the invention are capable of
- 15 modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SES protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, modulation of proteins
- 20 involved directly in transcription or translation (e.g., polymerases or ribosomes) such that they are increased in number or in activity should increase global cellular transcription or translation (or rates of these processes). This increased cellular gene expression should include those proteins involved in fine chemical biosynthesis, so an increase in yield, production, or efficiency of production of one or more desired
- 25 compounds may occur. Modifications to the transcriptional/translational protein machinery of *C. glutamicum* such that the regulation of these proteins is altered may also permit increased expression of genes involved in the production of fine chemicals. Modulation of the activity or number of proteins involved in polypeptide folding may permit an increase in the overall production of correctly folded molecules in the cell,
- 30 thereby increasing the possibility that desired proteins (e.g., fine chemical biosynthetic proteins) are able to function properly. Further, by mutating proteins involved in secretion from *C. glutamicum* such that they are increased in number or activity, it may be possible to increase the secretion of a fine chemical (e.g., an enzyme) from cells in fermentor culture, where it may be readily recovered.
- 35 Genetic modification of the SES molecules of the invention may also result in indirect modulation of production of one or more fine chemicals. For example, by increasing the number or activity of a DNA repair or recombination protein of the

invention, one may increase the ability of the cell to detect and repair DNA damage. This should effectively increase the ability of the cell to maintain a mutated gene within its genome, thereby increasing the likelihood that a transgene engineered into *in* *C. glutamicum* (e.g., encoding a protein which will increase biosynthesis of a fine chemical) will not be lost during culture of the microorganism. Conversely, by decreasing the number or activity of one or more DNA repair or recombination proteins, it may be possible to increase the genetic instability of the organism. Such manipulations should improve the ability of the organism to be modified by mutagenesis without the introduced mutation being corrected. The same holds true for proteins involved in transposition or rearrangement of genetic elements in *C. glutamicum* (e.g., transposons). By mutagenizing these proteins such that they are either increased or decreased in number or activity, it is possible to simultaneously increase or decrease the genetic stability of the microorganism. This has a profound impact on the ability of any other mutation to be introduced into *C. glutamicum*, and on the ability of introduced mutations to be retained. Transposons also offer a convenient mechanism by which mutagenesis of *C. glutamicum* may be performed; duplication of desired genes (e.g., fine chemical biosynthetic genes) is readily accomplished by transposon mutagenesis, as is disruption of undesired genes (e.g., genes encoding proteins involved in degradation of desired fine chemicals).

By modulating one or more proteins (e.g. sigma factors) involved in the regulation of transcription or translation in response to particular environmental conditions, it may be possible to prevent the cell from slowing or stopping protein synthesis under unfavorable environmental conditions, such as those found in large-scale fermentor culture. This should lead to increased gene expression, which in turn may permit increased biosynthesis of desired fine chemicals under such conditions. Many such secreted proteins have functions critical for cell viability (e.g., cell surface proteases or receptors). An alteration of a secretory pathway such that these proteins are more readily transported to their extracellular location may improve the overall viability of the cell, and thus result in greater numbers of *C. glutamicum* cells capable of producing fine chemicals during large-scale culture. Further, since certain bacterial protein secretion pathways (e.g., the sec system) are known to participate in the insertion of integral membrane proteins (such as receptors, channels, pores, or transporters) into the membrane, the modulation of activity of proteins involved in protein secretion from *C. glutamicum* may affect the ability of the cell to excrete waste products or to import necessary metabolites. If the activity of these secretory proteins is increased, then the ability of the cell to produce fine chemicals may be similarly increased (due to an increase in the presence of transporters/channels in the membrane which may import

nutrients or excrete waste products). If the activity of these proteins is decreased, then there may be insufficient nutrients available to support overproduction of desired compounds, or waste products may interfere with fine chemical biosynthesis.

The isolated nucleic acid sequences of the invention are contained within the
5 genome of a *Corynebacterium glutamicum* strain available through the American Type
Culture Collection, given designation ATCC 13032. The nucleotide sequence of the
isolated *C. glutamicum* SES DNAs and the predicted amino acid sequences of the *C.*
glutamicum SES proteins are shown in Appendices A and B, respectively.
Computational analyses were performed which classified and/or identified these
10 nucleotide sequences as sequences which encode proteins involved in the repair or
recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*,
the processes of transcription or translation), in protein folding, or in protein secretion in
Corynebacterium glutamicum.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

25 The SES protein or a biologically active portion or fragment thereof of the invention can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following
30 subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SES polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SES-encoding nucleic acid (e.g., SES DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic

DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SES nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SES DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (e.g., a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be

designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an

- 5 appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SES nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

- In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* SES DNAs of the invention. This DNA comprises sequences encoding SES proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix
- 15 A.

- For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5 digits (*i.e.*, RXA01278, RXN01559, or RXS00061). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated
- 25 into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, or RXS designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA01278, RXN01559, and RXS00061 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules
- 30 RXA01278, RXN01559, and RXS00061 respectively, in Appendix A. Each of the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1. For example, as set forth in Table 1, the nucleotide sequence of RXN01559 is SEQ ID NO:5, and the amino acid sequence of RXN01559 is SEQ ID NO:6.

- Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN or RXS designation. For example, SEQ ID NO:7, designated, as indicated on

Table 1, as "F RXA00935", is an F-designated gene, as are SEQ ID NOs: 9, 29, and 37 (designated on Table 1 as "F RXA01559", "F RXA00484", and "F RXA01670", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SES protein. The nucleotide sequences determined from the cloning of the SES genes from *C. glutamicum* allows for the generation of probes and primers

- designed for use in identifying and/or cloning SES homologues in other cell types and organisms, as well as SES homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes
- 5 under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone SES homologues.
- 10 Probes based on the SES nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-
- 15 factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SES protein, such as by measuring a level of an SES-encoding nucleic acid in a sample of cells, e.g., detecting SES mRNA levels or determining whether a genomic SES gene has been mutated or deleted.

- In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently
- 20 homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*. As used herein, the language "sufficiently homologous" refers to proteins
- 25 or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to participate in the repair or recombination of DNA, in the transposition of genetic
- 30 material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*. Proteins involved in *C. glutamicum* genetic stability, gene expression, protein folding or protein secretion, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of
- 35 an SES protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SES protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

- 5 Portions of proteins encoded by the SES nucleic acid molecules of the invention are preferably biologically active portions of one of the SES proteins. As used herein, the term "biologically active portion of an SES protein" is intended to include a portion, *e.g.*, a domain/motif, of an SES protein that participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of
- 10 transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has an activity as set forth in Table 1. To determine whether an SES protein or a biologically active portion thereof can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in
- 15 protein secretion in *Corynebacterium glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

- Additional nucleic acid fragments encoding biologically active portions of an SES protein can be prepared by isolating a portion of one of the sequences in Appendix
- 20 B, expressing the encoded portion of the SES protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SES protein or peptide.

- The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy
- 25 of the genetic code and thus encode the same SES protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is
- 30 substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

- It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to
- 35 the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank

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sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 71% identical to the nucleotide sequence designated RXA01278 (SEQ ID NO:1), a nucleotide sequence which is greater than and/or at least 38% identical to the nucleotide sequence designated RXA01020 (SEQ ID NO:25), and a nucleotide sequence which is greater than and/or at least 54% identical to the nucleotide sequence designated RXA02078 (SEQ ID NO:39). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SES nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SES proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the SES gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SES protein, preferably a *C. glutamicum* SES protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the SES gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SES that are the result of natural variation and that do not alter the functional activity of SES proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SES DNA of the invention can be isolated based on their homology to the *C. glutamicum* SES nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid

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molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SES protein.

In addition to naturally-occurring variants of the SES sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded SES protein, without altering the functional ability of the SES protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SES proteins (Appendix B) without altering the activity of said SES protein, whereas an "essential" amino acid residue is required for SES protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having SES activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SES activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SES proteins that contain changes in amino acid residues that are not essential for SES activity. Such SES proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the SES activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about

50% homologous to an amino acid sequence of Appendix B and is capable of participating in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (i.e., the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (e.g., one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (e.g., one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SES protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine,

proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SES protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SES coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SES activity described herein to identify mutants that retain SES activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SES proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SES coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SES protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXA01278) comprises nucleotides 1 to 2127). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SES. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SES disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SES mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SES mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SES mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in

- the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

- The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SES protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.*(1987) *Nucleic Acids.*

- 5 *Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*(1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*(1987) *FEBS Lett.* 215:327-330).

- In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are
10 capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SES mRNA transcripts to thereby inhibit translation of SES mRNA. A ribozyme having specificity for an SES-encoding nucleic acid can be designed based
15 upon the nucleotide sequence of an SES DNA disclosed herein (*i.e.*, SEQ ID NO. 1 (RXA01278 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SES-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No.
20 5,116,742. Alternatively, SES mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- Alternatively, SES gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SES nucleotide sequence (*e.g.*,
25 an SES promoter and/or enhancers) to form triple helical structures that prevent transcription of an SES gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.*(1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

30 *B. Recombinant Expression Vectors and Host Cells*

- Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SES protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid",
35 which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of

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- autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector.
- 10 However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which
- 15 means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which are operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression
- 20 of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,
- 25 Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *arny*-, *SPO2*-, *λ-P_R*- or *λ P_L*-, which are used preferably in bacteria. Additional regulatory sequences are, for
- 30 example, promoters from yeasts and fungi, such as *ADC1*, *MFα*, *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the
- 35 design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or

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peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., SES proteins, mutant forms of SES proteins, fusion proteins, etc.).

- The recombinant expression vectors of the invention can be designed for expression of SES proteins in prokaryotic or eukaryotic cells. For example, SES genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: *More Gene Manipulations in Fungi*, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: *Applied Molecular Genetics of Fungi*, Peberdy, J.F. et al., eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

- Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SES protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from

the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SES protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

- 5 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier et al., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 10 Pouwels et al., eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by
- 15 host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation
- 20 of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels et al., eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman,
- 25 S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada et al. (1992) *Nucleic Acids Res.* 20:
- 30 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

- In another embodiment, the SES protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S cerevisiae* include pYepSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234, 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23,
- 35 pMfa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the

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filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, et al., eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the SES proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the SES proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements.

For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto

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and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SES mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA.

The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) (1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SES protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related

to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., linear DNA or RNA (e.g., a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (e.g., a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SES protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SES gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the SES gene. Preferably, this SES gene is a *Corynebacterium glutamicum* SES gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SES gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SES gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous SES protein). In the homologous recombination vector, the altered portion

of the SES gene is flanked at its 5' and 3' ends by additional nucleic acid of the SES gene to allow for homologous recombination to occur between the exogenous SES gene carried by the vector and an endogenous SES gene in a microorganism. The additional flanking SES nucleic acid is of sufficient length for successful homologous

- 5 recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SES gene has homologously recombined with the
- 10 endogenous SES gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an SES gene on a vector placing it under control of the lac operon permits expression of the SES gene only in the presence of IPTG. Such

- 15 regulatory systems are well known in the art.

In another embodiment, an endogenous SES gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SES gene in a host cell has been altered by one or more point mutations,

20 deletions, or inversions, but still encodes a functional SES protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SES gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SES gene is modulated. One of ordinary skill in the art will appreciate that host cells containing

25 more than one of the described SES gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SES protein. Accordingly, the

30 invention further provides methods for producing SES proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SES protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SES protein) in a suitable medium until SES protein is produced. In another

35 embodiment, the method further comprises isolating SES proteins from the medium or the host cell.

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C. Isolated SES Proteins

Another aspect of the invention pertains to isolated SES proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SES protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SES protein having less than about 30% (by dry weight) of non-SES protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SES protein, still more preferably less than about 10% of non-SES protein, and most preferably less than about 5% non-SES protein. When the SES protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SES protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SES protein having less than about 30% (by dry weight) of chemical precursors or non-SES chemicals, more preferably less than about 20% chemical precursors or non-SES chemicals, still more preferably less than about 10% chemical precursors or non-SES chemicals, and most preferably less than about 5% chemical precursors or non-SES chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SES protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SES protein in a microorganism such as *C. glutamicum*.

An isolated SES protein or a portion thereof of the invention can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene

expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SES protein of the invention has an amino acid sequence shown in

5 Appendix B. In yet another preferred embodiment, the SES protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the SES protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%,

10 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or

15 a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SES proteins of the present invention also preferably possess at least one of

20 the SES activities described herein. For example, a preferred SES protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium*

25 *glutamicum*, or which has one or more of the activities set forth in Table 1.

In other embodiments, the SES protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation

30 or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SES protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%,

35 or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one

of the SES activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended

- 5 to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

- Biologically active portions of an SES protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SES protein, e.g., the an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an SES protein, which include fewer amino acids than a full length SES protein or the full length protein which is homologous to an SES protein, and exhibit at least one activity of an SES protein. Typically, biologically active portions (peptides, e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SES protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SES protein include one or more selected domains/motifs or portions thereof having
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20 biological activity.

- SES proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SES protein is expressed in the host cell. The SES protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SES protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SES protein can be isolated from cells (e.g., endothelial cells), for example using an anti-SES antibody, which can be produced by standard techniques utilizing an SES protein or fragment thereof of this invention.
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- The invention also provides SES chimeric or fusion proteins. As used herein, an SES "chimeric protein" or "fusion protein" comprises an SES polypeptide operatively linked to a non-SES polypeptide. An "SES polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SES protein, whereas a "non-SES polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SES protein, e.g., a protein which is different from the SES protein and which is derived from the same or a different
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organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SES polypeptide and the non-SES polypeptide are fused in-frame to each other. The non-SES polypeptide can be fused to the N-terminus or C-terminus of the SES polypeptide. For example, in one embodiment the fusion protein is a GST-SES

- 5 fusion protein in which the SES sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SES proteins. In another embodiment, the fusion protein is an SES protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of an SES protein can be increased through use
- 10 of a heterologous signal sequence.

- Preferably, an SES chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
- 15 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
- 20 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An SES-
- 25 encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SES protein.

- Homologues of the SES protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the SES protein. As used herein, the term "homologue" refers to a variant form of the SES protein which acts as an agonist or antagonist of the
- 30 activity of the SES protein. An agonist of the SES protein can retain substantially the same, or a subset, of the biological activities of the SES protein. An antagonist of the SES protein can inhibit one or more of the activities of the naturally occurring form of the SES protein, by, for example, competitively binding to a downstream or upstream member of a biochemical cascade which includes the SES protein, by binding to a target
- 35 molecule with which the SES protein interacts, such that no function interaction is possible, or by binding directly to the SES protein and inhibiting its normal activity.

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In an alternative embodiment, homologues of the SES protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SES protein for SES protein agonist or antagonist activity. In one embodiment, a variegated library of SES variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of SES variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SES sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SES sequences therein.

10 There are a variety of methods which can be used to produce libraries of potential SES homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SES sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SES protein coding can be used to generate a variegated population of SES fragments for screening and subsequent selection of homologues of an SES protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SES coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SES protein.

30 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SES homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a

desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SES homologues (Arkin and Yourvan (1992) *PNAS*

5 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SES library, using methods well known in the art.

D. Uses and Methods of the Invention

10 The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SES protein
15 regions required for function; modulation of an SES protein activity; and modulation of cellular production of a desired compound, such as a fine chemical.

The SES nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum*
20 or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

25 Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli
30 secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and
35 the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SES nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SES nucleic acid molecules of the invention may result in the production of SES proteins having functional differences from the wild-type SES proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SES protein, either by interacting with the protein itself or a substrate or binding partner of the SES protein, or by modulating the transcription or translation of an SES nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SES proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SES protein is assessed.

The modulation of activity of proteins involved in *C. glutamicum* DNA repair, recombination, or transposition should impact the genetic stability of the cell. For example, by decreasing the number or activity of proteins involved in DNA repair mechanisms, one may decrease the ability of the cell to correct genetic errors, which should permit the simplified introduction of desired mutations into the genome (such as those encoding proteins involved in fine chemical production). Increasing the activity or number of transposons should result in a similarly increased mutation rate in the genome, and can permit facile duplication of desired genes (e.g., those encoding fine chemical biosynthetic proteins) or disruption of undesired genes (e.g., those encoding fine chemical degradation proteins). Conversely, by decreasing the number or activity of transposons or by increasing the number or activity of DNA repair proteins, it may be possible to increase the genetic stability of *C. glutamicum*, which in turn should result in better retention of introduced mutations in this microorganism through multiple generations in culture. Ideally, during mutagenesis and strain construction, one or more DNA repair systems would be decreased in activity and one or more transposons may be increased in activity, but once the desired mutation had been achieved in a strain, these the reverse would occur. Such manipulation is possible by placement of one or more DNA repair genes or transposons under control of an inducible repressor.

Modulation of proteins involved in transcription and translation in *C. glutamicum* can have both direct and indirect effects on the production of a fine chemical from these microorganisms. For example, by manipulating a protein which directly translates a gene (e.g., a polymerase) or which directly regulates transcription (e.g., a repressor or activator protein), it is possible to directly affect the expression of the target gene. In the case of genes encoding a protein involved in the biosynthesis or degradation of a fine chemical, this type of genetic manipulation should have a direct effect on the production of this fine chemical. Mutagenesis of a repressor protein such that it can no longer repress its target gene, or mutagenesis of an activator protein such that it is optimized in activity should lead to an increase in transcription of the target gene. If the target gene is, for example, a fine chemical biosynthetic gene, then an increase in production of that chemical may result, due to the overall greater number of

transcripts present for the gene, which should result in greater numbers of the protein as well. Increasing the number or activity of a repressor protein for a target sequence or decreasing the number or activity of an activator protein for a target sequence when this sequence is, for example, a fine chemical degradative protein, then a similar increase in production of the fine chemical should result.

Indirect effects on fine chemical production may also arise due to manipulation of proteins involved in transcription and translation. For example, by modulating the activity or number of transcription factors (e.g., the sigma factors) or translational repressors/activators which globally regulate transcription in *C. glutamicum* in response to environmental or metabolic factors, it should be possible to uncouple cellular transcription from environmental or metabolic regulation. In turn, this may permit continued transcription under conditions which would normally slow or altogether stop gene expression, such as those unfavorable conditions (e.g., high temperature, low oxygen, high waste product levels) which exist in large-scale fermentor cultures. By increasing the rate of gene (e.g., fine chemical biosynthetic gene) expression in such situations, the overall rate of fine product production may also be increased, at least due to the relatively greater number of fine chemical biosynthetic proteins in the cell. Principles and examples for modification of transcription and transcriptional regulation are described in, e.g., Lewin, B. (1990) Genes IV, Part 3: "Controlling procaryotic genes by transcription" Oxford Univ. Press: Oxford, p. 213-301.

Modulation of the activity or number of proteins involved in polypeptide folding (e.g., chaperones) may permit an increase in the overall production of correctly folded molecules in the cell. This has two effects: first, an overall increase in the number of proteins in the cell, due to the fact that fewer proteins are misfolded and degraded, and second, an increase in the number of any given protein that is correctly folded and thus active (see, e.g., Thomas, J.G., Baneyx, F. (1997) *Protein Expression and Purification* 11(3): 289-296; Luo, Z.H., and Hua, Z.C. (1998) *Biochemistry and Molecular Biology International* 46(3): 471-477; Dale, G.E., et al. (1994) *Protein Engineering* 7(7): 925-931; Amrein, K.E. et al. (1995) *Proc. Natl. Acad. Sci. U.S.A.* 92(4): 1048-1052; and Caspers, P. et al. (1994) *Cell. Mol. Biol.* 40(5): 635-644). While such mutations result in an increase in the number of active proteins of all kinds, when coupled with additional mutations increasing the activity or number of, e.g., a fine chemical biosynthetic protein, an additive effect in the amount of correctly folded, active desired protein may be obtained.

Manipulation of proteins involved in secretion of polypeptides from *C. glutamicum* such that they are improved in activity or number may directly improve the secretion of a proteinaceous fine chemical (e.g., an enzyme) from this microorganism. It

is significantly easier to harvest and purify fine chemicals when they are secreted into the medium of large-scale cultures than when they are retained in the cell, so the yield and production of a fine chemical should be increased through such secretion system engineering. Genetic manipulation of these secretion proteins may also result in indirect improvements in the production of one or more fine chemicals. First, increased or decreased activity of one or more *C. glutamicum* secretion systems (as brought about by mutagenesis of one or more SES proteins involved in such pathways) may result in increased or decreased global secretion rates from the cell. Many such secreted proteins have functions critical for cell viability (e.g., cell surface proteases or receptors). An alteration of a secretory pathway such that these proteins are more readily transported to their extracellular location may improve the overall viability of the cell, and thus result in greater numbers of *C. glutamicum* cells capable of producing fine chemicals during large-scale culture. Second, certain bacterial secretion systems, (e.g., the sec system) are known to play a significant role in the process by which integral membrane proteins (e.g. channels, pores, or transporters) insert into cellular membranes. If the activity of one or more secretory pathway proteins is increased, then the ability of the cell to produce fine chemicals may be similarly increased, due to the presence of increased intracellular nutrient levels or decreased intracellular waste levels. If the activity of one or more such secretory pathway protein is decreased, then there may be insufficient nutrients available to support overproduction of desired compounds, or waste products may interfere with the biosynthesis of desired fine chemicals.

The aforementioned mutagenesis strategies for SES proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SES nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents,

published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

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Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l pantothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. et al. (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. et al. (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to one of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g.,

- Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

- Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

- Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

- Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known

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methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones - Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (eds. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if

necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

- Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the microorganisms, the pH can also be controlled using gaseous ammonia.

- The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

- If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

- The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well

- within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) 5 Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 10 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

- The activity of proteins which bind to DNA can be measured by several well- 15 established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as 20 beta-galactosidase, green fluorescent protein, and several others.

- The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

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Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

- The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified 30 microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical 35 chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. et al., (1987) "Applications of HPLC in Biochemistry" in:

Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: *Ulmann's Encyclopedia of Industrial Chemistry*, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- 10 In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in *Applied Microbial Physiology, A Practical Approach*, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art.
- 25 If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

- The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate

chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

- There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

- The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

20 **Example 11: Analysis of the Gene Sequences of the Invention**

- The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SES nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SES protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN
5 program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

10 The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the
15 GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, e.g., Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (e.g., a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (e.g., a
25 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
30 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
35 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment

homology percentages set forth in Table 4 under the heading “% homology (GAP)” are listed in the European numerical format, wherein a ‘,’ represents a decimal point. For example, a value of “40,345” in this column represents “40.345%”.

5 Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.*(1995) *Science* 270: 467-470; Wodicka, L. *et al.*(1997) *Nature Biotechnology* 15: 1359-1367;

- 10 DeSaizieu, A. *et al.*(1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.*(1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

- The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.*(1995) *Science* 270: 467-470).

- Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.*(1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

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The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.*(1995) *supra*; Wodicka, L. *et al.*(1997), *supra*; and DeSaizieu A. *et al.*(1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.*(1995) *supra* and fluorescent labels may be detected, for example, by the method of Shalon *et al.*(1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the

consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

- Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the
- 5 following claims.

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What is claimed :

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an
5 SES protein, or a portion thereof, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule
encodes an SES protein involved in the production of a fine chemical.
- 10 3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the
group consisting of those sequences set forth in Appendix A, or a portion thereof,
provided that the nucleic acid molecule does not consist of any of the F-designated
genes set forth in Table 1.
- 15 4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected
from the group consisting of those sequences set forth in Appendix B, provided that
the nucleic acid molecule does not consist of any of the F-designated genes set forth
in Table 1.
- 20 5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant
of a polypeptide selected from the group of amino acid sequences consisting of those
sequences set forth in Appendix B, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
- 25 6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least
50% homologous to a nucleotide sequence selected from the group consisting of
those sequences set forth in Appendix A, or a portion thereof, provided that the
nucleic acid molecule does not consist of any of the F-designated genes set forth in
30 Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides
of a nucleic acid comprising a nucleotide sequence selected from the group
consisting of those sequences set forth in Appendix A, provided that the nucleic acid
35 molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1
5 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of claim 1.
11. The vector of claim 10, which is an expression vector.
- 10 12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
- 15 14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
- 20 16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
- 25 17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
- 30 18. An isolated SES polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical production.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 5 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 15 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 20 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 30 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 35 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoredutum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

5 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

10 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

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CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN GENETIC STABILITY, GENE EXPRESSION, AND PROTEIN SECRETION AND FOLDING

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Abstract of the Disclosure

Isolated nucleic acid molecules, designated SES nucleic acid molecules, which encode novel SES proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SES nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SES proteins, mutated SES proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SES genes in this organism.

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN GENETIC STABILITY, GENE EXPRESSION, AND PROTEIN SECRETION AND FOLDING

X is attached hereto.

_____ was filed on _____ as

Application Serial No. _____

and was amended on _____
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

0000290.65820960

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

- ☐ no such applications have been filed.
- ☒ such applications have been filed as follows

**EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19931412.8	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932928.1	07/14/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
			<input type="checkbox"/> Yes No <input type="checkbox"/>
			<input type="checkbox"/> Yes No <input type="checkbox"/>
			<input type="checkbox"/> Yes No <input type="checkbox"/>

**ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

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CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031
(Application Serial No.)

June 25, 1999
(Filing Date)

60/143,752
(Application Serial No.)

July 14, 1999
(Filing Date)

60/151,671
(Application Serial No.)

August 31, 1999
(Filing Date)

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CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

 (Application Serial No.)

 (Filing Date)

 (Status)
 (patented,pending,aband.)

 (Application Serial No.)

 (Filing Date)

 (Status)
 (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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TABLE 1: GENES IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
1	2	RXA01278	GR00389	2425	299	Protein Translation Elongation Factor G (EF-G)
3	4	RXA01513	GR00547	1856	2880	Protein Translation Elongation Factor Ts (EF-Ts)
5	6	RXA01559	VV0171	7795	5654	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
7	8	F RXA00935	GR00254	654	4	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
9	10	F RXA01589	GR00434	1983	1741	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
11	12	RXA01558	GR00707	1735	527	PREPROTEIN TRANSLLOCATION SECA SUBUNIT
13	14	RXA02429	GR00744	4823	7111	SIGNAL RECOGNITION PARTICLE PROTEIN
15	16	RXA02748	GR00764	2434	4074	SIGNAL PEPTIDASE (EC 3.4.21.89)
17	18	RXA01555	GR00393	2877	3662	GLUTAREDOXIN-LIKE PROTEIN NBDH
19	20	RXA00107	GR00014	17940	18176	GLUTATHIONE REDUCTASE (EC 1.6.4.2)
21	22	RXA01513	GR00449	7055	5841	GLUTATHIONE PEROXIDASE (EC 1.11.9)
23	24	RXA00539	GR00139	1460	1936	
25	26	RXA01020	GR00291	998	1744	URACIL-DNA GLYCOSYLASE (EC 3.2.2.1)
27	28	RXN00484	VV0086	47365	46286	DEOXYRIBODIPYRIMIDINE PHOTOLYASE (EC 4.1.99.3)
29	30	F RXA00484	GR00119	21602	20588	DEOXYRIBODIPYRIMIDINE PHOTOLYASE (EC 4.1.99.3)
31	32	RXA02476	GR00715	10514	9636	AG-SPECIFIC ADENINE GLYCOSYLASE (EC 3.2.2.1)
33	34	RXA00102	GR00014	11288	10521	FORAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23)
35	36	RXA01670	VV0079	18911	18105	FORAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23)
37	38	F RXA01670	GR00466	3	614	FORAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23)
39	40	RXA02078	GR00648	8170	9027	FORAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23)
41	42	RXA01596	GR00447	4370	6148	DNA REPAIR PROTEIN RECN
43	44	RXA01493	GR00423	7530	6220	DNA REPAIR PROTEIN RECN
45	46	RXA02671	GR00753	11718	12296	DNA REPAIR PROTEIN RADA HOMOLOG
47	48	RXA02291	VV0127	18678	18025	ALKB PROTEIN (DNA repair - alkylated DNA)
49	50	F RXA02291	GR00662	1518	865	DNA repair gene specific for alkylated DNA
51	52	RXA01733	VV0221	70	1251	RECF PROTEIN
53	54	F RXA01733	GR00492	2	544	RECF PROTEIN
55	56	RXA01252	GR00365	643	1296	RECOMBINATION PROTEIN RECR
57	58	RXA01878	GR00337	1239	2117	DIMETHYLADENSINE TRANSFERASE (EC 2.1.1.1)
59	60	RXA01566	GR00038	849	854	METHYLPHOSPHOTRIESTER-DNA ALKYL-TRANSFERASE
61	62	RXA00553	GR00033	1162	8554	MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE)
63	64	RXA00280	GR00043	4196	4696	MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE)

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
65	66	FXA0333	GR00657	16166	16699	MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE) (8-OXODGTPASE) (EC 3.6.1.-)
67	68	FXA02110	GR00632	3641	4268	MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE) (8-OXODGTPASE) (EC 3.6.1.-)
69	70	FXA02290	GR00662	663	295	DNA-3-METHYLADEINE GLYCOSIDASE I (EC 3.2.2.20)
71	72	FXA02557	GR00731	3766	3179	DNA-3-METHYLADEINE GLYCOSIDASE I (EC 3.2.2.20)
73	74	FXA02130	GR00638	1	87	DNA REPAIR HELICASE RAD25
75	76	FXA02742	GR00703	12394	10036	Hypothetical DNA Repair Helicase
77	78	FXA02445	GR00709	9362	518	ATP-DEPENDENT DNA HELICASE RECQ
79	80	FXA00627	GR00253	1606	518	HOLLIDAY JUNCTION DNA HELICASE RUVB
81	82	FXA00628	GR00253	2233	1616	HOLLIDAY JUNCTION DNA HELICASE RUVB
83	84	FXA00172	GR00707	7949	8560	RESOLVASE
85	86	FXA00172	GR00707	455	9411	RESOLVASE
87	88	FXA00164	GR00028	8239	16258	DNA repair exonuclease
89	90	FXA00019	GR00002	14399	16258	SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECQ (EC 3.1.-)
91	92	FXA00629	GR00253	2359	2276	CROSSOVER JUNCTION ENDONUCLEASE RUVG (EC 3.1.22.4)
93	94	FXA00629	GR00253	16327	16686	EXONUCLEASE ABC SUBUNIT C
95	96	FXA02252	GR00634	18322	20655	EXONUCLEASE ABC SUBUNIT C
97	98	FXA02252	GR00634	18322	20655	EXONUCLEASE ABC SUBUNIT C
99	100	FXA02416	GR00705	10457	2642	EXONUCLEASE ABC SUBUNIT A
101	102	FXA02563	GR00732	1515	2246	Exonuclease ATPase subunit
103	104	FXA02731	GR00762	3263	5359	EXONUCLEASE ABC SUBUNIT B
105	106	FXA00998	GR00283	2871	2410	COMA OPERON PROTEIN 2
107	108	FXA02366	VO0176	388	826	COMA OPERON PROTEIN 1
109	110	FXA02366	GR00693	1180	776	COME OPERON PROTEIN 1, DNA binding and uptake (competence)
111	112	FXA02388	VO0176	826	2487	COME OPERON PROTEIN 1, DNA binding and uptake (competence)
113	114	FXA02385	GR00693	776	6	COME OPERON PROTEIN 3, DNA binding and uptake (competence)
115	116	FXA02388	GR00694	1770	925	COME OPERON PROTEIN 3, DNA binding and uptake (competence)
117	118	FXA01975	GR00571	242	2137	PUTATIVE TYPE II RESTRICTION ENDONUCLEASE, AND PUTATIVE TYPE I OR TYPE III RESTRICTION ENDONUCLEASE GENES, COMPLETE CDS
119	120	FXA01954	GR00562	3326	4165	TYPE III RESTRICTION-MODIFICATION SYSTEM ECP151 ENZYME MOD (EC 2.1.1.72)
121	122	FXA02236	GR00654	4249	4566	Integration host factor
123	124	FXA01795	VO0093	722	1318	MODIFICATION METHYLASE (EC 2.1.1.73)
125	126	FXA02267	VO0020	10928	10056	DNA (CYTOSINE-5-METHYL)TRANSFERASE (EC 2.1.1.37)
127	128	FXA02267	VO0093	231	836	MODIFICATION METHYLASE SCRP-A (EC 2.1.1.73)
129	130	FXA00127	VO0124	9789	10253	COMPETENCE PROTEIN F
131	132	FXA02358	VO0097	23587	24097	MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE) (8-OXODGTPASE) (EC 3.6.1.-)
133	134	FXA001102	VO0067	5293	4762	PUTATIVE COMPETENCE DAMAGE PROTEIN
135	136	FXA001318	VO0093	1330	2139	PUTATIVE TYPE II RESTRICTION ENDONUCLEASE, AND PUTATIVE TYPE I OR TYPE III RESTRICTION ENDONUCLEASE GENES, COMPLETE CDS
137	138	FXA02989	VO0073	118	1257	RECA PROTEIN
139	140	FXA02166	VO0327	1777	896	RECA PROTEIN
141	142	FXA02431	VO0090	1	876	RIIONUCLEASE BN (EC 3.1.-)
143	144	FXA02985	VO0009	1182	850	UMUC PROTEIN
						EBSC PROTEIN

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
145	146	RXN02986	VV0009	801	664	EBSC PROTEIN
147	148	RXS0061	VV0044	4256	1590	DNA POLYMERASE I (EC 2.7.7)
149	150	RXS0012	VV0036	12413	10854	DNA LIGASE (EC 6.5.12)
151	152	RXS00213	VV0086	12894	12322	DNA LIGASE (EC 6.5.12)
153	154	RXS0024	VV0052	1217	3193	ATP-DEPENDENT DNA HELICASE REGG (EC 3.6.1.)
155	156	RXS0024	VV0052	1217	3193	ATP-DEPENDENT DNA HELICASE REGG (EC 3.6.1.)
157	158	RXS0088	VV0054	22014	22793	ENDONUCLEASE III (EC 4.2.99.18)
159	160	RXS01066	VV0030	4753	5543	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)
161	162	RXS02145	VV0030	21112	21837	DNA REPAIR PROTEIN RECO
163	164	RXS02476	VV0008	12448	3864	ENDONUCLEASE III (EC 4.2.99.18)
165	166	RXS02990	VV0008	46453	4679	ADP-SPECIFIC ADENINE GLYCOSYLASE (EC 3.2.2.)
167	168	RXS03098	VV0064	1952	1639	REGULATORY PROTEIN RECOX
169	170	RXS03175	VV0331	2100	2723	DNA replication repair enzyme
				1248	466	EXODEOXYRIBONUCLEASE III (EC 3.1.11.2)

Transposon, IS elements, Transposase, Integrase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
171	172	RXN03069	VV0039	5816	4734	INTEGRASE
173	174	F RXA02890	GR10027	112	1134	INTEGRASE
175	176	RXA01601	GR00447	11128	12039	INTEGRASE/RECOMBINASE XERO
177	178	RXA01228	GR00355	1668	1883	TRANSPOSASIS IN/OUT AND IN/OUT RESOLVASE
179	180	RXN03130	VV0123	14282	15569	DNA TRANSPOSABLE ELEMENT IS31831
181	182	RXN01969	VV0155	139	504	DNA TRANSPOSABLE ELEMENT IS31831
183	184	F RXA00263	GR00040	2243	966	DNA TRANSPOSABLE ELEMENT IS31831
185	186	RXN01541	VV0015	56012	56738	PLASMID PASU1 TRANSPOSASE
187	188	F RXA01541	GR00428	3865	3095	INSERTION ELEMENT IS1415 TRANSPOSASE (IS1) GENES, COMPLETE CDS
189	190	RXA002590	GR00741	14837	13902	IS3 RELATED INSERTION ELEMENT
191	192	RXA00016	GR00002	8857	7964	IS3 RELATED INSERTION ELEMENT
193	194	RXA00255	GR00040	2840	3289	TRANSPOSASE
195	196	RXA00938	GR00256	670	927	TRANSPOSASE
197	198	RXA01284	GR00367	12003	11788	TRANSPOSASE
199	200	RXA01265	GR00367	12616	12467	TRANSPOSASE
201	202	RXA01327	GR00386	753	896	TRANSPOSASE
203	204	RXA01327	GR00386	991	1365	TRANSPOSASE
205	206	RXA01328	GR00386	1407	1697	TRANSPOSASE
207	208	RXA01443	GR00418	13570	12740	TRANSPOSASE
209	210	RXA01444	GR00418	13528	12662	TRANSPOSASE
211	212	RXA01648	GR00457	8292	841	TRANSPOSASE
213	214	RXA01649	GR00457	1360	841	TRANSPOSASE
215	216	RXA01650	GR00457	1437	1324	TRANSPOSASE
217	218	RXA01651	GR00457	1618	1484	TRANSPOSASE
219	220	RXN01680	VV0179	17470	17060	TRANSPOSASE

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
221	222	F RXA01690	GR00467	9590	9180	TRANSPPOSASE
223	224	RXN00794	VV0084	13161	12880	TRANSPPOSASE
225	226	F RXA01794	GR00505	3	551	TRANSPPOSASE
227	228	RXA01862	GR00529	4961	6166	TRANSPPOSASE
229	230	RXA01953	GR00562	928	548	TRANSPPOSASE
231	232	RXA01998	GR00586	1345	2082	TRANSPPOSASE
233	234	RXA02837	GR00829	179	6	TRANSPPOSASE
235	236	RXA00005	GR00001	4724	6331	TRANSPPOSASE
237	238	RXA00017	GR00002	9150	8657	TRANSPPOSASE
239	240	RXA00057	GR00009	2461	2383	TRANSPPOSASE
241	242	RXA00227	GR00032	27991	27194	TRANSPPOSASE
243	244	RXA01819	GR00515	8287	7841	transposase
245	246	RXN03052	VV0024	5310	4555	INTEGRASE
247	248	RXN02915	VV0135	43798	44175	TRANSPPOSASE
249	250	RXN02919	VV0084	14653	15486	TRANSPPOSASE
251	252	RXN03033	VV0012	3942	5099	TRANSPPOSASE
253	254	RXN03035	VV0013	667	1824	TRANSPPOSASE
255	256	RXN03049	VV0020	29526	28985	TRANSPPOSASE
257	258	RXN03070	VV0039	8897	8070	TRANSPPOSASE
259	260	RXN03121	VV0101	645	4	TRANSPPOSASE
261	262	RXN03161	VV0193	884	1267	TRANSPPOSASE
263	264	RXN03165	VV0312	1562	1242	TRANSPPOSASE
265	266	RXN00083	VV0048	3416	3117	TRANSPPOSASE
267	268	RXN02004	VV0290	588	382	TRANSPPOSASE
269	270	RXN02287	VV0127	69201	69752	TRANSPOSON TNS201 RESOLVASE
271	272	RXN02963	VV0102	6547	5240	DNA, TRANSPOSABLE ELEMENT IS31031
Aminoacyl-tRNA synthetases / tRNAs and RNA metabolism						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
273	274	RXA02788	GR00777	2359	5022	ALANYL-tRNA SYNTHETASE (EC 6.1.1.7)
275	276	RXN00975	VV0149	7820	9469	ARGINYL-tRNA SYNTHETASE (EC 6.1.1.19)
277	278	F RXA00975	GR00275	780	4	POSSIBLE ARGINYL-tRNA SYNTHETASE (EC 6.1.1.19)
279	280	F RXA00976	GR00275	1423	824	POSSIBLE ARGINYL-tRNA SYNTHETASE (EC 6.1.1.19)
281	282	RXN01730	VV0137	1709	6	ASPARTYL-tRNA SYNTHETASE (EC 6.1.1.12)
283	284	F RXA01730	GR00490	298	1974	ASPARTYL-tRNA SYNTHETASE (EC 6.1.1.12)
285	286	RXA00314	GR00053	5406	4027	CYSTEINYL-tRNA SYNTHETASE (EC 6.1.1.6)
287	288	RXA00224	GR00646	8756	7497	CYSTEINYL-tRNA SYNTHETASE (EC 6.1.1.6)
289	290	RXA01124	GR00312	2	1610	GLUTAMYL-tRNA SYNTHETASE (EC 6.1.1.7)
291	292	RXN00468	VV0076	8169	8804	GLUTAMYL-tRNA SYNTHETASE (EC 6.1.1.7)

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METHYLTRANSFERASE (CYTIDINIC ACID-2-THIOURIDYLATE)
PEPTIDYL-RNA HYDROLASE (EC 3.1.1.61)
PERYDYL-RNA HYDROLASE (EC 3.1.1.29)
PENTYL-RNA HYDROLASE (EC 3.1.1.29)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit A (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit B (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit C (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit D (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit E (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit F (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit G (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit H (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit I (EC 6.3.5.
1)
L-glutaryl-RNA(Gin)-dependent amidotransferase subunit J (EC 6.3.5.
1)

Nucleic Acid	Amino Acid	Identification Code	Contig	NT Start	NT Stop	Function
SEQ ID NO	SEQ ID NO					
383	384	RYA02228	GR00653	1876	2778	TRNA DELTA(2)-ISOPENITEMUTYLPHOSPHATE TRANSFERASE (EC 2.5.1.8)
385	386	RYA02502	GR00720	15150	16901	GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-)
387	388	RYA02192	GR00461	17875	18648	GLUTAMINE CYCLOTRANSFERASE PRECURSOR (EC 2.3.2.6), Glutaminyl-HRNA
389	390	RXN00211	VW0096	10126	10788	Cyclotransferase
391	392	RXN00669	VW0095	38825	39706	L-glutaryl-RNA(Gln)-dependent amidotransferase subunit B (EC 6.3.5.-)
393	394	RXN02551	VW0090	6842	7771	PSEUDOURIDYLATE SYNTHASE (EC 4.2.1.70) SFHB PROTEIN

Transcription

Nucleic Acid	Amino Acid	Identification Code	Contig	NT Start	NT Stop	Function
SEQ ID NO	SEQ ID NO					
395	396	RYA01344	GR00399	2551	5	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
397	398	RYA01387	GR00407	372	4	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
399	400	RYA01388	GR00369	439	459	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
401	402	RYA01283	GR00369	7208	5817	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
403	404	RYA01433	GR00417	9696	8004	DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
405	406	RYA02466	GR00712	1127	510	SIGMA FACTOR
407	408	RYA00304	GR00051	666	4	RNA POLYMERASE SIGMA-H FACTOR
409	410	RYA00495	GR00123	1210	1773	RNA POLYMERASE SIGMA FACTOR
411	412	RYA00532	GR00137	3	567	PUTATIVE RNA POLYMERASE SIGMA FACTOR CY78.15
413	414	RYA01530	GR00426	1724	1063	PROBABLE RNA POLYMERASE SIGMA FACTOR CY49.08
415	416	RYA01531	GR00626	5348	5995	RNA POLYMERASE SIGMA FACTOR RHO
417	418	RYA02065	GR00488	7429	7812	EXTRACRYTOPLASMIC FUNCTIONAL TERNAL
419	420	RYA00588	VW0037	13672	14193	TRANSCRIPTION ELONGATION FACTOR GRETA
421	422	RXN01724	VW0037	2128	809	TRANSCRIPTION TERMINATION FACTOR RHO
423	424	F RYA01723	GR00488	6600	7436	TRANSCRIPTION TERMINATION FACTOR RHO
425	426	RYA01724	GR00488	7429	7812	TRANSCRIPTION TERMINATION FACTOR RHO
427	428	RXN01726	VW0037	825	619	TRANSCRIPTION TERMINATION FACTOR RHO
429	430	F RYA01725	GR00488	7887	8004	TRANSCRIPTION TERMINATION FACTOR RHO
431	432	RYA01726	GR00488	8000	8572	TRANSCRIPTION TERMINATION FACTOR RHO
433	434	RYA00738	VW0094	1	1867	TRANSCRIPTION-REPAIR COUPLING FACTOR
435	436	F RYA00737	VW0094	2673	1661	TRANSCRIPTION-REPAIR COUPLING FACTOR
437	438	F RYA00737	GR00200	1	480	TRANSCRIPTION-REPAIR COUPLING FACTOR
439	440	F RYA01812	VW0248	2141	2968	TRANSCRIPTION-REPAIR COUPLING FACTOR
441	442	RXN02413	GR00335	768	4	TRANSCRIPTIONAL REGULATORY PROTEIN
443	444	RXN02413	VW0703	3029	2538	TRANSCRIPTIONAL REGULATORY PROTEIN
445	446	RXN02827	VW0735	3	1001	TRANSCRIPTIONAL REGULATORY PROTEIN
447	448	RXN02827	VW0735	3	1001	TRANSCRIPTIONAL REGULATORY PROTEIN
449	450	RXN02722	VW0146	3915	9475	TRANSCRIPTION-REPAIR COUPLING FACTOR
451	452	RXN0671	VW0079	17865	18717	TRANSCRIPTION-REPAIR COUPLING FACTOR
453	454	RXN00671	VW0005	37121	38134	TRANSCRIPTION-REPAIR COUPLING FACTOR
455	456	RXN02760	VW0025	31807	32780	TRANSCRIPTION-REPAIR COUPLING FACTOR
457	458	RXN02830	VW0168	3	650	TRANSCRIPTION-REPAIR COUPLING FACTOR
459	460	RXN02830	VW0168	3	650	TRANSCRIPTION-REPAIR COUPLING FACTOR

DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (EC 2.7.7.6)
 TRANSCRIPTION ANTIMINATION PROTEIN NUSG
 Helix-loop-helix containing transcription regulator
 RNA POLYMERASE SIGMA FACTOR

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Translation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
461	462	RXA02418	GR00705	5101	5667	Bacterial Protein Translation Initiation Factor 3 (IF-3)
463	464	RXAN0496	VW0139	12846	32966	Bacterial Protein Translation Initiation Factor 2 (IF-2)
465	466	F RXA00755	GR00203	2890	6	Protein Translation Initiation Factor 2 (IF-2)
467	468	F RXA001466	GR00423	10308	9181	Bacterial Protein Translation Initiation Factor 2 (IF-2)
469	470	RXA001986	GR00178	1624	1839	Bacterial Protein Translation Initiation Factor 1 (IF-1)
471	472	RXAN01294	VW0212	510	4	Bacterial Protein Translation Elongation Factor Tu (EF-Tu)
473	474	F RXA01284	GR00070	510	4	Bacterial Protein Translation Elongation Factor Tu (EF-Tu)
475	476	RXA00138	GR00022	1914	2474	Protein Translation Elongation Factor P (EF-P)
477	478	RXA00331	GR00083	15141	14785	Hypothetical Translational Inhibitor Protein
479	480	RXA002822	GR00003	1	570	Bacterial Peptide Chain Release Factor 1 (RF-1)
481	482	RXA00011	GR00002	2739	2285	Bacterial Peptide Chain Release Factor 2 (RF-2)
483	484	RXA00012	GR00002	3487	2432	Bacterial Peptide Chain Release Factor 2 (RF-2)
485	486	RXAN01926	VW0284	1	747	PEPTIDE CHAIN RELEASE FACTOR 3
487	488	F RXA01926	GR00654	1	672	PEPTIDE CHAIN RELEASE FACTOR 3
489	490	RXAN02002	VW0111	141	518	PEPTIDE CHAIN RELEASE FACTOR 3
491	492	F RXA02002	GR00592	383	3522	POLYPEPTIDE DEFORMYLASE (EC 3.5.1.31)
493	494	RXA00896	GR00244	2884	11091	POLYPEPTIDE DEFORMYLASE (EC 3.5.1.31)
495	496	RXA02242	GR00654	10589	11091	POLYPEPTIDE DEFORMYLASE (EC 3.5.1.31)
497	498	RXS02308	VW0127	13156	12727	TRANSLATION INITIATION INHIBITOR

Protein translocation, secretion, and folding

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
499	500	RXA01710	GR00484	850	443	PEPTIDE METHIONINE SULFOXIDE REDUCTASE
501	502	RXAN0462	VW0124	11932	13749	PREPROTEIN TRANSLOCASE SECA SUBUNIT
503	504	F RXA00124	GR00020	737	6	PREPROTEIN TRANSLOCASE SECA SUBUNIT
505	506	F RXA02462	GR00712	7563	6739	PREPROTEIN TRANSLOCASE SECA SUBUNIT
507	508	RXA00126	GR00020	1467	703	PREPROTEIN TRANSLOCASE SECA SUBUNIT
509	510	RXA00280	GR00178	9121	10440	PREPROTEIN TRANSLOCASE SECA SUBUNIT
511	512	RXA02240	GR00654	30280	30510	PREPROTEIN TRANSLOCASE SECA SUBUNIT
513	514	RXAN00046	VW0119	3583	6058	SIGNAL RECOGNITION PARTICLE GTPase
515	516	F RXA00046	GR00007	3583	6058	SIGNAL RECOGNITION PARTICLE GTPase
517	518	RXA00753	GR00202	23301	21880	PSI PROTEIN PRECURSOR (PSI), one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>
519	520	RXAN0308	VW017	42941	43666	PSI PROTEIN PRECURSOR (PSI), one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>
521	522	F RXA01719	GR00355	4639	5161	PSI PROTEIN PRECURSOR (PSI), one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>
523	524	RXA01274	GR00367	27146	28242	<i>Corynebacterium glutamicum</i> (PSI, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
525	526	RAA01449	GR00419	1046	6	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
527	528	RAA01798	GR00609	276	4	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
529	530	RAA01818	GR00515	6453	7439	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
531	532	RAA02807	GR00742	13971	14189	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
533	534	RAA02808	GR00742	14248	15942	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
535	536	RXN03054	VW0026	1906	3486	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
537	538	F RAA02886	GR10021	1907	2737	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
539	540	RXN03039	VW0018	2	631	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
541	542	F RAA02884	GR10036	1017	232	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
543	544	F RAA02804	GR10042	686	12	PS1 PROTEIN PRECURSOR (PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i>)
545	546	RAA02025	GR00614	862	212	PEPTIDE METHIONINE SULFOXIDE REDUCTASE
547	548	RAA01431	GR00417	7858	7538	THIOREDOXIN REDUCTASE (EC 1.6.4.5) / THIOREDOXIN
549	550	RAA01432	GR00417	8886	7946	THIOREDOXIN REDUCTASE (EC 1.6.4.5) / THIOREDOXIN
551	552	RXN00337	VW0079	42335	42706	THIOREDOXIN
553	554	F RAA00937	GR00256	1	123	THIOREDOXIN
555	556	RAA01199	GR00343	3813	4583	THIOREDOXIN
557	558	RAA00824	GR00221	4356	4913	THIOREDOXIN
559	560	RXN01941	GR00522	116	477	THIOREDOXIN
561	562	RXN01963	VW0206	1172	24	THIOREDOXIN
563	564	F RAA01863	GR00530	830	34	THIOREDOXIN
565	566	RAA02323	GR00568	1429	595	THIOREDOXIN
567	568	RAA01072	GR00368	377	147	THIOREDOXIN
569	570	RXN02396	GR00708	1596	1036	THIOREDOXIN
571	572	RXN01837	VW0310	7103	7879	THIOREDOXIN
573	574	F RAA01837	GR00518	858	466	THIOREDOXIN
575	576	RXN01777	VW0009	32155	34158	THIOREDOXIN
577	578	F RAA02847	GR00624	1	192	THIOREDOXIN
579	580	RAA02174	GR00041	9280	8937	THIOREDOXIN
581	582	RAA00668	GR00152	2928	1582	THIOREDOXIN
583	584	RXN03040	VW0018	1089	1089	THIOREDOXIN
585	586	RXN03051	VW0022	2832	3586	THIOREDOXIN
587	588	RXN02346	VW0025	31243	31575	THIOREDOXIN
589	590	RXN00833	VW0150	8039	8333	THIOREDOXIN
591	592	RXN01576	VW0179	12659	11304	THIOREDOXIN
593	594	RAA00380	VW0223	636	216	THIOREDOXIN

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Nucleic Acid		Amino Acid		Identification Code	Contig	NT Start		NT Stop	Function
SEQ ID NO		SEQ ID NO							
596		596		RXNM2325	VW0047	5527	6393		THIOREDOXIN
597		598		RXNM0493	VW0086	14389	16002		60 KD CHAPERONIN
599		600		RXNM2543	VW0057	22031	20178		DNAAK PROTEIN
601		602		RXNM01345	VW0123	4883	3432		Molecular chaperones (HSP70/DnaK family)
603		604		RXNM2735	VW0074	13600	14556		PUTATIVE OXPPCYCLE PROTEIN OPCA
605		606		RXNM2280	VW0152	1849	26		TRAP1
607		608		RXSM0170	VW0031	4882	3029		PS1 PROTEIN PRECURSOR
609		610		RXSM2641	VW0098	49070	51145		PS1 PROTEIN PRECURSOR
611		612		RXSM2650	VW0090	6261	6839		LIPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.38)
613		614		RXSM0076	VW0154	2752	4122		NADPH-FERREDOXIN OXIDOREDUCTASE PRECURSOR (EC 1.18.1.2)
616		616		RXSM1438	VW0089	25340	23976		NADPH-FERREDOXIN OXIDOREDUCTASE PRECURSOR (EC 1.18.1.2)

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TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains." Patent: EP 0358940-A 3 0321/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase." Patent: WO 9519442-A 5 07/2095
AB003132	murC; fisQ; fisZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the fisZ gene from corynebacterium bacteria." <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; fisQ		Wachi, M. et al. "A murC gene from Corynebacterium bacteria." <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ." <i>Biosect. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2		
AB020624	murI	D- glutamate racemase	
AB023372	tki	transketolase	
AB024708	glitB; glitD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	Cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	Wehmeier, L. et al "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB;	N-acetylglutaminylphosphate reductase;	
	argD; argF; argR;	ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor;	
	argG; argH	argininosuccinate synthase;	
		argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cell.</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-Phosphoribosyltransferase	
AF114233	aroA	Pyrophosphohydrolyase	
AF116184	panD	5-enolpyruvylshikimate 3-phosphate synthase	
		L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothemate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	arod, aroE	3-dehydroquinase, shikimate dehydrogenase	
AF124600	aroc, arok, aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AI001436	ecp	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EcpP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AI004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ." <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AI007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; β , high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AI010319	fts Y, glnB, glnD, srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> . Isolation of genes involved in biochemical characterization of corresponding proteins." <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AI132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (aceptor) from <i>Corynebacterium glutamicum</i> ." <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lehninger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> . The channel is formed by a low molecular mass polypeptide." <i>Biochemistry</i> , 37(43):15024-15032 (1998)
DJ7429		Transposable element IS31831	Veres, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ." <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	cdhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) cdhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hcdL, htk	Homoserine dehydrogenase, homoserine kinase	Kusumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 198723292-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Kusumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 198723292-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL, trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
T01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
F03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino peptidic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopeptidic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Deshiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopeptidic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isoctic acid lyase	Kusumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isoctic acid lyase N-terminal fragment	Kusumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Stouch, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
T05108		Aspartokinase	Fujino, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
T05112		Dihydro-dipicolinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kobayashi, M. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
T06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetylhydroxy acid synthetase	Imai, M. et al. "Gene capable of coding Acetylhydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Homo, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
F08177		Aspartokinase	Sao, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
H08178, H08179, H08180, H08181, H08182		Feedback inhibition-released Aspartokinase	Sao, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
F08232		Acetylhydroxy-acid isomerase	Imai, M. et al. "Gene DNA coding acetylhydroxy acid isomerase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
F08643		FT aminotransferase and deshydrobiotin synthase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031476-A 1 02/03/95
F08646		Biotin synthase	Hatakeyama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031476-A 1 02/03/95

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Genbank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Asparatase	Kohama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031478-A 1 0203095
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 032095
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 032095
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 020497
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 031897
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 031897
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 031897
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 031897
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 031897
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 0902097
L01508	IlvA	Threonine dehydratase	Mooskel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinosephosphonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinosephosphonate-7-phosphate synthase gene," <i>FEBS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB, ilvN, ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomerase	Keilhauser, C. et al. "Solvent synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PlsM	Phosphoenolpyruvate sugar phosphotransferase	Foster, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria." <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J. K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence." <i>FEBS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	acdB	Malate synthase	Lee, H.-S. et al. "Molecular characterization of acdB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jelen, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	acca	Isocitrate lyase	
L33906	dxr	Diphtheria toxin repressor	Oguita, J. A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dxr from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follette, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167(695-702) (1986)
M16175	5S rRNA		Park, Y.-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes." <i>J. Gen. Microbiol.</i> 138:1167-1175 (1992)
M89931	acdD, brnQ, yhbW	Bea C-S lyase; branched-chain amino acid uptake carrier; hypodermal protein yhbW	Russell, L. et al. "The Corynebacterium glutamicum acdD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminodihydroxyisovaline." <i>J. Bacteriol.</i> 174(9):2968-2977 (1992); Tsuchi, A. et al. "Isotoluene uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product." <i>Arch. Microbiol.</i> 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence." <i>Appl. Environ. Microbiol.</i> 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Grada, J.P. and Dunne, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schäfer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergenic configuration with Escherichia coli." <i>J. Bacteriol.</i> 176(23):7309-7319 (1994); Schäfer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain." <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step." <i>J. Bacteriol.</i> 178(15):4412-4419 (1996)
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step." <i>J. Bacteriol.</i> 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step." <i>J. Bacteriol.</i> 178(15):4412-4419 (1996)
U31230	obe; proB; unkdh	?gamma glutamyl kimes; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step." <i>J. Bacteriol.</i> 178(15):4412-4419 (1996)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Szeberitskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiH; acsBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	apbA-3	3'-5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(2):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase; EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(D):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Elkann, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepoint, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of C. glutamicum fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.32)	Bornasie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

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GemBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AtbB-related site	Chantotto, N. et al. "DNA sequence homology between atB-related sites of <i>Corynebacterium diptheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the atp site of <i>lambdacorynephage</i> ." <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS, lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene." <i>Mol. Microbiol.</i> , 4(1):1819-1830 (1990)
X55994	trpL, trpE	Purative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene." <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	trnC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene." <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	atbB-related site	Attachment site	Chantotto, N. et al. "DNA sequence homology between atB-related sites of <i>Corynebacterium diptheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the atp site of <i>lambdacorynephage</i> ." <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kallinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ." <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kallinowski, J. et al. "Aspartokinase genes lysC-alpha and lysC-beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ." <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap-pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Elkmanns, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase." <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bornmann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase." <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Siepp-Fellhans, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake." <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	PSI protein	Jolliff, G. et al. "Cloning and nucleotide sequence of the <i>cspI</i> gene encoding PSI, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> . The deduced N-terminal region of PSI is similar to the Mycobacterium antigen 85 complex." <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992).
X66112	glc	Citrate synthase	Elkrmann, B. J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> glcA gene encoding citrate synthase." <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	Peyret, J.L. et al. "Characterization of the <i>cspB</i> gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ." <i>Mol. Microbiol.</i> , 9(1):97-109 (1993).
X69103	csp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis." <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X69104		IS3 related insertion element	Palet, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of <i>leuA</i> , and effect of <i>leuA</i> inactivation on lysine synthesis." <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X70959	leuA	Isopropylmalate synthase	Elkrmann, B. J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> <i>icd</i> gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme." <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X71489	icd	Isocitrate dehydrogenase (NADP+)	
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083	mitrA	5-methyltryptophan resistance	Hery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan." <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X70584			Fitzpatrick, R. et al. "Construction and characterization of <i>recA</i> mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ." <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75085	recA		Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme." <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X75504	aceA, thix	Partial Isocitrate lyase; ?	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes." <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1995)
X76875		ATPase beta-subunit	

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes." <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA	recA	Bilman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinischer, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pte-ack operon encoding phosphotransacylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; glub; gluC; gluD	Glutamate uptake system	Kroneneyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(3):1152-1158 (1995)
X81379	dapE	Succinyl/diaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Rumy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 43(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	arop; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of arp, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

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Genbank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl- γ -amino- glutanyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N- acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta, ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of ph1 AAU2 infecting "Atrhobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Paack, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment H45	Paek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Paek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Paek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Paek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Paek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Paek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Stew, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	bepP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> bepP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X93649	orf4		Paek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X93671	lysE, lysG	Lysine exporter protein; Lysine export regulator protein	Viljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB, panC, xyb	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Salim, H. et al. "D-pantoic acid synthase in <i>Corynebacterium glutamicum</i> and use of panB and genes encoding L-valine synthase for D-pantoic acid overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	
Y00140	thrB	Homoserine kinase	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00151	ddl	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00476	thrA	Homoserine dehydrogenase	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00546	hom, thrB	Homoserine dehydrogenase; homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y08964	muC, ftsQ/diV, ftsZ	UDP-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y09163	putP	High affinity proline transport system	Horubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09548	pyc	Pyruvate carboxylase	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09578	leuB	3-isopropylmalate dehydrogenase	Peters-Wentisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y12472		Attachment site bacteriophage Phi-16	Puck, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
			Moreau, S. et al. "Site-specific integration of bacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctB." <i>J. Bacteriol.</i> 180(22):6005-6012 (1998)
Y13221	gluA	Glutamine synthetase I	Jacoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> gluA gene encoding glutamine synthetase I." <i>FEBS Microbiol. Lett.</i> 154(1):81-88 (1997)
Y16642	hpd	Dihydrodipicolinate dehydrogenase	Moreau, S. et al. "Analysis of the integration functions of <i>ArgR</i> .3041: An integrase module among corynephages." <i>Virology</i> , 255(1):150-159 (1999)
Y18059		Attachment site Coryneophage 3041.	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine." <i>J. Bacteriol.</i> 175(22):7356-7362 (1993)
Z21501	argS, lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pacharao, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function." <i>J. Bacteriol.</i> 175(9):2743-2749 (1993)
Z21502	dapA, dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Malumbres, M. et al. "Analysis and expression of the thnC gene of the encoded threonine synthase." <i>Appl. Environ. Microbiol.</i> 60(7):2209-2219 (1994)
Z29563	thnC	Threonine synthase	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB." <i>J. Bacteriol.</i> 178(2):550-553 (1996)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dimR gene." <i>Gene</i> , 177:103-107 (1996)
Z49822	sigA	Sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB." <i>J. Bacteriol.</i> 178(2):550-553 (1996)
Z49823	galE, dirK	Catalytic activity UDP-galactose 4-epimerase; diptheria toxin regulatory protein	Correa, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869." <i>Gene</i> , 170(1):91-94 (1996)
Z49824	orf1, sigB	?; SigB sigma factor	
Z66534		Transposase	

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

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TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRL	CECT	NCIMB	CBS	NCIC	DSMZ
Brevibacterium	ammoniaenes	21054							
Brevibacterium	ammoniaenes	19380							
Brevibacterium	ammoniaenes	19351							
Brevibacterium	ammoniaenes	19352							
Brevibacterium	ammoniaenes	19353							
Brevibacterium	ammoniaenes	19354							
Brevibacterium	ammoniaenes	19355							
Brevibacterium	ammoniaenes	19356							
Brevibacterium	ammoniaenes	21055							
Brevibacterium	ammoniaenes	21077							
Brevibacterium	ammoniaenes	21553							
Brevibacterium	ammoniaenes	21580							
Brevibacterium	ammoniaenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477						
Brevibacterium	flavum			B11478						
Brevibacterium	flavum	21127								
Brevibacterium	flavum			B11474						
Brevibacterium	breclii	15527								
Brevibacterium	kefoglutamicum	21004								
Brevibacterium	kefoglutamicum	21089								
Brevibacterium	ketosoroductum	21914								
Brevibacterium	lactofermentum				70					
Brevibacterium	lactofermentum				74					
Brevibacterium	lactofermentum				77					
Brevibacterium	lactofermentum	21798								
Brevibacterium	lactofermentum	21799								
Brevibacterium	lactofermentum	21800								
Brevibacterium	lactofermentum	21801								
Brevibacterium	lactofermentum			B11470						
Brevibacterium	lactofermentum			B11471						
Brevibacterium	lactofermentum	21086								
Brevibacterium	lactofermentum	21420								
Brevibacterium	lactofermentum	21086								
Brevibacterium	lactofermentum	31269								
Brevibacterium	linens	9174								
Brevibacterium	linens	19391								
Brevibacterium	linens	8377								
Brevibacterium	parafimnolyticum					11160				
Brevibacterium	spec.						717.73			
Brevibacterium	spec.						717.73			
Brevibacterium	spec.	14604								
Brevibacterium	spec.	21860								
Brevibacterium	spec.	21864								
Brevibacterium	spec.	21865								

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Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetosclodophilum	21476							
Corynebacterium	acetosclodophilum	13870							
Corynebacterium	aceto-glutamicum			B11473					
Corynebacterium	aceto-glutamicum			B11475					
Corynebacterium	aceto-glutamicum	15806							
Corynebacterium	aceto-glutamicum	21491							
Corynebacterium	aceto-glutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammonigenes	6872						2399	
Corynebacterium	ammonigenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium			P973					
Corynebacterium	nitrilophilus	21419					11594		
Corynebacterium	spec.			P4445					
Corynebacterium	spec.	31088		P4446					
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

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Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd, Aberdeen, UK

CBS: Centraalbureau voor Schimmecultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saitama, Japan.

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TABLE 4: ALIGNMENT RESULTS

ID #	length	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	%homology (GAP)	Date of Deposit
na00006 1731	NTD	GB_BAI.CCGNA	3666	Y13221	Cornelabacterium glutamicum glpA gene	Cornelabacterium glutamicum	37.555	28-Aug-97
na00006 1731		GB_BAI.CCGPROMF45	60	X10383	C. glutamicum DNA for promoter fragment F45	Cornelabacterium glutamicum	100.000	4-Nov-96
na00011 480		GB_BAI.DCGNA	3666	Y13221	Cornelabacterium glutamicum glpA gene	Cornelabacterium glutamicum	37.251	28-Aug-97
na00011 480		GB_BAI.DCGNA	5555	DB8821	Streptomyces coelicolor DNA for P _{6A} , P _{6B} and P _{6B} complete cfs	Streptomyces coelicolor	69.729	7-Feb-99
na00011 480		GB_BAI.MTCV14	38150	205150	Mycobacterium tuberculosis H37Rv complete genome, segment 130/162	Mycobacterium tuberculosis	35.639	19-Jun-98
na00011 480		GB_BAI.MTCV14	43254	205271	Mycobacterium bovis cosmid B1779	Mycobacterium bovis	37.555	6-Aug-97
na00011 480		GB_BAI.MTCV14	5555	205150	Streptomyces coelicolor DNA for P _{6A} , P _{6B} and P _{6B} complete cfs	Streptomyces coelicolor	63.089	7-Feb-99
na00011 480		GB_BAI.MTCV14	38150	205150	Mycobacterium tuberculosis H37Rv complete genome, segment 130/162	Mycobacterium tuberculosis	38.985	19-Jun-98
na00016 1017		GB_BAI.CCGNA	1279	X69104	C. glutamicum IS3 related insertion element	Cornelabacterium glutamicum	82.881	8-Aug-97
na00017 417		GB_PAT.E12760	1279	E12760	DNA encoding Brachydictyon trypsinase	Cornelabacterium glutamicum	83.201	24-Jun-98
na00017 417		GB_PAT.A038104	1279	X69104	Sequence 9 from patient US 580414	Cornelabacterium glutamicum	83.201	24-Jun-98
na00017 417		GB_PAT.A038104	1279	E12760	C. glutamicum IS3 related insertion element	Cornelabacterium glutamicum	78.947	24-Jun-98
na00017 417		GB_PAT.E12760	1279	E12760	DNA encoding Brachydictyon trypsinase	Cornelabacterium glutamicum	77.885	24-Jun-98
na00019 1983		GB_PAT.A038104	30679	209713	Human DNA sequence from cosmid H2C046, on chromosome 22 contains STS	Human sapiens	37.556	25-Sep-99
na00019 1983		GB_PAT.HSND046	151996	AC015177	Human sapiens clone T2_P_19, LOH-PASS SEQUENCE SAMPLES	Human sapiens	34.506	07-Oct-99
na00019 1983		GB_HTC3.AC015177	4170	AW0000587	614059409.x1.614 - not cDNA library from Whitehead Lab Zee maye cDNA, mRNA sequence	Zee maye	41.578	8-Sep-99
na00046 819		GB_EST17.C73675	391	C73675	3163 Rice particle (longer than 10cm) Oryza sativa cDNA clone E20128_2A, mRNA sequence	Oryza sativa	42.014	23-Sep-97
na00046 819		GB_EST17.A1704169	275	A1704169	U-R-ACD-y-d-08-U-L1 U-R-ACD Rattus norvegicus cDNA clone U-R-ACD-y-d-08-U-L1 3' mRNA sequence	Rattus norvegicus	38.182	3-Jun-99
na00053 516		GB_EST35.A1846290	390	A1846290	U-M-AK1-aez-b-06-U-L1 NIH_3MMP_MH1V N Mus musculus cDNA clone U-M-AK1-aez-b-06-U-L1 3' mRNA sequence	Mus musculus	34.872	14-Jul-99
na00053 516		GB_PL2.AF072675	3127	AF072675	Kluyveromyces fragilis HapA (HAP4) gene, complete cds	Kluyveromyces fragilis	36.914	13-MAR-1999
na00053 516		GB_VI.AB010886	3367	AB010886	Cydia pomonella granulovirus genes for chitinase and caltropin, complete cds	Cydia pomonella granulovirus	35.375	13-Feb-99
na00053 516		GB_FR2.H17175	96256	AL022315	Human DNA sequence from clone 117715 on chromosome 22q13.1. Contains part of a putative novel gene, the gene for serum oncofibrin protein M5E55 downstream of a putative CpG island and the GSA152 gene for Lactin, Galactose-binding, soluble, 2. Galactin 2, S-Lac Lactin 2, HL14). Contains ESTs and GSSs, complete sequence	Human sapiens	36.884	23-Nov-99
na00057 222		GB_BAI.CCGNA	1290	X69104	C. glutamicum IS3 related insertion element	Cornelabacterium glutamicum	61.261	9-Aug-95
na00057 222		GB_PAT.A038104	1279	A038104	Sequence 9 from patient US 580414	Unknown	66.512	25-Sep-99
na00057 222		GB_PAT.E12760	1279	E12760	DNA encoding Brachydictyon trypsinase	Cornelabacterium glutamicum	66.512	24-Jun-98
na00059 1506		GB_BAI.MTCV27	27548	295208	Mycobacterium tuberculosis H37Rv complete genome, segment 104/162	Mycobacterium tuberculosis	38.029	17-Jun-98
na00059 1506		GB_BAI.MSCB1229CS	30679	L78812	Mycobacterium bovis cosmid B1728 DNA sequence	Mycobacterium bovis	64.940	15-Jun-96
na00059 1506		GB_BAI.MSCB989CS	10000	L78812	Mycobacterium bovis cosmid B998 DNA sequence	Mycobacterium bovis	64.940	15-Jun-96
na00102 891		GB_PRC.HS4P21	170001	AL021917	Human DNA sequence from clone 45P21 on chromosome 9p21.3-22.2 Contains butyrophilin (BTFL3, BTFL5, BTFL7, BTFL4, EST STS, complete sequence	Human sapiens	37.882	23-Nov-99
na00102 891		GB_PRC.AC005330	40507	AC005330	Human sapiens chromosome 19, cosmid R34047, complete sequence	Human sapiens	35.666	26-Jul-98

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TABLE 4: ALIGNMENT RESULTS

rs000227 921	GB_GSSX.A067431	502	A067431	HS_5592_A2_C01_7TA.RPCL1+Human Male BAC Library Homo sapiens	Homo sapiens	37,000	25-Jun-99
rs000107 360	GB_PL2.A0007153	103223	A0007153	Arabisopsis italiana chromosome 1BAC (3720 genomic sequence), complete sequence.	Arabisopsis italiana	33,427	17-MAY-1999
rs000138 684	GB_BA2.PPUB983	4642	UB983	Pseudomonas putida P28K, antisense, nitrite hydratase alpha subunit, nitrite hydratase beta subunit, and P14K genes, complete cds.	Pseudomonas putida	40,998	2-Jun-98
rs000172 735	GB_PAT.A0041193	1440	AR041193	Sequence 17 from patient US 5611286.	Unknown	40,988	29-Sep-99
rs000125 886	EM_PAT.E0063	2538	E0063	gDNA encoding seed protein.	Corynebacterium glutamicum	94,028	07-OCT-1997 (Rel 52, Crealid)
rs000184 1296	GB_BA1.NSJB031	2968	UB031	Myobacterium megamatis ScaA (ScaA) gene, complete cds.	Myobacterium megamatis	71,216	28-Aug-96
rs000138 684	GB_BA2.SLUT2102	4006	LU2102	Streptomyces lividans ScaA (ScaA) gene, complete cds.	Streptomyces lividans	63,472	3-Sep-96
rs000172 735	GB_BA1.BLE10NP	738	XB0289	B. lachnospirum gDNA encoding oligonucleotide P.	Corynebacterium glutamicum	98,332	14-Nov-98
rs000172 735	GB_BA1.MTCY159	33818	ZS983	Myobacterium tuberculoidis H37Rv complete genome, segment 1117162.	Myobacterium tuberculoidis	37,946	17-Jun-98
rs000172 735	GB_BA1.NSG3897CS	38914	L78820	Myobacterium leprae cosmid B597 DNA sequence.	Myobacterium leprae	62,281	15-Jun-96
rs000172 735	GB_EST28.A064755	572	A064755	EST28016 (partial ovary, rRNA) Lycopodium esculentum cDNA, clone cLE28016, rRNA sequence.	Lycopodium esculentum	38,171	28-Jun-99
rs000172 735	GB_EST28.A064755	610	A064755	EST284932 (partial ovary, rRNA) Lycopodium esculentum cDNA, clone cLE284932, rRNA sequence.	Lycopodium esculentum	46,452	28-Jun-99
rs000184 1296	GB_P383.HS390D17	152562	ALU08634	Human DNA sequence from clone 390D17 on chromosome 1p33-35.3 Contains EST, 5'UT, GSS, complete sequence.	Homo sapiens	33,080	23-Nov-99
rs000184 1296	GB_BA1.MTCY90	38030	Z77137	Myobacterium tuberculoidis H37Rv complete genome, segment 557162.	Myobacterium tuberculoidis	47,823	17-Jun-98
rs000184 1296	GB_BA1.AB013462	19497	AB013462	Bacillus halodurans C-123 genomic DNA, 5'UT, fragment, clone ALBAC001.	Bacillus halodurans	30,234	3-Aug-99
rs000184 1296	GB_P383.A0005738	134506	AC005738	Homo sapiens chromosome 5, BAC clone 7912 (LBRM, HT20), complete sequence.	Homo sapiens	37,127	20-OCT-1999
rs000209 1614	GB_BA1.MNTV012	70287	AL021287	Myobacterium tuberculoidis H37Rv complete genome, segment 1327162.	Myobacterium tuberculoidis	37,632	23-Jun-99
rs000210 420	GB_BA1.NCIB537	44882	Z86263	Streptomyces leprae cosmid B597.	Streptomyces leprae	65,765	17-Sep-97
rs000210 420	GB_P383.SC009	38681	AL003669	Streptomyces coelicolor cosmid 829.	Streptomyces coelicolor	63,795	26-Feb-98
rs000210 420	GB_P383.MCR0731	103	AL007031	Myobacterium granulicella microsatellite ST1A2 DNA.	Myobacterium granulicella	46,545	3-Aug-98
rs000210 420	GB_HTG1.CEY48G10_4	110000	AL021450	Caenorhabditis elegans chromosome 1 clone Y48G10, *** SEQUENCING IN PROGRESS *** in undervet pieces.	Caenorhabditis elegans	37,101	28-Jul-99
rs000217 1218	GB_HTG1.CEY48G10_4	110000	AL021450	Caenorhabditis elegans chromosome 1 clone Y48G10, *** SEQUENCING IN PROGRESS *** in undervet pieces.	Caenorhabditis elegans	37,101	28-Jul-99
rs000217 1218	GB_BA1.MNTV012	70287	AL021287	Myobacterium tuberculoidis H37Rv complete genome, segment 1327162.	Myobacterium tuberculoidis	35,122	23-Jun-99
rs000217 1218	GB_HTG2.AC008092	88749	AC008092	22 F2 map BAC-84D strain Y, on bw sp, *** SEQUENCING IN PROGRESS *** in undervet pieces.	Drosophila melanogaster	33,001	2-Aug-99
rs000217 1218	GB_HTG2.AC008092	88749	AC008092	22 F2 map BAC-84D strain Y, on bw sp, *** SEQUENCING IN PROGRESS *** in undervet pieces.	Drosophila melanogaster	33,001	2-Aug-99
rs000227 921	GB_BA1.LLUDHE	1651	X70926	Drosophila melanogaster chromosome 3 clone BACR22F22 (D824) RPCL-98	Drosophila melanogaster	33,001	2-Aug-99
rs000227 921	GB_GSSX.A0158666	731	A0158666	L. plantinum gene for lactate dehydrogenase.	Lactobacillus plantinum	37,294	17-Feb-94
rs000227 921	GB_BA1.LLUDHE	1651	X70926	nb400011 INDB6 CUGI Rice BAC Library Oryza sativa genomic clone nb400011 INDB6 Oryza sativa genomic survey sequence.	Oryza sativa	39,041	12-Sep-98
rs000227 921	GB_BA1.LLUDHE	1651	X70926	L. plantinum gene for lactate dehydrogenase.	Lactobacillus plantinum	34,947	17-Feb-94

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TABLE 4: ALIGNMENT RESULTS

rs00066 573	GB_PRR.ACO07368	94024	AC007368	Homo sapiens 12q24.2 PAC RPCC4-B09F-18 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	40,037	31-Jul-99
	GB_PRR.ACO07368	94024	AC007368	Homo sapiens 12q24.2 PAC RPCC4-B09F-18 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	36,121	31-Jul-99
rs000280 624	GB_EST19.A658595	532	A658595	0970D4.YT Zebrafish WASHU MPMING EST Dario rio cDNA, 5' similar to WP-FC2D8.4 CE05783 LACTATE DEHYDROGENASE... mRNA sequence.	Dario rio	34,242	21-Apr-99
	GB_VID7382	1593	D7382	Rotavirus sp. mRNA for nonstructural protein 1, complete cds.	Rotavirus sp.	35,217	22-Jan-98
	GB_EST19.A658595	532	A658595	0970D4.YT Zebrafish WASHU MPMING EST Dario rio cDNA, 5' similar to WP-FC2D8.4 CE05783 LACTATE DEHYDROGENASE... mRNA sequence.	Dario rio	36,118	21-Apr-99
rs000314 1503	GB_PAT.AB008345	1344	AB008345	Sequence 1 from patient US 6753480	Unknown	50,763	04-DEC-1988
	GB_BA1.AB008346	333	AB008346	A. brasiliense jPKC, gIX, & gIYS genes.	Azoarcillum brasiliense	37,244	9-Jan-98
	GB_PAT.AB008346	333	AB008346	Sequence 3 from patient US 6753480	Unknown	64,545	04-DEC-1988
rs000331 480	GB_BA1.CGT-HRC	3120	X58037	Cornebacterium glutamicum tbc gene for threonine synthase (EC2.9.9.2).	Cornebacterium glutamicum	40,393	17-Jun-97
	GB_PAT.108078	3146	108078	Sequence 4 from Patient NO 80080810.	Unknown	38,462	02-DEC-1994
rs000333 657	GB_BA1.SA.Y14370	7791	Y14370	Staphylococcus aureus RF3, mufE, ynfP genes.	Staphylococcus aureus	34,526	24-Jun-98
	GB_PRR.ACO04788	39438	AC004788	Homo sapiens chromosome 7 clone UNGC.G1564327 from 7p14-16, complete sequence.	Homo sapiens	37,618	2-Jun-98
	GB_PRR.ACO04788	39438	AC004788	Homo sapiens chromosome 7 clone UNGC.G1564327 from 7p14-16, complete sequence.	Homo sapiens	34,169	2-Jun-98
rs000454 1416	GB_BA2.AE00147	10577	AE00147	Escherichia coli K-12 MG1655 section 37 of 400 of the complete genome.	Escherichia coli	48,925	12-Nov-98
	GB_PRR.DJ270M14	192126	AF107865	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor/homo sapiens beta 3 (TGF-beta 3) gene, complete cds, and unknown genes.	Homo sapiens	36,043	14-Jul-99
	GB_BA1.ECOTGT	1823	M83939	E. coli tRNA-guanine-thiarylsylase (tly) gene, complete cds.	Escherichia coli	48,925	26-Apr-99
rs000458 736	GB_BA1.SCAQ2	30590	AL031371	Pseudomonas coelicolor cosmid 432.	Streptomyces coelicolor	34,836	5-Sep-98
	GB_BA2.AF024619	4038	AF024619	Pseudomonas fluorescens hybrid histidine kinase homolog (hys) and response regulatory protein (bcr) genes, complete cds.	Pseudomonas fluorescens	39,251	22-Mar-99
	GB_BA1.SCAQ2	30590	AL031371	Streptomyces coelicolor cosmid 432.	Streptomyces coelicolor	40,186	5-Sep-98
rs000464 1203	GB_PRR.ACO07267	3019	AB012627	Adiantum capillus-venereis CRT2 mRNA for blue-light photoreceptor complete cds.	Adiantum capillus-venereis	43,959	5-Feb-99
	GB_PRR.ACO07267	3019	AB012627	Adiantum capillus-venereis CRT2 gene for blue-light photoreceptor, complete cds.	Adiantum capillus-venereis	39,765	5-Feb-99
	GB_PRR.ACO07267	3019	AB012627	Saccharomyces cerevisiae chromosome VI phage 6562.	Saccharomyces cerevisiae	37,133	7-Feb-99
rs000465 867	GB_HTC3.ACO08863	54169	AC008863	Homo sapiens chromosome 5 clone C17B-H1_2178P21... SEQUENCING IN PROGRESS... 66 undetected pieces.	Homo sapiens	36,471	3-Aug-99
	GB_HTC3.ACO08863	54169	AC008863	Homo sapiens chromosome 5 clone C17B-H1_2178P21... SEQUENCING IN PROGRESS... 66 undetected pieces.	Homo sapiens	36,090	3-Aug-99
rs000532 608	GB_HTC3.ACO08863	54169	AC008863	Homo sapiens chromosome 5 clone C17B-H1_2178P21... SEQUENCING IN PROGRESS... 66 undetected pieces.	Homo sapiens	38,992	18-Nov-93
	GB_EBGR751	5409	X54455	E. coli plasmid 3751 (pA, 5' end), frag, int1, tral, trkA and hml (5' end) genes Escherichia coli of the transfer region.	Escherichia coli	38,992	18-Nov-93

TABLE 4: ALIGNMENT RESULTS

GB_BAZEAMJ07194	53339	U0184	Enterobacter aerogenes plasmid R751, complete plasmid sequence.	Enterobacter aerogenes	38,892	19-OCT-1989
GB_BA1DB2327	1626	D08327	Rhodococcus erythropolis DNA for catabolite 1,2-dioxanase, complete cds.	Rhodococcus erythropolis	37,232	1-Sep-89
GB_PL2-AF053311	1110	AF053311	Zaradokasia aethiopica glutathione peroxidase (gpx) mRNA, nuclear gene encoding chloroplast protein, complete cds.	Zaradokasia aethiopica	48,552	20-Nov-88
GB_PL2-AF053311	1110	AF053311	Zaradokasia aethiopica glutathione peroxidase (gpx) mRNA, nuclear gene encoding chloroplast protein, complete cds.	Zaradokasia aethiopica	36,301	20-Nov-88
GB_PAT192046	2203	192046	Sequence 13 from patent US 5726299.	Unknown	37,129	01-DEC-1989
GB_PAT178757	2203	178757	Sequence 13 from patent US 5693781.	Unknown	37,129	3-Apr-89
GB_P44-AC005642	192218	AC005642	Mycobacterium tuberculosis H37Rv complete genome, segment 481/62.	Mycobacterium tuberculosis	37,672	14-Jun-99
GB_P44-MT017	67200	AL021687	Pseudomonas aeruginosa dihydrodipicolinate reductase (diprd) gene, partial cds.	Pseudomonas aeruginosa	38,150	24-Jun-89
GB_BA1PAU61259	7265	U81259	carbamoylphosphate synthetase large subunit (carS) gene, and rrs1 homolog (rrs1) gene, partial cds.		45,463	22-DEC-1986
GB_IN2-AC005643	80389	AC005643	Drosophila melanogaster, chromosome 2R, region 50C5-50C6, P1 done D50C072.Drosophila melanogaster complete sequence.	Drosophila melanogaster	40,705	15-DEC-1989
GB_BA1MLC31222	34714	AL048491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	40,549	27-Aug-99
GB_BA1MEU15140	2136	U13140	Mycobacterium bovis tuberculin proteins If-1 (infA), L36 (pnu), S13 (psaM) and S11 (psk) genes, complete cds, and S4 (psd) gene, partial cds.	Mycobacterium bovis	64,881	28-OCT-1999
GB_BA1MTY13E12	43401	Z93390	Mycobacterium tuberculosis H37Rv complete genome, segment 1477/62.	Mycobacterium tuberculosis	41,896	17-Jun-88
GB_BA1BR1SECY	1516	D14162	Mycobacterium flavum gene for SecY protein (complete cds) and gene for adenylyate kinase (partial cds).	Mycobacterium flavum	68,436	3-Jul-99
GB_PAT.E07701	1323	E07701	Brevibacterium seckii gene.	Corynebacterium glutamicum	68,262	28-Sep-97
GB_BA1MTV041	28628	AL021958	Mycobacterium tuberculosis H37Rv complete genome, segment 351/62.	Mycobacterium tuberculosis	60,724	17-Jun-88
GB_EST17.C81980	216	C81980	C81980 Yujl Kohara unpublished cDNA Caenorhabditis elegans cDNA done yk272b 5' mRNA sequence.	Caenorhabditis elegans	43,030	22-Sep-97
GB_RO1MANNT12	5141	X01815	Mouse gene for H-2K(b) antigen.	Mus musculus	37,317	03-OCT-1987
GB_P44-AC003001	101981	AC003001	Homo sapiens chromosome X, clone HRCQ328E24, complete sequence.	Homo sapiens	34,127	6-Jul-99
GB_PL2.AT7C1A0	200576	Z97355	Aradopsis thaliana DNA chromosome 4, ESSA1 FGA coding fragment No. 0	Aradopsis thaliana	36,527	36-Jul-99
GB_P44-AC006443	210636	AC006443	Homo sapiens chromosome 9, clone hRPK_494_N_15, complete sequence.	Homo sapiens	34,401	30-Jun-99
GB_P44-AC006443	210636	AC006443	Homo sapiens chromosome 9, clone hRPK_494_N_15, complete sequence.	Homo sapiens	34,401	30-Jun-99
GB_GSS12.A0403148	432	A0403148	HS_5052_A2_F07 SPEE RPKC114 Human HaBAC Library Homo sapiens genomic clone P1as-628 Col=14 Rom+K genomic survey sequence.	Homo sapiens	41,371	13-MAR-1999
GB_HTF6-AC009821	184689	AC009821	Homo sapiens clone PPI1-115018.WORKING DRAFT SEQUENCE. 17 unorderd pieces.	Homo sapiens	37,223	03-DEC-1999
GB_HTF6-AC009821	184689	AC009821	Homo sapiens clone PPI1-115018.WORKING DRAFT SEQUENCE. 17 unorderd pieces.	Homo sapiens	38,438	03-DEC-1999
GB_BA1MTCV227	36946	Z77774	Mycobacterium tuberculosis H37Rv complete genome, segment 114/162.	Mycobacterium tuberculosis	38,493	17-Jun-88
GB_BA1U00011	40929	U00011	Mycobacterium leprae cosmid B1177.	Mycobacterium leprae	37,978	01-MAR-1994

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TABLE 4: ALIGNMENT RESULTS

rs000829_786	GB_BA1D08029	20277	D90829	E. coli genomic DNA, Kohara clone #327(41.4-42.3 min).	Escherichia coli	35,750	21-MAR-1987
rs000828_741	GB_P122HS112118	138145	AL031653	Human DNA sequence from clone 112118 on chromosome 20. Contains ESTs, STS, GSSs, a c. repeat polymorphism and genomic marker D205115, complete sequence.	Homo sapiens	37,997	23-Nov-99
	GB_P122HS112118	138145	AL031653	Human DNA sequence from clone 112118 on chromosome 20. Contains ESTs, STS, GSSs, a c. repeat polymorphism and genomic marker D205115, complete sequence.	Homo sapiens	38,701	23-Nov-99
	GB_H1FG3AC08715	101012	AC08715	Homo sapiens chromosome 5, clone C17875(SKG_14413, ** SEQUENCING IN PROGRESS *** 7 unordered Homo sapiens	Homo sapiens	38,189	3-Aug-99
	GB_H1FG3AC00480	220000	AC00480	Homo sapiens chromosome 4, ** SEQUENCING IN PROGRESS *** 7 unordered Homo sapiens	Homo sapiens	37,131	2-Sep-99
	GB_H1FG3AC00480	220000	AC00480	Homo sapiens chromosome 4, ** SEQUENCING IN PROGRESS *** 7 unordered Homo sapiens	Homo sapiens	37,131	2-Sep-99
	GB_H1FG3AC00480	220000	AC00480	Homo sapiens chromosome 4, ** SEQUENCING IN PROGRESS *** 7 unordered Homo sapiens	Homo sapiens	37,775	2-Sep-99
rs000837_495	GB_GSS3B67298	592	B67298	Arabisopsis thaliana chromosome 1 BAC F5K7 genomic sequence, complete sequence.	Arabisopsis thaliana	36,884	08-MAR-1989
	GB_P122ATAC000413	86059	AC000413	Arabisopsis thaliana chromosome 1 BAC F5K7 genomic sequence, complete sequence.	Arabisopsis thaliana	36,884	08-MAR-1989
	GB_EST8AA052151	282	AA052151	mitig103.1 Soares mouse embryo NHEK13.5 14.5 Mus musculus cDNA clone IMAGE 420724.5, mRNA sequence.	Mus musculus	38,652	13-Sep-96
rs000938_381	GB_BA2AF121000	19751	AF121000	Corynebacterium glutamicum strain Z2243 R-plasmid pNGL, complete sequence.	Corynebacterium glutamicum	38,410	14-Apr-99
	GB_BA1FV6FOA2A	45919	D26094	Flavobacterium sp. plasmid pOAO2 DNA, whole sequence.	Flavobacterium sp.	37,228	6-Feb-99
	GB_BA1FV6FOA2A	45919	D26094	Flavobacterium sp. plasmid pOAO2 DNA, whole sequence.	Flavobacterium sp.	63,102	6-Feb-99
rs000968_640	GB_BA1MLC8628	40789	Y14967	Mycobacterium leprae cosmid B528.	Mycobacterium leprae	60,538	28-Aug-97
	GB_BA1MLC8170	37821	Z70722	Mycobacterium leprae cosmid B1770.	Mycobacterium leprae	60,538	28-Aug-97
	GB_BA1MTCV21D4	20760	Z80775	Mycobacterium tuberculosis H37Rv complete genome, segment 3/282.	Mycobacterium tuberculosis	59,375	24-Jun-99
	GB_BA1MTCV21D4	38721	AC000013	Mycobacterium tuberculosis sequence from clone Y219.	Mycobacterium tuberculosis	36,077	10-DEC-1999
rs000968_1054	GB_BA1MTCV21D4	20760	Z80775	Mycobacterium tuberculosis H37Rv complete genome, segment 3/282.	Mycobacterium tuberculosis	67,536	24-Jun-99
	GB_BA1MLC8628	40789	Y14967	Mycobacterium leprae cosmid B528.	Mycobacterium leprae	65,990	28-Aug-97
	GB_PAT.E14508	3579	E14508	DNA encoding flavobacterium diaminopimic acid decarboxylase and arginyl-RNA synthase.	Corynebacterium glutamicum	99,887	28-Jun-99
rs000975_1773	GB_PAT.AR038110	3579	AR038110	Sequence 15 from patient US 590414.	Unknown	99,887	25-Sep-99
	GB_PAT.E16355	3579	E16355	Brevibacterium agens and Ysa genes.	Corynebacterium glutamicum	34,674	28-Jun-99
rs000978_738	GB_P122HSAC00372	41730	AC000372	Human cosmid p18004186, complete sequence.	Homo sapiens	34,674	12-MAR-1987
	GB_P122HSAC00372	40988	AC000372	Human cosmid p18004186, complete sequence.	Homo sapiens	34,674	12-MAR-1987
	GB_PR2AC005603	40988	AC005603	Human cosmid p18004186, complete sequence.	Homo sapiens	38,881	20-Aug-98
	GB_PR2HSAC00372	41730	AC000372	Human cosmid p18004186, complete sequence.	Homo sapiens	38,881	20-Aug-98
rs000885_2652	GB_BA1MTCV21D4	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 1/281/162.	Mycobacterium tuberculosis	38,126	17-Jun-98
	GB_BA1MTCV21D4	3168	X77239	B. subtilis vaxs gene.	Bacillus subtilis	52,036	16-Apr-97
	GB_BA1ECOLUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,971	17-Apr-96

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TABLE 4. ALIGNMENT RESULTS

ra00998 565	GB_PAT1E960	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Corynebacterium glutamicum	38,398	24-Jun-98
	GB_HJG2A.F64115	94757	AF164115	PROGRESS *** in unrefined pieces.	Homo sapiens	33,563	12-Jul-99
	GB_HJG2A.F64115	94757	AF164115	Homo sapiens chromosome 8 clone BAC 644F.1, *** SEQUENCING IN PROGRESS *** in unrefined pieces.	Homo sapiens	33,563	12-Jul-99
ra001020 870	GB_EST193.A65371	418	A65371	h28D06.x1 NC1 CGAP Brn25 homo sapiens cDNA clone IMAGE 2168115.3 similar to contains element T1A1 T1A1 repetitive element. mRNA sequence.	Homo sapiens	36,655	12-MAY-1999
	GB_EST193.A671115	508	AB71115	similar to TR075176.075176 KIAA0882 PROTEIN contains element MERT15 repetitive element. mRNA sequence.	Homo sapiens	37,549	30-Aug-99
	GB_EST172.A430328	520	A430328	mtf8505.v1 f1 mouse embryo NM01613.5 14.5 Mus musculus cDNA clone IMAGE 419216.5. mRNA sequence.	Mus musculus	37,765	09-MAR-1999
ra001061 1061	GB_BA1MTCY21D4	2070	Z80775	Mycobacterium tuberculosis H37RV complete genome, segment 3282.	Mycobacterium tuberculosis	62,606	24-Jun-99
	GB_BA1MTCY21D4	38721	AC000013	Mycobacterium tuberculosis H37RV complete genome, segment 3282.	Mycobacterium tuberculosis	41,171	10-DEC-1999
ra001072 354	GB_BA1MLCB2828	40789	Y14867	Mycobacterium leprae cosmid B528.	Mycobacterium leprae	61,022	28-Aug-97
	GB_BA2AF12535	4383	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	99,718	9-Aug-99
	GB_BA1CANRDFGEN	6054	Y09572	Corynebacterium ammoniagenes nrdH, nrdI, nrdE, nrdF genes.	Corynebacterium ammoniagenes	62,393	18-Apr-98
ra001124 1602	GB_BA1MTCY22D7	31659	Z83886	Mycobacterium tuberculosis H37RV complete genome, segment 133162.	Mycobacterium tuberculosis	37,714	17-Jun-98
	GB_BA1SC1C2	42210	AL031124	Streptomyces coelicolor cosmid TC2.	Streptomyces coelicolor	60,616	15-Jan-99
	GB_BA1MTCV012	70287	AL021287	Mycobacterium tuberculosis H37RV complete genome, segment 132162.	Mycobacterium tuberculosis	37,913	23-Jun-99
ra001189 871	GB_PRA1MCE837	44882	Z82933	Mycobacterium leprae cosmid B537.	Mycobacterium leprae	61,216	17-Sep-97
	GB_PRA1MCE837	2153	AF046873	Homo sapiens synapsin IIIa mRNA, complete cds.	Homo sapiens	37,164	28-Apr-98
	GB_EST30.A64949	691	AB49494	h3A303.x1 Sugano mouse kidney m1a Mus musculus cDNA clone IMAGE:1970609.3 similar to gb.X15694 Mouse mRNA for liver-type glucose transporter protein (MOLISE)., mRNA sequence.	Mus musculus	37,226	30-Apr-99
	GB_EST23A112163	468	A1121163	ud7D04.x1 Sugano mouse liver m1a Mus musculus cDNA clone IMAGE:1461215 similar to gb.X00310 GLUCOSE TRANSPORTER TYPE 2, LIVER (HUMAN). gb.X15694 Mouse mRNA for liver-type glucose transporter protein (MOLISE)., mRNA sequence.	Mus musculus	35,057	2-Sep-98
ra001223 735	GB_PRA1AC007396	176742	AC007396	Homo sapiens BAC clone NH0359K10 from 2, complete sequence.	Homo sapiens	38,551	22-OCT-1989
	GB_PRA1AC007396	176742	AC007396	Homo sapiens BAC clone NH0359K10 from 2, complete sequence.	Homo sapiens	38,678	22-OCT-1989
ra001226 663	GB_PRA1H621F7	150789	AL033375	Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.	Homo sapiens	37,309	23-Nov-99
	GB_PRA1AF023268	75270	AF023268	Homo sapiens cdk2 kinase (CLK2), ppp1r1, cdk1, glucocorticoid-induced (GBA), and Homo sapiens melanin genes, complete cds, melanin pseudogene and glucocorticoidase pseudogene, and thrombospondin3 (THBS3) gene, partial cds.	Homo sapiens	38,923	26-OCT-1997
	GB_BA2AF016465	191346	AF016465	Halobacterium sp. NRC-1, plasmid pNRC100, complete plasmid sequence.	Halobacterium sp. NRC-1	39,938	28-MAR-1999

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TABLE 4: ALIGNMENT RESULTS

rs601228	339	GB_PRC2-HIS148E12	163871	AL031594	Human DNA sequence from clone 115EE12 on chromosome Xp11.23-11.4. Contains EST, STS, GSS, CGP island, complete sequence.	Homo sapiens	34,718	23-Nov-99
rs601228	777	GB_HTRG/AC008180_0	110006	AC008180	Homo sapiens clone RP11-102L5. *** SEQUENCING IN PROGRESS ***. 152 unspliced pieces.	Homo sapiens	31,212	29-Jul-99
rs601228	777	GB_PRA/AC000498	139251	AC000498	Homo sapiens P1AC clone D1085521, complete sequence.	Homo sapiens	37,082	15-Jan-99
rs601228	777	GB_BA1/SC6913	121125	AL022121	Mycobacterium tuberculosis H37RV complete genome, segment 159/162.	Mycobacterium tuberculosis	38,171	24-Jun-99
rs601228	777	GB_BA1/SC6913	35101	AL070348	Streptomyces coelicolor strain 6673.	Streptomyces coelicolor	35,401	18-Jun-99
rs601228	777	GB_BA2/AF151381	1286	AF151381	Streptomyces coelicolor recombinant protein RecR (recR) gene, complete cds. and unknown gene.	Streptomyces coelicolor	53,826	20-Aug-99
rs601284	339	GB_GSS10/AQ181653	617	AQ181653	RP11-16823.T1, RP11-11 Homo sapiens genomic clone RP11-16823, genomic survey sequence.	Homo sapiens	41,016	20-Apr-99
rs601285		GB_HTRG/AC00016	194000	AC00016	Homo sapiens chromosome 4. *** SEQUENCING IN PROGRESS ***. 9 unspliced pieces.	Homo sapiens	38,253	16-MAY-1998
rs601285		GB_STS/GS3604	617	GS3604	SHGC-66312 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	41,016	25-Jun-99
rs601274	1218	GB_PAT/16823	2323	E16823	DNA encoding cell surface protein from Corynebacterium ammoniagenes.	Corynebacterium ammoniagenes	52,523	26-Jul-99
rs601274	1218	GB_HTRG/AF182108	167065	AF182108	Homo sapiens chromosome 8 clone BAC R-1118 map 8p12.8. ***SEQUENCING IN PROGRESS***. In unrotated pieces.	Homo sapiens	35,377	08-OCT-1999
rs601278	2250	GB_HTRG/AF182108	167085	AF182108	Homo sapiens chromosome 8 clone BAC R-1118 map 8p12.8. ***SEQUENCING IN PROGRESS***. In unrotated pieces.	Homo sapiens	35,377	08-OCT-1999
rs601278	2250	GB_BA1/MLB17803	37617	Z14314	Maize genes p1L, p2L, p3C, end, p4L, p5G, e1g, u1L, p5L, p1C for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and mkl gene.	Mycobacterium leprae	70,031	11-Feb-93
rs601283	1316	GB_BA1/MTV040	15100	AL021943	Mycobacterium tuberculosis H37RV complete genome, segment 339/162.	Mycobacterium tuberculosis	70,704	17-Jun-98
rs601283	1316	GB_BA1/AF151381	3412	X86673	A tumefaciens tshA and tshB genes.	Agrobacterium tumefaciens	64,042	11-Nov-96
rs601283	1316	GB_BA1/MLB17803	37617	Z14314	Maize genes p1L, p2L, p3C, end, p4L, p5G, e1g, u1L, p5L, p1C for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and mkl gene.	Mycobacterium leprae	65,865	11-Feb-93
rs601284	967	GB_BA1/CGT1F	11891	X77034	C glutamum tuf gene for elongation factor Tu.	Corynebacterium glutamicum	100,000	1994
rs601284	967	GB_BA1/MTV210	38604	Z84395	Mycobacterium tuberculosis H37RV complete genome, segment 341/162.	Mycobacterium tuberculosis	74,622	17-Jun-98
rs601284	967	GB_BA1/MSG142	38626	AD000005	Mycobacterium tuberculosis sequence from clone y42.	Mycobacterium tuberculosis	37,419	05-DEC-1999

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TABLE 4: ALIGNMENT RESULTS

rs01327 207	GB_SYSCUS5567	4546	US5367	Artificial Corynebacterium glutamicum (S1207-derived transposon transposase gene, complete cds, and 35' amino-glycylidic phosphotransferase (gppA-3) gene, complete cds.	synthetic construct	60,674	06-MAY-1996
	GB_BA1BUS13869	1940	Z65534	Ribacterium (S13989) DNA and transposase gene.	Corynebacterium glutamicum	62,172	16-Jul-96
	EM_PAT1E10H19	1469	E10419	Insertion sequence derived from C. glutamicum	Corynebacterium glutamicum	60,674	08-OCT-1997 (Rel 62, Created)
rs01328 498	GB_BA1BUS13869	1840	Z65534	Ribacterium (S13989) DNA and transposase gene.	Corynebacterium glutamicum	73,038	16-Jul-96
	GB_SYSCUS5567	4546	US5367	Artificial Corynebacterium glutamicum (S1207-derived transposon transposase gene, complete cds, and 35' amino-glycylidic phosphotransferase (gppA-3) gene, complete cds.	synthetic construct	60,613	06-MAY-1996
	GB_PAT1A3826	1462	143826	Sequence 1 from patient US 563154.	Unknown	60,014	07-OCT-1997
rs01329 414	GB_BA1BUS13869	1840	Z65534	Ribacterium (S13989) DNA and transposase gene.	Corynebacterium glutamicum	73,966	16-Jul-96
	GB_PAT1E10H19	1463	E12758	DNA encoding Brevibacterium transposase.	Corynebacterium glutamicum	73,020	24-Jun-98
	GB_PAT1E10H19	1463	103166	Sequence 1 from patient US 559157.	Unknown	73,020	04-Feb-97
rs01344 2047	GB_BA1MSU4494	3752	U24484	Mycobacterium smegmatis DNA polymerase (rpoD) gene, complete cds.	Mycobacterium smegmatis	73,086	07-MAR-1996
	GB_BA1MTC376	19770	Z26972	Mycobacterium tuberculosis H37Rv complete genome, segment 32/162.	Mycobacterium tuberculosis	71,385	17-Jun-98
	GB_BA1MSGPR08	5004	L21769	Mycobacterium tuberculosis beta subunit rpoC gene, partial cds.	Mycobacterium tuberculosis	71,429	13-Sep-94
rs01355 909	GB_HITG4AC009135	168607	AC009135	Homo sapiens chromosome 16, clone RP4-11.509E10, *** SEQUENCING IN PROGRESS ***.	Homo sapiens	37,166	31-OCT-1989
	GB_HITG4AC009135	168607	AC009135	Homo sapiens chromosome 16, clone RP4-11.509E10, *** SEQUENCING IN PROGRESS ***.	Homo sapiens	37,166	31-OCT-1989
	GB_BA1PLEPALP	1381	X56466	P. fluorescens lepa (partial) and lep gene for leader peptidase 1.	Pseudomonas fluorescens	44,023	04-Feb-92
rs01387 469	GB_BA1MTAB7803	37617	Z14314	Malpue genes rplA, rpoB, rpoC, and, rplA, rplB, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and mkl gene.	Mycobacterium leprae	71,429	11-Feb-93
	GB_BA1MTC376	19770	Z26972	Mycobacterium tuberculosis H37Rv complete genome, segment 32/162.	Mycobacterium tuberculosis	73,176	17-Jun-98
	GB_BA1BUSU001	213080	Z89194	Bacillus subtilis complete genome (section 1 of 21).	Bacillus subtilis	63,853	26-Nov-97
rs01388 295	GB_HITG2HSB76L13	117045	AL034347	Homo sapiens chromosome 6, clone RP4-676J13 map q14, *** SEQUENCING IN PROGRESS ***.	Homo sapiens	36,863	03-DEC-1989
	GB_HITG2HSB76L13	117045	AL034347	Homo sapiens chromosome 6, clone RP4-676J13 map q14, *** SEQUENCING IN PROGRESS ***.	Homo sapiens	36,863	03-DEC-1989
	GB_HITG2HSB76L13	117045	AL034347	Homo sapiens chromosome 6, clone RP4-676J13 map q14, *** SEQUENCING IN PROGRESS ***.	Homo sapiens	29,804	03-DEC-1989
rs01398 659	GB_BA1MTAV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162.	Mycobacterium tuberculosis	36,547	23-Jun-99
	GB_BA1S70345	5077	570345	SpaA-antigenomic immunodominant antigen (Streptococcus sobrinus, MUCOB 263, Genomic, 5077 nt).	Streptococcus sobrinus	35,139	23-Sep-94
	GB_BA1STRPAGA	5100	D80354	S. sobrinus pag gene for surface protein antigen (PAg).	Streptococcus sobrinus	35,604	7-Feb-99

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TABLE 4: ALIGNMENT RESULTS

ra01431	444	GB_BA2.AE01648	13965	AE01648	Chlamydia pneumoniae section 6a of 103 of the complete genome.	44,218	08-MAR-1989
ra01432	1074	GB_BA2.AE01648	13965	AE01648	Chlamydia pneumoniae section 6a of 103 of the complete genome.	35,520	08-MAR-1989
ra01433	726	GB_BA2.AF105341	3010	AF105341	Mycobacterium tuberculosis sequence from clone y67.	37,860	03-DEC-1986
ra01434	1074	GB_BA1.MSCT9367	35336	ADD00008	Mycobacterium tuberculosis H37Rv complete genome; segment 162/162.	61,891	17-Jun-98
ra01435	11381	GB_BA1.MNTV028	11381	AL021426	Mycobacterium smegmatis thiothoxon reductase (trxB) and thiothoxon (trx) genes, complete cds.	64,105	13-OCT-1997
ra01436	1175	GB_BA1.AFC023161	1175	AFC023161	Listeria monocytogenes threonine dehydratase (tdhD) gene, partial cds; alpha acetolactate decarboxylase gene, complete cds; and pyrimidine nucleoside phosphorylase (pdp1) gene, partial cds.	36,254	04-MAR-1989
ra01437	3010	GB_BA2.AF105341	3010	AF105341	Listeria monocytogenes threonine dehydratase (tdhD) gene, partial cds; alpha acetolactate decarboxylase gene, complete cds; and pyrimidine nucleoside phosphorylase (pdp1) gene, partial cds.	35,303	04-MAR-1989
ra01443	864	GB_BA1.CG15468	1290	X69104	C. glutamicum (LS) related insertion element; Sequence 4 from patent US 5591877.	72,823	9-Aug-95
ra01444	380	GB_PAT193168	1279	193168	DNA encoding Mycobacterium transposase.	72,853	6-Feb-97
ra01444	380	GB_BA1.CG15468	1280	E12760	C. glutamicum (LS) related insertion element.	69,694	24-Jun-98
ra01444	380	GB_PAT193168	1279	X69104	DNA encoding Mycobacterium transposase.	69,318	9-Aug-95
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	24-Jun-98
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449	1141	GB_PAT193168	1279	193168	Sequence 4 from patent US 5591877.	69,318	6-Feb-97
ra01449							

TABLE 4: ALIGNMENT RESULTS

GB_ESTF6A002802	396	AA002802	mg3a12.11 Soares mouse embryo NM613.5 14.5 Mus musculus cDNA, clone	Mus musculus	42,333	19-Jul-96
GB_PRR2SHJUT3633	42845	U75633	IMAGE428046.5, mRNA sequence.	Mus musculus	37,412	19-Jun-97
GB_RC0MMU70209	14141	U70209	Human chromosome 11 14p12 cosmid, complete sequence.	Human sapiens	37,412	31-MAY-
GB_HJG2AC007303	170591	AC007303	Mus musculus polyoviscy kidney disease 1 (pvd1) mRNA, complete cds.	Mus musculus	42,536	1987
GB_BA1MTC2272	35046	277724	Homo sapiens chromosome 18, clone 655_L_9 map 18, *** SEQUENCING IN PROGRESS *** 6 uncloned pieces.	Homo sapiens	34,898	23-Jun-99
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	38,567	17-Jun-98
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	53,364	27-Aug-99
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	38,498	1984
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	37,945	17-Jun-98
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	51,117	27-Aug-99
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	37,513	1984
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	80,245	17-Jun-98
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	59,547	15-Jun-96
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	37,473	8-Sep-96
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	38,573	18-Jun-96
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	38,989	20-Aug-98
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	39,220	18-Jun-98
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	38,386	16-Aug-99
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	53,052	17-Jun-96
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	49,393	2-Jun-96
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	54,801	17-Jun-96
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	59,577	24-Jun-97
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	39,476	28-Sep-94
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	52,216	17-Jun-98
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	52,216	18-Jul-97
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	36,145	3-Aug-99
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	36,776	17-Jun-98
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	60,525	93 DEC-
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	36,288	17-Jun-98
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	76,483	9-Aug-95
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	75,574	28-Sep-99
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	75,574	24-Jun-98
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	67,978	9-Aug-95
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	67,857	28-Sep-99
GB_BA1MTC2272	35046	277724	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	67,857	24-Jun-98
GB_BA1MTC1259	39807	AC023591	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	42,241	22-Jul-99
GB_BA1U00011	40428	U00011	Myobacterium tuberculosis H37Rv complete genome, segment 1141/62.	Myobacterium tuberculosis	33,766	22-Jul-99

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TABLE 4: ALIGNMENT RESULTS

GB_P1:1/SCVDR012W	2732	Z74308	S. cerevisiae chromosome 11, reading frame ORF YDR012w.	30,804	12-Aug-88
GB_BA1:CGISAB1	1230	X69104	C. glutamicum (DS) related insertion element.	69,643	9-Aug-95
GB_PAT:AR03104	1279	AR03104	Sequence 9 from patient US 595441.4.	67,265	28-Sep-99
GB_PAT:133188	1279	133188	Sequence 4 from patient US 595157.2.	67,265	6-Feb-97
GB_BA2:SMUG696	3303	UG696	Serially propagated DNA virus (SV4) gene, complete cds.	36,186	7-Jan-98
GB_BA1:DP0902	122056	DP0902	Synchocystis sp. PCC6803 complete genome, 4271_402250-524945.	37,814	7-Feb-99
GB_HTG2:MSDJB16K9	144277	AL117349	Homo sapiens chromosome 1 clone RP4-816V1, "" SEQUENCING IN PROGRESS "" in undetected pieces.	41,799	30-Nov-99
rm001680					
rm001704 1100					
GB_HTG2:AF128075	195012	AF128075	Homo sapiens chromosome 21, clone 1121100; E0479, map 21q22.1, ""SEQUENCING IN PROGRESS"" in undetected pieces.	40,187	03-MAR-1999
GB_HTG2:AF128075	195012	AF128075	Homo sapiens chromosome 21, clone 1121100; E0479, map 21q22.1, ""SEQUENCING IN PROGRESS"" in undetected pieces.	40,187	03-MAR-1999
GB_HTG2:AC007271	164289	AC007271	Homo sapiens clone PH0004812, "" SEQUENCING IN PROGRESS "" 2 undetected pieces.	38,667	16-Apr-99
rm001710 531					
GB_BA1:MTCV441	35107	Z80225	Mycobacterium tuberculosis H37Rv complete genome, segment 118162.	56,309	18-Jun-98
GB_EST16:AAQ40562	665	AAQ40562	LD20282, spine LD Drosophila melanogaster embryo Bluescript Drosophila melanogaster cDNA, clone LD20282, spine, mRNA sequence.	51,357	28-Nov-98
GB_EST37:AB944677	580	AB944677	b6g4004.Y1 Drosophila melanogaster adult testis library Drosophila melanogaster cDNA, clone b6g4004.5, mRNA sequence.	50,728	17-Aug-99
rm001724 1343					
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	37,412	03-MAR-1999
rm001725 330					
GB_BA1:MTCV373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome, segment 571162.	47,819	17-Jun-98
GB_HTG2:AC007608	170057	AC007608	Homo sapiens chromosome 16, clone 40179, "" SEQUENCING IN PROGRESS"" 59 undetected pieces.	37,236	20-MAY-1999
GB_BA1:MTCV373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome, segment 571162.	75,610	17-Jun-98
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	38,355	03-MAR-1999
rm001726 666					
GB_BA1:PSEPHO	1479	L27278	Pseudomonas fluorescens no gene, complete cds.	63,303	9-Jan-95
GB_BA1:MTCV373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome, segment 571162.	72,889	17-Jun-98
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	37,500	03-MAR-1999
rm001730 1804					
GB_BA1:SLRHOENE	2966	X95444	S. lividans Rio gene.	69,005	1-Feb-96
GB_BA1:MTCV227	35946	Z77774	Mycobacterium tuberculosis H37Rv complete genome, segment 114162.	39,943	17-Jun-98
GB_BA1:MLC81259	38607	AL023591	Mycobacterium leprae cosmid B1259.	65,120	27-Aug-99
GB_BA2:SE8288	2209	SE8288	Mycobacterium leprae ASPs and antigen T3 genes, complete cds.	40,715	22-Jul-98
rm001733 1274					
GB_BA1:MSORREP	10430	X92503	M. smegmatis origin of replication and genes prnH, dnaK, trnA, and recF- gyrB, gyrA.	52,740	26-Aug-97
GB_BA1:MSG3VBA	6000	X94224	M. smegmatis gyrB and gyrA genes.	52,277	12-Feb-97
GB_HTG2:AC010890	175554	AC010890	Homo sapiens chromosome unknown clone NT0449.24, WORKING DRAFT SEQUENCE, in undetected pieces.	36,601	28-OCT-1999
rm001736 2891					
GB_BA1:MTV014	56280	AL021665	Mycobacterium tuberculosis H37Rv complete genome, segment 137162.	38,918	16-Jun-98
GB_FL2:AF156928	2280	AF156928	Candida albicans (poly)glutamate synthase (pgs) gene, complete cds.	34,854	22-Jun-99

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TABLE 4: ALIGNMENT RESULTS

nc01862_1329	GB_BAI1U00011	40429	U00011	<i>Mycobacterium leprae</i> cosmid B11177	<i>Mycobacterium leprae</i>	37,690	01-MAR-1994
	GB_BAI1R1DCTA	5620	21559	R. leguminosarum dcd4 gene encoding C4-dicarboxylate permease.	Rhizobium leguminosarum	39,401	23-Sep-92
	GB_BAI1R1DCTB	3620	X06233	Rhizobium leguminosarum dcd4 and dcd5 genes involved in C4-dicarboxylate transport.	Rhizobium leguminosarum	39,401	12-Sep-93
nc01863_1219	GB_BAI1R1DCTA	5620	21559	Rhizobium leguminosarum dcd4 gene encoding C4-dicarboxylate permease.	Rhizobium leguminosarum	39,269	23-Sep-92
	GB_BAI1R1DCTB	20840	299108	Radial subunits complete genome (section 5 of 21; from 802821 to 1011250).	Radial subunits	36,673	26-Nov-97
	GB_BAI1D89E07	22197	D8987	Radial subunits complete genome (section 5 of 21; from 802821 to 1011250).	Radial subunits	57,261	20-Nov-97
	GB_BAI1STAT1B	300	M2033	S. aureus bacteriophage phi-11 attachment site (attB).	Staphylococcus aureus	99,595	26-Jun-93
nc01872_928	GB_GSS15_A0651661	422	A0651661	Sheread DNA-5N18 T7E Sheread DNA-Tyranosoma brucei genomic clone	Tyranosoma brucei	42,034	22-Jun-99
	GB_GSS15_A0651661	175	A0639444	Sheread DNA-5N18 genomic survey sequence.			
	GB_HTTG3_A009819	134724	AC009819	g27P1-17G6 TV g27P1 Tyranosoma brucei genomic clone g27P1-17G6, genomic survey sequence.	Homo sapiens	61,786	8-Jul-99
nc01878_1002	GB_HTTG1CEY64F11	17748	298776	Homo sapiens clone 115_123 LON-PA55 SEQUENCE SAMPLING.	Ceornothoditis elegans	37,222	8-Sep-99
	GB_HTTG1CEY64F11	17748	298776	PROGESSES **, in uncloned pieces.	Ceornothoditis elegans	37,564	14-OCT-1998
	GB_HTTG1CEY64F11	17748	298776	PROGESSES **, in uncloned pieces.	Ceornothoditis elegans	37,564	14-OCT-1998
	GB_HTTG1CEY64F11	17748	298776	PROGESSES **, in uncloned pieces.	Ceornothoditis elegans	37,576	14-OCT-1998
nc01913_348	GB_BAI1HTC274	39891	274024	Ceornothoditis elegans chromosome IV clone 164F11, *** SEQUENCING IN PROGRESSES **, in uncloned pieces.	Ceornothoditis elegans	39,631	18-Jun-98
	GB_BAI1SC2E1	38982	AL023797	Ceornothoditis elegans chromosome IV clone 164F11, *** SEQUENCING IN PROGRESSES **, in uncloned pieces.	Streptomyces coelicolor	58,226	4-Jun-96
	GB_B42AF130345	965	AF130346	Streptomyces coelicolor cosmid ZC1.	Streptomyces ramosissimus	36,009	15-OCT-1999
nc01938_1561	GB_BAI1MTCY24A1	20270	293207	Streptomyces ramosissimus elongation factor Ts (tsf) gene, complete cds.	<i>Mycobacterium tuberculosis</i>	38,976	17-Jun-98
	GB_GSS1TCONS00WZ	720	AL094292	<i>Mycobacterium tuberculosis</i> H37Rv complete genome; segment 124/162.	Arabidopsis thaliana	54,026	20-Jun-99
				Arabidopsis thaliana genome survey Sra and of BAC 11208 of T4M4 library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.			
nc01953_504	GB_PFR2_AP000056	100000	AP000056	Homo sapiens genomic DNA, chromosome 21q22.1, segment 21728, complete sequence.	Homo sapiens	36,967	20-Nov-99
	GB_BAI1M5G1NP	2276	MT9495	<i>Plasmodium falciparum</i> insertion element thpR and thpA genes, complete cds.	<i>Mycobacterium smegmatis</i>	38,153	28-Apr-96
	GB_B42E12PHEAB	6164	MF7500	Plasmodium falciparum putative transposase (trnpA), catalytic 1,2-alkyltransferase (phd), phenol monooxygenase (phdA), and putative transposase (trnpA) genes, complete cds.	Plasmodium falciparum	56,338	21-OCT-1999
	GB_PFR2HS179N16	172048	295152	Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33.	Homo sapiens	34,490	23-Nov-99
				Contains the SAPK4 (MAPK, p38delta) gene, and the alternatively spliced SAPK4 gene coding for Csk1s binding protein (CSBP2) and a MAPK, p38delta LIME protein. Contains ESTs, STSs, and two predicted CpG islands, complete sequence.			
nc01954_963	GB_BAI1SC4H8	15560	AL020856	Streptomyces coelicolor cosmid 4H8.	Streptomyces coelicolor	37,960	10-DEC-1997
	GB_GSS3B91274	183	B91274	CT-HSP-2168G14 T7 CT-HSP Homo sapiens genomic clone 2168G14, genomic survey sequence.	Homo sapiens	36,066	26-Jun-98

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TABLE 4: ALIGNMENT RESULTS

GB_BA1SC4H8	15560	ALU20958	Streptomyces coelicolor cosmid 418	Streptomyces coelicolor	39,457	10-DEC-1987
GB_BQ2CBU13622	4412	U13922	Corynebacterium glutamicum putative type II 5-cytosine methyltransferase (cgjII)	Corynebacterium glutamicum	99,950	3-Feb-98
GB_BA1SPN8BCDE	22440	Y11548	restriction endonuclease (GqfR) genes, complete cds	Streptomyces pristinaespiralis	36,657	25-Apr-97
GB_BA1SPN8BCGEN	22440	X98690	S pristinaespiralis smc gene & smcDE gene	Streptomyces pristinaespiralis	36,657	24-MAR-1987
GB_BQ2AF121000	19751	AF121000	Corynebacterium glutamicum strain 22243 p-plasmid pAG1, complete sequence	Corynebacterium glutamicum	40,520	14-Apr-89
GB_BQ2AF121000	19751	AF121000	Corynebacterium glutamicum strain 22243 p-plasmid pAG1, complete sequence	Corynebacterium glutamicum	54,699	14-Apr-89
GB_BA1TFCPOADA	45519	DD6904	Flavobacterium sp. plasmid pOQD2 DNA, whole sequence	Flavobacterium sp.	38,562	6-Feb-89
GB_BA1STYRFFC	2140	DD0436	Salmonella typhimurium gene for peptide release factor 3/Prf3, complete cds	Salmonella typhimurium	53,289	10-Feb-89
GB_BQ2UC2946	11650	U02946	Haemophilus influenzae Rd section 161 of 163 of the complete genome	Haemophilus influenzae Rd	47,265	28-MAY-1989
GB_BQ2AF072440	4316	AF072440	Enterobacter gergoviae GTRs (bpa) gene, partial cds; glutamine synthetase (gln) and nitrogen regulatory protein (nifS) genes, complete cds, and nitrogen regulatory protein (nifD) gene, partial cds	Enterobacter gergoviae	37,284	30-OCT-1989
GB_PL2AF015560	2681	AF015560	Neurospora crassa R011 (dc-11) gene, complete cds	Neurospora crassa	38,953	3-Sep-87
GB_GSS163AC497173	511	AC497173	HS_3193_E2_A10_174 RPO-11 Human Male BAC Library Homo sapiens genomic clone Hs4e-193 Col-20 Row-85 genomic survey sequence	Homo sapiens	37,095	26-Apr-89
GB_PL1SPAC2107	35692	AL009227	S pombe chromosome I cosmid c2707	Schizosaccharomyces pombe	39,016	25-MAR-1989
GB_BA1ECOUW63	336534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 100.1 minutes	Escherichia coli	38,108	17-Apr-86
GB_BQ2AECDH493	10819	AECDH493	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome	Escherichia coli	39,108	12-Nov-88
GB_BA1ECOUW63	1270	W69992	Escherichia coli penicillin methionine sulfoxide reductase gene, complete cds	Escherichia coli	50,329	26-Apr-83
GB_BQ2MSU87307	1520	U87307	Mycobacterium smegmatis extracytoplasmic function alternative sigma factor gene, complete cds	Mycobacterium smegmatis	59,533	07-MAY-1987
GB_BA1MTC61	13540	Z88260	Mycobacterium tuberculosis H37Rv complete genome, segment 53/162	Mycobacterium tuberculosis	57,833	17-Jun-88
GB_BQ2MTU87242	3690	U87242	Mycobacterium tuberculosis sigma factor SigE (SigE) and Hya (Hya) genes, complete cds	Mycobacterium tuberculosis	57,833	08-MAY-1987
GB_BA1MTCV38	29372	Z74687	Mycobacterium tuberculosis H37Rv complete genome, segment 127/162	Mycobacterium tuberculosis	38,080	17-Jun-88
GB_BA1MLCG1243	42926	AL026535	Mycobacterium leprae cosmid B1243 DNA sequence	Mycobacterium leprae	53,733	27-Aug-99
GB_BA1MSG81723CS	38477	L18825	095689 s1 NC1, CGAC_Kid3 Homo sapiens cDNA clone IMAGE:150220.3, mRNA sequence	Mycobacterium leprae	53,733	15-Jun-86
GB_EST20AA984760	281	AA984760	DKE2767B161.1, 761 (synonym: hamy2) Homo sapiens cDNA clone	Homo sapiens	39,028	9-Jun-86
GB_EST138.AL118293	323	AL118293	Human DNA sequence from clone RPS-103.18 on chromosome 20, complete sequence	Homo sapiens	34,579	27-Sep-89
GB_PFC3HSJ1031J8	155213	AL118523	Human DNA sequence from clone RPS-103.18 on chromosome 20, complete sequence	Homo sapiens	32,341	03-DEC-1989
GB_BA1MTC125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome, segment 76/162	Mycobacterium tuberculosis	63,215	17-Jun-88
GB_BA1MLCG1351	38936	Z98117	Mycobacterium leprae cosmid B1351	Mycobacterium leprae	38,240	24-Jun-87
GB_BA1U00021	39193	U00021	Corynebacterium jeikeium complete genome	Corynebacterium jeikeium	37,964	28-Sep-84
GB_BA1COGLTG	3013	X68112	C. glutamicum gII gene for citrate synthase and OTC	Corynebacterium glutamicum	100,000	17-Feb-85

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Ile Asn Arg Lys Val Gly Glu Thr His Asp Gly Gly Ala Thr Thr Asp
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Val	Glu	Ile	Leu	Arg	Val	Lys	Gly	Ala	Lys	Asp
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Glu	Arg	Asn	Ala	Thr	Glu	Gly	Leu	Val	Ala	Val
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gtc	gag	gtc	aac	tct	gag	acc	gac	ttc	gtt	gca
Val	Glu	Val	Asn	Ser	Glu	Thr	Asp	Phe	Val	Ala
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aag	gaa	ttc	gct	gca	aag	gtt	gca	gac	gca	gca
Lys	Glu	Phe	Ala	Ala	Lys	Val	Ala	Asp	Ala	Ala
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aac	tcc	cag	gaa	gag	ctc	gca	gca	gtt	gac	gtg
Asn	Ser	Gln	Glu	Glu	Leu	Ala	Ala	Val	Asp	Val
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gac	gca	gct	ctg	cag	gag	ttc	tcc	gca	aag	atc
Asp	Ala	Ala	Leu	Gln	Glu	Phe	Ser	Ala	Lys	Ile
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Leu	Arg	Arg	Ala	Val	Thr	Leu	Glu	Gly	Asp	Lys
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cac	cag	cgt	tcc	gct	gac	ctg	cca	cca	gca	ggt
His	Gln	Arg	Ser	Ala	Asp	Leu	Pro	Pro	Ala	Val
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Phe	Thr	Gly	Glu	Gly	Glu	Ala	Ala	Glu	Ala	Ala
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Met	Gln	Ile	Ala	Ala	Leu	Lys	Ala	Ser	Tyr	Leu
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cct	gca	gag	atc	atc	gag	aag	gag	cgc	tcc	atc
Pro	Ala	Glu	Ile	Ile	Glu	Lys	Glu	Arg	Ser	Ile
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cgc	gaa	gag	ggc	aag	cca	gag	gcn	gct	atc	cct
Arg	Glu	Glu	Gly	Lys	Pro	Glu	Gln	Ala	Ile	Pro
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cgt	ttg	aat	ggc	ttc	tac	aag	gag	aac	gta	ctt
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Arg	Leu	Asn	Gly	Phe	Tyr	Lys	Glu	Asn	Val	Leu	Leu	Glu	Gln	Ser	Ser	
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Lys	Asn	Ser	Asp	Phe	Lys	Glu	Phe	Ala	Ala	Lys	Val	Ala	Asp	Ala	Ala
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Ala	Ala	Ala	Lys	Ala	Asn	Ser	Gln	Glu	Glu	Leu	Ala	Ala	Val	Asp	Val
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Asp	Gly	Gln	Thr	Ala	Asp	Ala	Ala	Leu	Gln	Glu	Phe	Ser	Ala	Lys	Ile
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Gly	Glu	Lys	Leu	Glu	Leu	Arg	Arg	Ala	Val	Thr	Leu	Glu	Gly	Asp	Lys
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Thr	Ala	Val	Tyr	Leu	His	Gln	Arg	Ser	Ala	Asp	Leu	Pro	Pro	Ala	Val
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Gly	Val	Leu	Val	Ala	Phe	Thr	Gly	Glu	Gly	Glu	Ala	Ala	Glu	Ala	Ala
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Lys Ile Val Glu Gly Arg Leu Asn Gly Phe Tyr Lys Glu Asn Val Leu
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Val Leu Ile Val Val
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ggt gtt tat gcg ttg gtg ctg ttg aca ggc gat cgt tct gcc aca cca 163
Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro
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Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro
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cag ggg cag gat cca act cag gac cag ctg aat cag gca cgc acc att 259
Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile
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ctg gaa aac cgt gtg aac ggc atg ggc gtt tca ggt gca agc gtg gtc 307
Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val
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gct gac ggt aac acg ctg gtg atc act gtt ccc ggg gaa aat acc gca 355
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cag gcg caa tcc cta gga cag acc tcc cag ctg ctg ttc cgt ccc gtt 403
Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val
90 95 100

ggt cag gca gga atg ccc gat atg acc acg ttg atg cca gag ctg gaa 451
Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu
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gaa gcc tct gca act tgg tcc tct ctg acc agc cag tac ctg cag cag Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln 295 300 305			1027
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tac Tyr	tac Tyr	cgc Arg	gtc Val	ttc Phe	gga Gly	ttc Phe	ggt Val	tcc Ser	ctg Leu	ttc Phe	acc Thr	ctg Leu	ttt Phe	gcc Ala	gca Ala	1363
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ORGANIZATIONAL

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Lys

1965

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Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser
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Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro
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Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu
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Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu
100 105 110
Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val
115 120 125
Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala
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Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu
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Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile
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Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp
180 185 190
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Gln Cys Thr Thr Asp Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro
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Arg Leu Pro Leu Val Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val
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245 250 255
Ala Arg Leu Thr Gly Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly
260 265 270

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 Gln Tyr Leu Gln Gln Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile
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 Leu Arg Tyr Gly Ala Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu
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 Arg Gly Gly Thr Thr Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser
 370 375 380
 Leu Lys Ala Gly Leu Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala
 385 390 395
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 Thr Leu Phe Ala Ala Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu
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 485 490 495
 Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
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 Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
 515 520 525
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 530 535 540
 Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
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 Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
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 Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
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Asp Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr
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Arg Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu
50 55 60

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Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val
65 70 75 80

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Ser Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val
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Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln
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Leu Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr
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Leu Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly
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Val Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr
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Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val
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Ser Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val
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Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln
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Leu Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr
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Leu Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly
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Val Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr
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Ala Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro
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Glu Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser
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DECEMBER 2010

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 Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu
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 cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc 144
 Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile
 35 40 45
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 His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
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 act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag 240
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 35 40 45
 His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
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Met Thr Asp Ser Gln																		
1 5																		
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Thr Glu Ser Leu Ser Thr Gln Ser Val Lys Pro Ala Lys Lys Arg Ser																		
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Trp Phe Asn Ser Leu Tyr Thr Gly Asp Gly Gly Ile Asp Phe Ile Ala																		
25 30 35																		
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Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile Leu Leu Val Ile Ser																		
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Val Glu Glu Thr Thr Glu Ala Thr Gly Ile Thr Pro Glu Ile Val																		
90 95 100																		
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Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu Glu Ile Tyr Ser Gln																		
105 110 115																		
cga ctc agc gat gag gat gta gaa aaa gcc cgc ctg gcg atc tac gag																		499
Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg Leu Ala Ile Tyr Glu																		
120 125 130																		
gaa tac caa ccc cta aac tct gag ggc cag cca agc cca gat gcc atc																		547
Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro Ser Pro Asp Ala Ile																		
135 140 145																		
ggt aat tcc acg gtg tgc gaa tca tgg ggt tcc acc atc acc caa cgc																		595
Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser Thr Ile Thr Gln Arg																		
150 155 160 165																		
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Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile Ala Ala Ile Tyr Ile																		

2000

170										175										180										
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Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala Ala Met Ala Ala Leu																														
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Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr Ala Val Ile Gly Leu																														
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Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu Thr Val Leu Thr Phe																														
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Ser Ile Tyr Asp Thr Val Val Val Phe Asp Lys Val Arg Glu Asn Thr																														
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Glu Gly Phe Glu Gly Ser Arg Arg Thr Tyr Ala Glu Gln Ala Asn																														
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ctg gcg gtc aac cag acc ttc atg cgt tcg atc tcc acg aca atc atc	931																													
Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile Ser Thr Thr Ile Ile																														
265	270	275																												
tct gca ctt ccg atc atc gct ttg atg gtt gtc gcc gtc tgg atg atg	979																													
Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val Ala Val Trp Met Met																														
280	285	290																												
ggt gtt ggc acc ctc aaa gac ctc gca ctg atc cag ctg atc ggc gtc	1027																													
Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile Gln Leu Ile Gly Val																														
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Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala Thr Pro Leu Leu Val																														
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agc ctg aaa aac cgc ctg agc aaa acc aaa gcg cac acc gct tcc gtt	1123																													
Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala His Thr Ala Ser Val																														
330	335	340																												
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Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile Asp Ala Thr Pro His																														
345	350	355																												
acc aac gcc gac gcc ttc gcg cac ggc acc gaa agc gac act gac ggt	1219																													
Thr Asn Ala Asp Ala Phe Ala His Gly Thr Glu Ser Asp Thr Asp Gly																														
360	365	370																												
gtg acc ccc gaa gca cct gca aaa cgt aca gta agc aaa ccc att gtg	1267																													
Val Thr Pro Glu Ala Pro Ala Lys Arg Thr Val Ser Lys Pro Ile Val																														
375	380	385																												
gat gat cac cga tca agc gga acc tgg cga cca gcc aga agc	1309																													
Asp Asp His Arg Ser Ser Gly Thr Trp Arg Pro Gly Arg Ser																														
390	395	400																												
taaaccaatt ggagaacgaa gaa	1332																													

002290-662300

060928

Met	Thr	Asp	Ser	Gln	Thr	Glu	Ser	Leu	Ser	Thr	Gln	Ser	Val	Lys	Pro
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Ala	Lys	Lys	Arg	Ser	Trp	Phe	Asn	Ser	Leu	Tyr	Thr	Gly	Asp	Gly	Gly
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Ile	Asp	Phe	Ile	Ala	Lys	Thr	Lys	Leu	Trp	Tyr	Trp	Ile	Thr	Gly	Ile
		35					40					45			
Leu	Leu	Val	Ile	Ser	Ile	Leu	Phe	Ile	Ala	Ile	Arg	Gly	Phe	Ser	Leu
		50				55					60				
Ser	Ile	Asp	Phe	Gln	Gly	Gly	Thr	Lys	Met	Ser	Met	Pro	Ala	Ser	Asp
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Tyr	Ser	Thr	Glu	Gln	Val	Glu	Glu	Thr	Phe	Thr	Glu	Ala	Thr	Gly	Ile
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Thr	Pro	Glu	Ile	Val	Gln	Ile	Val	Gly	Ser	Gly	Asp	Ala	Arg	Thr	Leu
			100					105					110		
Glu	Ile	Tyr	Ser	Glu	Arg	Leu	Ser	Asp	Glu	Asp	Val	Glu	Lys	Ala	Arg
							120					125			
Leu	Ala	Ile	Tyr	Glu	Glu	Tyr	Gln	Pro	Leu	Asn	Ser	Glu	Gly	Gln	Pro
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Ser	Pro	Asp	Ala	Ile	Gly	Asn	Ser	Thr	Val	Ser	Glu	Ser	Trp	Gly	Ser
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Thr	Ile	Thr	Gln	Arg	Met	Val	Leu	Ala	Leu	Ile	Ala	Phe	Leu	Val	Ile
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Ala	Ala	Ile	Tyr	Ile	Ala	Phe	Arg	Leu	Glu	Arg	Glu	Met	Ala	Ile	Ala
			180					185					190		
Ala	Met	Ala	Ala	Leu	Val	Val	Asp	Gly	Ile	Val	Ile	Ala	Gly	Ile	Tyr
			195				200					205			
Ala	Val	Ile	Gly	Leu	Glu	Val	Ser	Pro	Ala	Thr	Val	Ile	Gly	Leu	Leu
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Thr	Val	Leu	Thr	Phe	Ser	Ile	Tyr	Asp	Thr	Val	Val	Val	Phe	Asp	Lys
					230					235					240
Val	Arg	Glu	Asn	Thr	Glu	Gly	Phe	Glu	Gly	Ser	Arg	Arg	Arg	Thr	Tyr
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Ala	Glu	Gln	Ala	Asn	Leu	Ala	Val	Asn	Gln	Thr	Phe	Met	Arg	Ser	Ile
			260					265					270		
Ser	Thr	Thr	Ile	Ile	Ser	Ala	Leu	Pro	Ile	Ile	Ala	Leu	Met	Val	Val
			275				280					285			
Ala	Val	Trp	Met	Met	Gly	Val	Gly	Thr	Leu	Lys	Asp	Leu	Ala	Leu	Ile

290	295	300
Gln Leu Ile Gly Val	Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala	
305	310	315
Thr Pro Leu Leu Val Ser Leu Lys Asn Arg	Leu Ser Lys Thr Lys Ala	
	325	330
His Thr Ala Ser Val Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile		
	340	345
Asp Ala Thr Pro His Thr Asn Ala Asp Ala Phe Ala His Gly Thr Glu		
	355	360
Ser Asp Thr Asp Gly Val Thr Pro Glu Ala Pro Ala Lys Arg Thr Val		
	370	375
Ser Lys Pro Ile Val Asp Asp His Arg Ser Ser Gly Thr Trp Arg Pro		
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		395
		400
Gly Arg Ser		

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 <213> Corynebacterium glutamicum

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 Val Ala Gly Phe Asp
 1 5
 tgg ttt tgg aag gcc ctt ggc ggc aaa tcg ggc aga aac caa aaa cgt 163
 Trp Phe Trp Lys Ala Leu Gly Gly Lys Ser Gly Arg Asn Gln Lys Arg
 10 15 20
 agc gtg gca att gtc aat cag gta gaa aac cat gca gcg gaa tta gac 211
 Ser Val Ala Ile Val Asn Gln Val Glu Asn His Ala Ala Glu Leu Asp
 25 30 35
 gcg ctg gat gat gtt gca ttg gcg cag cgt gcc aag gat cta gcc agt 259
 Ala Leu Asp Asp Val Ala Leu Ala Gln Arg Ala Lys Asp Leu Ala Ser
 40 45 50
 ggt gga cgc att gac aat cat gcg gaa ttc ctc gcc att ttg ggt gtg 307
 Gly Gly Arg Ile Asp Asn His Ala Glu Phe Leu Ala Ile Leu Gly Val
 55 60 65
 gca tcg cag cgg aca ttg ggg ctg aag ccg tat ccg gtg caa tca cag 355
 Ala Ser Gln Arg Thr Leu Gly Leu Lys Pro Tyr Pro Val Gln Ser Gln
 70 75 80 85

005290-682960
 09602839-062300

gcg gtg ttg cgt ctc att gaa ggc gat gtg gtg cac atg gct acc ggt 403
 Ala Val Leu Arg Leu Ile Glu Gly Asp Val Val His Met Ala Thr Gly
 90 95 100

gag ggc aag act ttg gtg ggc gcg atg gcg gcc acc ggt ctg ggg ttg 451
 Glu Gly Lys Thr Leu Val Gly Ala Met Ala Ala Thr Gly Leu Gly Leu
 105 110 115

atg ggc aag cga gtc cat tcg att acc gtc aat gat tat ttg gcg gtg 499
 Met Gly Lys Arg Val His Ser Ile Thr Val Asn Asp Tyr Leu Ala Val
 120 125 130

cgc gat gcc gaa tgg atg cgg cca ttg gtc gaa ttt ttc ggt ctg agc 547
 Arg Asp Ala Glu Trp Met Arg Pro Leu Val Glu Phe Phe Gly Leu Ser
 135 140 145

gtg gcg agc atc agc gag aag atg gat gca ggg gag cgt cga caa gca 595
 Val Ala Ser Ile Ser Glu Lys Met Asp Ala Gly Glu Arg Arg Gln Ala
 150 155 160 165

tat aaa gcc gca att gtc tac gga cct gtc aat gaa atc ggc ttt gac 643
 Tyr Lys Ala Ala Ile Val Tyr Gly Pro Val Asn Glu Ile Gly Phe Asp
 170 175 180

gtg ctg cgt gat cag cta att acc cgg cgc gaa gac gcc gtg cag cat 691
 Val Leu Arg Asp Gln Leu Ile Thr Arg Arg Glu Asp Ala Val Gln His
 185 190 195

ggc gcc gac gtc gcg att atc gat gag gcc gat tcc gtg ctt gtc gac 739
 Gly Ala Asp Val Ala Ile Ile Asp Glu Ala Asp Ser Val Leu Val Asp
 200 205 210

gag gcc ctg gtg cca ctc gtc ctc gcc ggc aac cag ccc gcc cat gcg 787
 Glu Ala Leu Val Pro Leu Val Leu Ala Gly Asn Gln Pro Gly His Ala
 215 220 225

ccg cgc ggc aaa atc acc gat gtg gtg cgc tcg ttg aaa gaa aac gac 835
 Pro Arg Gly Lys Ile Thr Asp Val Val Arg Ser Leu Lys Glu Asn Asp
 230 235 240 245

gat tac acc atc gac gat gat cgt cgc aac gtc ttc ctc acc gac aag 883
 Asp Tyr Thr Ile Asp Asp Arg Arg Asn Val Phe Leu Thr Asp Lys
 250 255 260

ggt gcc gcc aaa tta gag cag cag ctg gcc atc agc agc ctc tac gac 931
 Gly Ala Ala Lys Leu Glu Gln Gln Leu Gly Ile Ser Ser Leu Tyr Asp
 265 270 275

gat gag cac gtc ggc tcg acg ctc gtg cag gtc aac ctc gcc ctc cac 979
 Asp Glu His Val Gly Ser Thr Leu Val Gln Val Asn Leu Ala Leu His
 280 285 290

gcg cag gca ctg ctc atc cgc gac atc cac tac atc gtc cgc gac agc 1027
 Ala Gln Ala Leu Leu Ile Arg Asp Ile His Tyr Ile Val Arg Asp Ser
 295 300 305

aag gtc ttg ctt atc gac gcc tcc cgc ggc cgt gtc gcc gac ctg cag 1075
 Lys Val Leu Leu Ile Asp Ala Ser Arg Gly Arg Val Ala Asp Leu Gln
 310 315 320 325

cgc tgg ccc gac ggc ctg caa gca gca gtg gag gcc aag gaa ggt ctc 1123

00602339 002300

Arg	Trp	Pro	Asp	Gly 330	Leu	Gln	Ala	Ala 335	Val	Glu	Ala	Lys	Glu	Gly 340	Leu	
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tgt Leu	att Ile	ggt Gly 360	cgc Arg	tac Tyr	cca Pro	atg Met	gca Cys 365	tgc Cys	ggc Gly	atg Met	aca Thr	ggt Gly 370	acc Thr	gcc Ala	gtg Val	1219
gag Glu	gca Ala 375	acc Thr	gat Asp	cag Gln	cta Leu	cgc Arg 380	acc Thr	ttc Phe	tat Tyr	gac Asp	ttg Leu 385	cat His	ggt Val	tct Ser	gtc Val	1267
att Ile 390	gag Glu	cgc Arg	aat Asn	cat His	ccg Pro 395	ctg Leu	aag Lys	cgc Arg	ttt Phe	gat Asp 400	gaa Glu	gct Ala	gac Asp	cgt Arg	atc Ile 405	1315
tac Tyr	gcc Ala	acc Thr	atg Met	cgc Ala 410	gag Glu	aaa Lys	aac Asn	cgc Arg	gcc Ala 415	atc Ile	atc Ile	gat Asp	gaa Glu	atc Ile 420	gca Ala	1363
ctc Leu	ctt Leu	cac His	agc Ser 425	acg Thr	ggg Gly	cag Gln	cca Pro	gtc Val 430	ctg Leu	gtg Val	ggt Gly	acc Thr	cac His	gat Asp	gtg Val	1411
gca Ala	gag Glu	tgc Ser 440	gaa Glu	ctc Leu	gcc Ala	act Thr 445	gca Ala	ctg Leu	cgt Arg	gaa Glu	ctc Leu 450	aac Asn	atc Ile	gaa Glu		1459
gta Val	agc Ser	gtt Val	ctc Leu	aac Asn	gcc Ala	aag Lys 460	aat Asn	gat Asp	gcc Ala	gaa Glu	gaa Glu 465	gcc Ala	cag Gln	atc Ile	atc Ile	1507
gca Ala 470	gag Glu	gct Ala	ggc Gly	gat Asp	att Ile 475	gga Gly	cga Arg	gtg Val	acc Thr	ggt Val 480	tcc Ser	act Thr	cag Gln	atg Met	gcc Ala 485	1555
ggc Gly	cgc Arg	ggt Gly	acc Thr	gat Asp 490	att Ile	cgc Arg	ctc Leu	ggt Gly	ggc Gly 495	gcc Ala	gat Asp	gaa Glu	gcc Ala	gac Asp	tac Tyr	1603
gat Asp	gaa Glu	gtg Val	gtg Val 505	aaa Lys	ctc Leu	ggt Gly	gga Gly	ctc Leu 510	gcc Ala	ggt Val	atc Ile	ggc Thr	acc Thr 515	gcc Ala	cgc Arg	1651
cac His	cgt Ser	tct Ser	cag Gln	cgc Arg	ctg Leu	gac Asp	aac Asn 525	cag Gln	ctg Leu	cgc Arg	gga Gly	cgt Arg 530	gcg Ala	gga Gly	cga Arg	1699
caa Gln	gga Gly	gat Asp	cca Pro	ggc Gly	ctg Leu	agc Ser 540	ctt Leu	ttc Phe	ttt Phe	gtc Val	tcc Ser 545	ctc Leu	gat Asp	gat Asp	gat Asp	1747
gtg Val 550	gtg Val	gtc Val	tca Ser	ggc Gly 555	ggg Gly	tca Ser	agg Arg	gag Glu	agc Ser	gtg Val 560	agc Val	gcg Val	caa Gln	ccc Pro	gat Asp 565	1795
gcc Ala 1843	acc Thr	ggc Gly	ctg Leu	att Ile	gat Asp	tca Ser	gat Asp	cgc Ala	atc Ile	cgc Gat	gtg Trp	tgg Gln	gga Val	cac Gly		

	570	575	580	
tgc cag cgc gtc acc gaa gga cag ctg ctg gaa atc cac tcc cag agc				1891
Cys Gln Arg Val Thr Glu Gly Gln Leu Leu Glu Ile His Ser Gln Ser	585	590	595	
tggt aat tac aac aag ctc ctt gcc gat caa cgc gtg atc att gac gag				1939
Trp Asn Tyr Asn Lys Leu Leu Ala Asp Gln Arg Val Ile Asp Glu	600	605	610	
cgc cgc gaa cgc ctc ctc gac acc gcc tta gcg tgg gag gaa ctg gca				1987
Arg Arg Glu Arg Leu Leu Asp Thr Ala Leu Ala Trp Glu Glu Leu Ala	615	620	625	
cag cat gca cca gcg cgg gct gca gag ctt gaa gac ctt gat cag tcc				2035
Gln His Ala Pro Ala Arg Ala Ala Glu Leu Glu Asp Leu Asp Gln Ser	630	635	640	645
gtg agg gaa cag gca gca cga gac atc atg ctg tac cac ctc gat tac				2083
Val Arg Glu Gln Ala Ala Arg Asp Ile Met Leu Tyr His Leu Asp Tyr	650	655	660	
aac tgg tca gag cac ctc gcg ttg atg gat gat gtc cgc gaa tcc att				2131
Asn Trp Ser Glu His Leu Ala Leu Met Asp Asp Val Arg Glu Ser Ile	665	670	675	
cac ctg cgc gcc atc gcc agg gaa acc ccc ctt gat gaa tac cac cgc				2179
His Leu Arg Ala Ile Ala Arg Glu Thr Pro Leu Asp Glu Tyr His Arg	680	685	690	
atc gct gtg cgt gaa ttc aag gat ttg gca caa cgc gct gtc gat gat				2227
Ile Ala Val Arg Glu Phe Lys Asp Leu Ala Gln Arg Ala Val Asp Asp	695	700	705	
gcg gtg tcc acg ttc aag tct gtg acc atc gat cac gag ggt gcc cat				2275
Ala Val Ser Thr Phe Lys Ser Val Thr Ile Asp His Glu Gly Ala His	710	715	720	725
ttg gat gat gag gcc ttg gcg cgt cca tca gca acg tgg acc tac atg				2323
Leu Asp Asp Glu Gly Leu Ala Arg Pro Ser Ala Thr Trp Thr Tyr Met	730	735	740	
gtc tct gac aac cca ctt gcg ggt agt ggt aac tca gtg atc agt gcc				2371
Val Ser Asp Asn Pro Leu Ala Gly Ser Gly Asn Ser Val Ile Ser Gly	745	750	755	
ata gga aat atc ttt aga taacctgaga actatgaaat tcc				2412
Ile Gly Asn Ile Phe Arg	760			

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<212> PRT

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 Ala Ala Glu Leu Asp Ala Leu Asp Val Ala Leu Ala Gln Arg Ala
 35 40 45
 Lys Asp Leu Ala Ser Gly Gly Arg Ile Asp Asn His Ala Glu Phe Leu
 50 55 60
 Ala Ile Leu Gly Val Ala Ser Gln Arg Thr Leu Gly Leu Lys Pro Tyr
 65 70 75 80
 Pro Val Gln Ser Gln Ala Val Leu Arg Leu Ile Glu Gly Asp Val Val
 85 90 95
 His Met Ala Thr Gly Glu Gly Lys Thr Leu Val Gly Ala Met Ala Ala
 100 105 110
 Thr Gly Leu Gly Leu Met Gly Lys Arg Val His Ser Ile Thr Val Asn
 115 120 125
 Asp Tyr Leu Ala Val Arg Asp Ala Glu Trp Met Arg Pro Leu Val Glu
 130 135 140
 Phe Phe Gly Leu Ser Val Ala Ser Ile Ser Glu Lys Met Asp Ala Gly
 145 150 155 160
 Glu Arg Arg Gln Ala Tyr Lys Ala Ala Ile Val Tyr Gly Pro Val Asn
 165 170 175
 Glu Ile Gly Phe Asp Val Leu Arg Asp Gln Leu Ile Thr Arg Arg Glu
 180 185 190
 Asp Ala Val Gln His Gly Ala Asp Val Ala Ile Ile Asp Glu Ala Asp
 195 200 205
 Ser Val Leu Val Asp Glu Ala Leu Val Pro Leu Val Leu Ala Gly Asn
 210 215 220
 Gln Pro Gly His Ala Pro Arg Gly Lys Ile Thr Asp Val Val Arg Ser
 225 230 235 240
 Leu Lys Glu Asn Asp Asp Tyr Thr Ile Asp Asp Asp Arg Arg Asn Val
 245 250 255
 Phe Leu Thr Asp Lys Gly Ala Ala Lys Leu Glu Gln Gln Leu Gly Ile
 260 265 270
 Ser Ser Leu Tyr Asp Asp Glu His Val Gly Ser Thr Leu Val Gln Val
 275 280 285
 Asn Leu Ala Leu His Ala Gln Ala Leu Leu Ile Arg Asp Ile His Tyr
 290 295 300
 Ile Val Arg Asp Ser Lys Val Leu Leu Ile Asp Ala Ser Arg Gly Arg
 305 310 315 320
 Val Ala Asp Leu Gln Arg Trp Pro Asp Gly Leu Gln Ala Ala Val Glu
 325 330 335
 Ala Lys Glu Gly Leu Ala Val Ser Glu Gly Gly Lys Ile Leu Asp Thr
 340 345 350

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Ile Thr Leu Gln Ala Leu Ile Gly Arg Tyr Pro Met Ala Cys Gly Met
 355 360 365
 Thr Gly Thr Ala Val Glu Ala Thr Asp Gln Leu Arg Thr Phe Tyr Asp
 370 375 380
 Leu His Val Ser Val Ile Glu Arg Asn His Pro Leu Lys Arg Phe Asp
 385 390 395 400
 Glu Ala Asp Arg Ile Tyr Ala Thr Met Ala Glu Lys Asn Arg Ala Ile
 405 410 415
 Ile Asp Glu Ile Ala Leu Leu His Ser Thr Gly Gln Pro Val Leu Val
 420 425 430
 Gly Thr His Asp Val Ala Glu Ser Glu Glu Leu Ala Thr Ala Leu Arg
 435 440 445
 Glu Leu Asn Ile Glu Val Ser Val Leu Asn Ala Lys Asn Asp Ala Glu
 450 455 460
 Glu Ala Gln Ile Ile Ala Glu Ala Gly Asp Ile Gly Arg Val Thr Val
 465 470 475 480
 Ser Thr Gln Met Ala Gly Arg Gly Thr Asp Ile Arg Leu Gly Gly Ala
 485 490 495
 Asp Glu Ala Asp Tyr Asp Glu Val Val Lys Leu Gly Gly Leu Ala Val
 500 505 510
 Ile Gly Thr Ala Arg His Arg Ser Gln Arg Leu Asp Asn Gln Leu Arg
 515 520 525
 Gly Arg Ala Gly Arg Gln Gly Asp Pro Gly Leu Ser Leu Phe Phe Val
 530 535 540
 Ser Leu Asp Asp Asp Val Val Val Ser Gly Gly Ser Arg Glu Ser Val
 545 550 555 560
 Ser Ala Gln Pro Asp Ala Thr Gly Leu Ile Asp Ser Asp Arg Ile Arg
 565 570 575
 Asp Trp Val Gly His Cys Gln Arg Val Thr Glu Gly Gln Leu Leu Glu
 580 585 590
 Ile His Ser Gln Ser Trp Asn Tyr Asn Lys Leu Leu Ala Asp Gln Arg
 595 600 605
 Val Ile Ile Asp Glu Arg Arg Glu Arg Leu Leu Asp Thr Ala Leu Ala
 610 615 620
 Trp Glu Glu Leu Ala Gln His Ala Pro Ala Arg Ala Ala Glu Leu Glu
 625 630 635 640
 Asp Leu Asp Gln Ser Val Arg Glu Gln Ala Ala Arg Asp Ile Met Leu
 645 650 655
 Tyr His Leu Asp Tyr Asn Trp Ser Glu His Leu Ala Leu Met Asp Asp
 660 665 670

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Val	Arg	Glu	Ser	Ile	His	Leu	Arg	Ala	Ile	Ala	Arg	Glu	Thr	Pro	Leu
675							680					685			
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690						695					700				
Arg	Ala	Val	Asp	Asp	Ala	Val	Ser	Thr	Phe	Lys	Ser	Val	Thr	Ile	Asp
705					710					715					720
His	Glu	Gly	Ala	His	Leu	Asp	Asp	Glu	Gly	Leu	Ala	Arg	Pro	Ser	Ala
				725					730					735	
Thr	Trp	Thr	Tyr	Met	Val	Ser	Asp	Asn	Pro	Leu	Ala	Gly	Ser	Gly	Asn
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	Val Phe Glu Ser Leu	5
	1	
tcc gat cgg ttg aat agc gcg ctt tcc ggc ctg cgc ggc aaa gga aag	163	
Ser Asp Arg Leu Asn Ser Ser Ala Leu Ser Gly Leu Arg Gly Lys Gly Lys	20	
	10 15	
ctc acc gag gca gac atc aat gca acc aca cgc gag atc cgt ctc gcg	211	
Leu Thr Glu Ala Ala Asp Ile Asn Ala Thr Thr Arg Glu Ile Arg Leu Ala	25 30 35	
	25	
ctg ctg gaa gct gac gtt tca tta acg gtt gtt cgt gcc ttc att aac	259	
Leu Leu Glu Ala Asp Val Ser Leu Thr Val Val Arg Ala Phe Ile Asn	40 45 50	
	40	
cga atc aag gaa cgc gcc gct ggt gca gaa gtt tct cag gca ctc aac	307	
Arg Ile Lys Glu Arg Ala Ala Gly Ala Glu Val Ser Gln Ala Leu Asn	55 60 65	
	55	
ccc gcg cag caa gtc atc aag atc gtc aac gag gaa ctg gtt cag atc	355	
Pro Ala Gln Gln Val Ile Lys Ile Val Asn Glu Glu Leu Val Gln Ile	70 75 80 85	
	75	
ctc ggt ggc gaa acc cgc cga ctg tca ctg gcc aaa aac cca ccg acc	403	
Leu Gly Gly Glu Thr Arg Arg Leu Ser Leu Ala Lys Asn Pro Pro Thr	90 95 100	
	90	
gtc atc atg ctg gca ggt ctg cag ggt gca ggt aag acc acc ctc gca	451	

Val Ile Met Leu Ala Gly Leu Gln Gly Ala Gly Lys Thr Thr Leu Ala
105 110 115

ggt aaa ctg tcc aag cac ctg gtc aag cag ggt cac act cct atg ctt 499
Gly Lys Leu Ser Lys His Leu Val Lys Gln Gly His Thr Pro Met Leu
120 125 130

gtt gcc tgt gac ctt cag cgt cca ggc gca gtt cag cag ctg caa att 547
Val Ala Cys Asp Leu Gln Arg Pro Gly Ala Val Gln Gln Leu Gln Ile
135 140 145

gtg ggt gaa cgc gca ggc gtt acc act ttc gca ccg gat cca ggc acc 595
Val Gly Glu Arg Ala Gly Val Thr Thr Phe Ala Pro Asp Pro Gly Thr
150 155 160 165

agc atc gac tcc ctc gag cac gaa atg ggc acc tcc cac ggt gat cca 643
Ser Ile Asp Ser Leu Glu His Glu Met Gly Thr Ser His Gly Asp Pro
170 175 180

gtc gag gta gcg cgc gca ggt atc gaa gaa gcc aag cgc acc cag cac 691
Val Glu Val Ala Arg Ala Gly Ile Glu Glu Ala Lys Arg Thr Gln His
185 190 195

gac atc gtg atc gtg gat acc gca ggt cgc ctc ggt atc gat gaa acc 739
Asp Ile Val Ile Val Asp Thr Ala Gly Arg Leu Gly Ile Asp Glu Thr
200 205 210

ctg atg act cag gca cgc aac atc cgc gaa gcc atc aac cct gat gaa 787
Leu Met Thr Gln Ala Arg Asn Ile Arg Glu Ala Ile Asn Pro Asp Glu
215 220 225

gtg ctc ttt gtc att gac tcc atg att ggt caa gac gcc gta gac acc 835
Val Leu Phe Val Ile Asp Ser Met Ile Gly Gln Asp Ala Val Asp Thr
230 235 240 245

gcc gaa gca ttc cgc gac ggc gtc gac ttc acc ggt gtt gtc ctg acc 883
Ala Glu Ala Phe Arg Asp Gly Val Asp Phe Thr Gly Val Val Leu Thr
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aag ctt gat ggc gac gcc cgc ggt ggt gct gca cta tcc atc cgt gaa 931
Lys Leu Asp Gly Asp Ala Arg Gly Gly Ala Ala Leu Ser Ile Arg Glu
265 270 275

gtc acc ggc aag ccc atc atg ttt gcc tcc act ggt gaa aaa ctc gac 979
Val Thr Gly Lys Pro Ile Met Phe Ala Ser Thr Gly Glu Lys Leu Asp
280 285 290

gac ttc gac gtc ttc cac cca gag cgc atg gcc agc cga atc ctg ggc 1027
Asp Phe Asp Val Phe His Pro Glu Arg Met Ala Ser Arg Ile Leu Gly
295 300 305

atg ggt gac gta ctg tca ctc atc gag cag gcc gaa gca gtc atg gat 1075
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310 315 320 325

cag gaa aag gca gag gtc gct gcc cag aag ttg ggc tcc ggc gag ctc 1123
Gln Glu Lys Ala Glu Val Ala Ala Gln Lys Leu Gly Ser Gly Glu Leu
330 335 340

acc ctg gaa gac ttc ctt gac caa atg ctg atg atc cgc cgc atg gga 1171
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345	350	355	
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caa atg gcg gac atg gtt gat gag aag caa ctc gac cgc atc cag gcg Gln Met Ala Asp Met Val Thr Asp Gln Lys Gln Leu Asp Arg Ile Gln Ala 375 380 385			1267
att atc cgc ggt atg acc ccg gcc gag cgc gat aat cca aag atc ctc Ile Ile Arg Gly Met Thr Pro Ala Glu Arg Asp Asn Pro Lys Ile Leu 390 395 400 405			1315
aac gct tcc agg cgc aag cgc atc gcc aac ggt tcc ggt gtg acc gtg Asn Ala Ser Arg Arg Lys Arg Ile Ala Asn Gly Ser Gly Val Thr Val 410 415 420			1363
tcc gaa gta aac aaa ctt gtt gaa cgc ttc ttc gag gct cgc aag atg Ser Glu Val Asn Lys Leu Val Glu Arg Phe Phe Glu Ala Arg Lys Met 425 430 435			1411
atg ggt caa atg gct ggc cag ttt ggc atg ggt cct gga tcc cgc agt Met Gly Gln Met Ala Gly Gln Phe Gly Met Gly Pro Gly Ser Arg Ser 440 445 450			1459
gca acc aag aag caa gcc aag ggc cgc aag ggt aag aac gcc aag cgt Ala Thr Lys Lys Gln Ala Lys Gly Arg Lys Gly Lys Asn Gly Lys Arg 455 460 465			1507
aaa cca gcc aag aag ggc cca acc cag cca aag atg cca atg ggc ggt Lys Pro Ala Lys Lys Gly Pro Thr Gln Pro Lys Met Pro Met Gly Gly 470 475 480 485			1555
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<212> PRT

<213> Corynebacterium glutamicum

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Arg Gly Lys Gly Lys Leu Thr Glu Ala Asp Ile Asn Ala Thr Thr Arg
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 Glu Ile Arg Leu Ala Leu Leu Glu Ala Asp Val Ser Leu Thr Val Val
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 Arg Ala Phe Ile Asn Arg Ile Lys Glu Arg Ala Ala Gly Ala Glu Val
 50 55 60
 Ser Gln Ala Leu Asn Pro Ala Gln Gln Val Ile Lys Ile Val Asn Glu
 65 70 75 80
 Glu Leu Val Gln Ile Leu Gly Gly Glu Thr Arg Arg Leu Ser Leu Ala
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 Lys Asn Pro Pro Thr Val Ile Met Leu Ala Gly Leu Gln Gly Ala Gly
 100 105 110
 Lys Thr Thr Leu Ala Gly Lys Leu Ser Lys His Leu Val Lys Gln Gly
 115 120 125
 His Thr Pro Met Leu Val Ala Cys Asp Leu Gln Arg Pro Gly Ala Val
 130 135 140
 Gln Gln Leu Gln Ile Val Gly Glu Arg Ala Gly Val Thr Thr Phe Ala
 145 150 155 160
 Pro Asp Pro Gly Thr Ser Ile Asp Ser Leu Glu His Glu Met Gly Thr
 165 170 175
 Ser His Gly Asp Pro Val Glu Val Ala Arg Ala Gly Ile Glu Glu Ala
 180 185 190
 Lys Arg Thr Gln His Asp Ile Val Ile Val Asp Thr Ala Gly Arg Leu
 195 200 205
 Gly Ile Asp Glu Thr Leu Met Thr Gln Ala Arg Asn Ile Arg Glu Ala
 210 215 220
 Ile Asn Pro Asp Glu Val Leu Phe Val Ile Asp Ser Met Ile Gly Gln
 225 230 235 240
 Asp Ala Val Asp Thr Ala Glu Ala Phe Arg Asp Gly Val Asp Phe Thr
 245 250 255
 Gly Val Val Leu Thr Lys Leu Asp Gly Asp Ala Arg Gly Gly Ala Ala
 260 265 270
 Leu Ser Ile Arg Glu Val Thr Gly Lys Pro Ile Met Phe Ala Ser Thr
 275 280 285
 Gly Glu Lys Leu Asp Asp Phe Asp Val Phe His Pro Glu Arg Met Ala
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 Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu Ile Glu Gln Ala
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              Val Thr Asp Phe Ser
              1          5
aqt gct tca aat gct gac gat tcc acg cag gac ggt cgt cct ggt cga      163

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Ser	Ala	Ser	Asn	Ala	Asp	Asp	Ser	Thr	Gln	Asp	Gly	Arg	Pro	Gly	Arg	
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cgt	gct	gga	aag	tct	aag	aag	gaa	tcg	aag	cca	act	ccg	tgg	tac	atc	211
Arg	Ala	Gly	Lys	Ser	Lys	Lys	Glu	Ser	Lys	Pro	Thr	Pro	Trp	Tyr	Ile	
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gaa	att	cca	gtg	gtt	gtg	gtt	ttg	acc	ctc	gcg	ctg	att	ttc	gtg	ctc	259
Glu	Ile	Pro	Val	Val	Val	Val	Leu	Thr	Leu	Ala	Leu	Ile	Phe	Val	Leu	
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cag	acg	ttt	gtc	gga	cgc	atg	tac	atg	att	ccg	agt	ggg	tgc	atg	gaa	307
Gln	Thr	Phe	Val	Gly	Arg	Met	Tyr	Met	Ile	Pro	Ser	Gly	Ser	Met	Glu	
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Pro	Thr	Leu	His	Gly	Cys	Glu	Gly	Cys	Thr	Gly	Asp	Arg	Ile	Leu	Val	
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Glu	Lys	Val	Ser	Tyr	Tyr	Phe	Thr	Asp	Pro	Glu	Pro	Gly	Asp	Val	Val	
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Val	Phe	Lys	Gly	Thr	Asp	Ser	Trp	Asn	Val	Gly	Phe	Thr	Thr	Gln	Arg	
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tcc	gat	aat	tgc	gtg	atc	cgc	ggc	ctg	cag	aac	ctg	ggg	tct	tac	gtg	499
Ser	Asp	Asn	Ser	Val	Ile	Arg	Gly	Leu	Gln	Asn	Leu	Gly	Ser	Tyr	Val	
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ggg	ctt	gtc	gca	cct	gat	gaa	aat	gac	ctg	gtc	aag	cgc	att	atc	gcc	547
Gly	Leu	Val	Ala	Pro	Asp	Glu	Asn	Asp	Leu	Val	Lys	Arg	Ile	Ile	Ala	
				135					140					145		
acc	ggc	ggg	cag	act	gtt	tgc	tgc	caa	gcc	ggg	gat	cct	gga	atc	atg	595
Thr	Gly	Gly	Gln	Thr	Val	Ser	Cys	Gln	Ala	Gly	Asp	Pro	Gly	Ile	Met	
				150					155					160		
gtt	gac	ggc	aag	gaa	gtc	gat	gac	agc	tac	acg	ctg	caa	cct	gca	caa	643
Val	Asp	Gly	Lys	Glu	Val	Asp	Asp	Ser	Tyr	Thr	Thr	Leu	Gln	Pro	Ala	
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ttc	ccc	atc	gat	gag	acc	tcc	ggg	tcc	acc	gaa	tgc	ggc	ggc	aac	tat	691
Phe	Pro	Ile	Asp	Glu	Thr	Ser	Gly	Ser	Thr	Glu	Cys	Gly	Gly	Asn	Tyr	
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ttc	ggc	ccc	atc	acc	gtg	cct	ggc	ggc	aac	tac	ttc	atg	atg	ggg	gac	739
Phe	Gly	Pro	Ile	Thr	Val	Pro	Gly	Gly	Asn	Tyr	Phe	Met	Met	Gly	Asp	
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aac	cgc	acc	aac	tcc	atg	gat	tcc	cgc	tac	cac	ctg	ggc	gat	cag	tac	787
Asn	Arg	Thr	Asn	Ser	Met	Asp	Ser	Arg	Tyr	His	Leu	Gly	Asp	Gln	Tyr	
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caa	gga	acc	atc	cct	gag	gaa	aac	atc	aag	ggc	aaa	gtt	caa	gca	att	835
Gln	Gly	Thr	Ile	Pro	Glu	Glu	Asn	Ile	Lys	Gly	Lys	Val	Gln	Ala	Ile	
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255

260

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Gly

909

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<212> PRT

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50 55 60

Ser Gly Ser Met Glu Pro Thr Leu His Gly Cys Glu Gly Cys Thr Gly
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Asp Arg Ile Leu Val Glu Lys Val Ser Tyr Tyr Phe Thr Asp Pro Glu
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Pro Gly Asp Val Val Val Phe Lys Gly Thr Asp Ser Trp Asn Val Gly
100 105 110

Phe Thr Thr Gln Arg Ser Asp Asn Ser Val Ile Arg Gly Leu Gln Asn
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Leu Gly Ser Tyr Val Gly Leu Val Ala Pro Asp Glu Asn Asp Leu Val
130 135 140

Lys Arg Ile Ile Ala Thr Gly Gly Gln Thr Val Ser Cys Gln Ala Gly
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Asp Pro Gly Ile Met Val Asp Gly Lys Glu Val Asp Asp Ser Tyr Thr
165 170 175

Leu Gln Pro Ala Gln Phe Pro Ile Asp Glu Thr Ser Gly Ser Thr Glu
180 185 190

Cys Gly Gly Asn Tyr Phe Gly Pro Ile Thr Val Pro Gly Gly Asn Tyr
195 200 205

Phe Met Met Gly Asp Asn Arg Thr Asn Ser Met Asp Ser Arg Tyr His
210 215 220

Leu Gly Asp Gln Tyr Gln Gly Thr Ile Pro Glu Glu Asn Ile Lys Gly
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Lys Val Gln Ala Ile Ile Leu Pro Phe Ser Arg Ile Gly Gly Val Asp
245 250 255

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Asp Pro Ala Ile Lys Gly
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<223> RXA00107

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Met Ser Asn Val Thr 5
att tac gcc aca gat tgg tgc cct tac tgc cga tcc ctc ctc aaa ggt 163
Ile Tyr Ala Thr Asp Trp Cys Pro Tyr Cys Arg Ser Leu Leu Lys Gly 20
10 15
ctc gac ggc caa gag tac gac ctc atc gac gtc gac caa gat gag gaa 211
Leu Asp Gly Gln Glu Tyr Asp Leu Ile Asp Val Asp Gln Asp Glu Glu 35
25 30
gcc ggc gag tgg gtt aag tca gtc aac gac ggc aac cgc atc gtc cca 259
Ala Gly Glu Trp Val Lys Ser Val Asn Asp Gly Asn Arg Ile Val Pro 50
40 45
acc gtg cgc tac tcc gat ggc acc cac gca act aat ccc cta gct gcg 307
Thr Val Arg Tyr Ser Asp Gly Thr His Ala Thr Asn Pro Leu Ala Ala 60 65
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Glu Val Ile Ala Lys Ile Glu Ala Leu Ala 75
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tcg 360

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35 40
Asn Arg Ile Val Pro Thr Val Arg Tyr Ser Asp Gly Thr His Ala Thr 60
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Asn Pro Leu Ala Ala Glu Val Ile Ala Lys Ile Glu Ala Leu Ala
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Met Ser Glu Gln Pro
1 5
gct tcc att aag cat tat gac ctc atc atc att ggt acc ggc tct gga 163
Ala Ser Ile Lys His Tyr Asp Leu Ile Ile Gly Thr Gly Ser Gly
10 15 20
aac tcc att cct gga cca gag ttt gat gat aaa tca att gcc atc gtg 211
Asn Ser Ile Pro Gly Pro Glu Phe Asp Asp Lys Ser Ile Ala Ile Val
25 30 35
gaa aag ggt gct ttc ggc gga act tgc ctc aat gtg ggc tgc atc cct 259
Glu Lys Gly Ala Phe Gly Gly Thr Cys Leu Asn Val Gly Cys Ile Pro
40 45 50
acc aag atg tac gtt tac gct gcg gat atc gct caa gaa att cag gag 307
Thr Lys Met Tyr Val Tyr Ala Ala Asp Ile Ala Gln Glu Ile Gln Glu
55 60 65
tct gct cgc ctg ggt atc gat gcg acg gtc aac agc gtg gat tgg cct 355
Ser Ala Arg Leu Gly Ile Asp Ala Thr Val Asn Ser Val Asp Trp Pro
70 75 80 85
tcc atc gtc agc cgc gtt ttc gac aag cgc atc gac ctc atc gcg caa 403
Ser Ile Val Ser Arg Val Phe Asp Lys Arg Ile Asp Leu Ile Ala Gln
90 95 100
ggc ggc gag gct tat cga cgt ggc ccc gaa act cca aac atc gat gtg 451
Gly Gly Glu Ala Tyr Arg Arg Gly Pro Glu Thr Pro Asn Ile Asp Val
105 110 115
tat gac atg cac gca tcg ttt gtt gat tcc aag aca atc tcc act ggt 499
Tyr Asp Met His Ala Ser Phe Val Asp Ser Lys Thr Ile Ser Thr Gly
120 125 130
att gcc ggc caa gaa cag ctg atc agc ggt act gac att gta atc gca 547
Ile Ala Gly Gln Glu Gln Leu Ile Ser Gly Thr Asp Ile Val Ile Ala
135 140 145
acc ggc tcc cgc cct tac atc cct gaa gct att gca gag tcc ggc gca 595
Thr Gly Ser Arg Pro Tyr Ile Pro Glu Ala Ile Ala Glu Ser Gly Ala
150 155 160 165

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 Arg Tyr Tyr Thr Asn Glu Asp Ile Met Arg Leu Ala Gln Gln Pro Glu
 170 175 180

tct ttg gtg att gtt ggt ggc ggt ttc atc gct ttg gaa ttt gct cac 691
 Ser Leu Val Ile Val Gly Gly Gly Phe Ile Ala Leu Glu Phe Ala His
 185 190 195

gtt ttt gaa gcg ctt ggc acc aag gtc acc atc ctc aac cgc tct gac 739
 Val Phe Glu Ala Leu Gly Thr Lys Val Thr Ile Leu Asn Arg Ser Asp
 200 205 210

gtg ctg ctg cgc gag gca gat gca gac atc tcc gcg aaa atc ctc gag 787
 Val Leu Leu Arg Glu Ala Asp Ala Asp Ile Ser Ala Lys Ile Leu Glu
 215 220 225

ctt tcc aaa aag cgt ttc gac gtc cgc ctc agc act gcg gtc acc gca 835
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 Val His Asn Lys Ala Asp Gly Gly Val Lys Ile Ser Thr Asp Thr Gly
 250 255 260

gac gac atc gag gca gat att ttg ctc gtt gcc act ggt cgc acc cct 931
 Asp Asp Ile Glu Ala Asp Ile Leu Leu Val Ala Thr Gly Arg Thr Pro
 265 270 275

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 Asn Gly Asn Gln Met Asn Leu Asp Ala Ala Gly Ile Glu Met Asn Gly
 280 285 290

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 295 300 305

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 310 315 320 325

aat gcg gaa atg cga gca atc aag cac aac ctt gcc aac cct aat gac 1123
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 330 335 340

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 345 350 355

cct cag atc tcg cag gtc ggc atg act gag cag gag gcg cgt gaa gct 1219
 Pro Gln Ile Ser Gln Val Gly Met Thr Glu Gln Ala Arg Glu Ala
 360 365 370

ggc ctc gac atc act gtg aag atc cag aac tac tct gat gtg gct tat 1267
 Gly Leu Asp Ile Thr Val Lys Ile Gln Asn Tyr Ser Asp Val Ala Tyr
 375 380 385

ggc tgg gcc atg gaa gat aag gat gga ttc gtt aag ctc aat tgc cga 1315
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1338

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<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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 35 40 45

Val Gly Cys Ile Pro Thr Lys Met Tyr Val Tyr Ala Ala Asp Ile Ala
 50 55 60

Gln Glu Ile Gln Glu Ser Ala Arg Leu Gly Ile Asp Ala Thr Val Asn
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Ser Val Asp Trp Pro Ser Ile Val Ser Arg Val Phe Asp Lys Arg Ile
 85 90 95

Asp Leu Ile Ala Gln Gly Gly Glu Ala Tyr Arg Arg Gly Pro Glu Thr
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Pro Asn Ile Asp Val Tyr Asp Met His Ala Ser Phe Val Asp Ser Lys
 115 120 125

Thr Ile Ser Thr Gly Ile Ala Gly Gln Glu Gln Leu Ile Ser Gly Thr
 130 135 140

Asp Ile Val Ile Ala Thr Gly Ser Arg Pro Tyr Ile Pro Glu Ala Ile
 145 150 155 160

Ala Glu Ser Gly Ala Arg Tyr Tyr Thr Asn Glu Asp Ile Met Arg Leu
 165 170 175

Ala Gln Gln Pro Glu Ser Leu Val Ile Val Gly Gly Gly Phe Ile Ala
 180 185 190

Leu Glu Phe Ala His Val Phe Glu Ala Leu Gly Thr Lys Val Thr Ile
 195 200 205

Leu Asn Arg Ser Asp Val Leu Leu Arg Glu Ala Asp Ala Asp Ile Ser
 210 215 220

Ala Lys Ile Leu Glu Leu Ser Lys Lys Arg Phe Asp Val Arg Leu Ser
 225 230 235 240

Thr Ala Val Thr Ala Val His Asn Lys Ala Asp Gly Gly Val Lys Ile
 245 250 255

Ser Thr Asp Thr Gly Asp Asp Ile Glu Ala Asp Ile Leu Leu Val Ala
 260 265 270

Thr Gly Arg Thr Pro Asn Gly Asn Gln Met Asn Leu Asp Ala Ala Gly

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275

280

285

Ile Glu Met Asn Gly Arg Ser Ile Lys Val Asp Glu Phe Gly Arg Thr
290 295 300

Ser Val Glu Gly Val Trp Ala Leu Gly Asp Val Ser Ser Pro Tyr Lys
305 310 315 320

Leu Lys His Val Ala Asn Ala Glu Met Arg Ala Ile Lys His Asn Leu
325 330 335

Ala Asn Pro Asn Asp Leu Gln Lys Met Pro His Asp Phe Val Pro Ser
340 345 350

Ala Val Phe Thr Asn Pro Gln Ile Ser Gln Val Gly Met Thr Glu Gln
355 360 365

Glu Ala Arg Glu Ala Gly Leu Asp Ile Thr Val Lys Ile Gln Asn Tyr
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Lys Leu Asn Cys Arg
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<223> RXA00539

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Met Thr Ser Ile His
1 5

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Asp Ile Ser Val Thr Leu Asn Asp Gly Thr Glu Thr Thr Met Ala Asp
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tgg gcg ggc cac ctt ttg ctc atc gtg aac gtg gca tcc aag tgc gga 211
Trp Ala Gly His Leu Leu Leu Ile Val Asn Val Ala Ser Lys Cys Gly
25 30 35

ctc acg cca cag tat gaa ggg ctt caa aaa ctg tat gag gaa tac caa 259
Leu Thr Pro Gln Tyr Glu Gly Leu Gln Lys Leu Tyr Glu Glu Tyr Gln
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gat cga ggc ttc ttt gtc att ggc gtg ccc tgc aat caa ttc aac ggc 307
Asp Arg Gly Phe Phe Val Ile Gly Val Pro Cys Asn Gln Phe Asn Gly
55 60 65

cag gaa cct gga acc gac gct gag gtg tgt gct ttc gcg caa aat cag 355

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 Tyr Asp Val Thr Phe Pro Leu Leu Ser Lys Thr Glu Val Asn Gly Glu
 90 95 100
 ggt gcc cac ccc ctg tac aag gtg ctc aaa gag gca act gat ggt agc 451
 Gly Ala His Pro Leu Tyr Lys Val Leu Lys Glu Ala Thr Asp Gly Ser
 105 110 115
 gaa atc gag tgg aat ttt gag aaa ttc ctg gta gat gca gaa ggt aat 499
 Glu Ile Glu Trp Asn Phe Glu Lys Phe Leu Val Asp Ala Glu Gly Asn
 120 125 130
 acg att aag cgc ttt gct cct cgg acg gaa cca tct gca gct gag gta 547
 Thr Ile Lys Arg Phe Ala Pro Arg Thr Glu Pro Ser Ala Ala Glu Val
 135 140 145
 gtg gaa gca atc gag gag aat ctc cct atc taagggtggtg ctagggttga 597
 Val Glu Ala Ile Glu Glu Asn Leu Pro Ile
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 cca 600
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 <213> *Corynebacterium glutamicum*
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 Ala Ser Lys Cys Gly Leu Thr Pro Gln Tyr Glu Gly Leu Gln Lys Leu
 35 40 45
 Tyr Glu Glu Tyr Gln Asp Arg Gly Phe Phe Val Ile Gly Val Pro Cys
 50 55 60
 Asn Gln Phe Asn Gly Gln Glu Pro Gly Thr Asp Ala Glu Val Cys Ala
 65 70 75 80
 Phe Ala Gln Asn Gln Tyr Asp Val Thr Phe Pro Leu Leu Ser Lys Thr
 85 90 95
 Glu Val Asn Gly Glu Gly Ala His Pro Leu Tyr Lys Val Leu Lys Glu
 100 105 110
 Ala Thr Asp Gly Ser Glu Ile Glu Trp Asn Phe Glu Lys Phe Leu Val
 115 120 125
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 <211> 870
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(847)
 <223> RXA01020

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 Met Thr Asn Thr Leu
 1 5
 tgg aat tca gta gac gaa ctc ccc atc cac gac tcc tgg aaa cca gta 163
 Trp Asn Ser Val Asp Glu Leu Pro Ile His Asp Ser Trp Lys Pro Val
 10 15 20
 ctc aaa cca gtc gaa gac gcc atc cga aaa ctc ggt gta ttc ctc gcg 211
 Leu Lys Pro Val Glu Asp Ala Ile Arg Lys Leu Gly Val Phe Leu Ala
 25 30 35
 gaa gaa gaa ttc ctt cca cca gta gat gac gta ttc aga gca ttt agc 259
 Glu Glu Glu Phe Leu Pro Pro Val Asp Asp Val Phe Arg Ala Phe Ser
 40 45 50
 tac ccc ttt gac gca gta aaa gta ctg atc atg gga caa gac cca tat 307
 Tyr Pro Phe Asp Ala Val Lys Val Leu Ile Met Gly Gln Asp Pro Tyr
 55 60 65
 ccc acc cca gga cat gcc atg gga ctg agc ttt tcc acc caa cca gac 355
 Pro Thr Pro Gly His Ala Met Gly Leu Ser Phe Ser Thr Gln Pro Asp
 70 75 80 85
 gta cga cca ctg cca cgg agc ctg aac aat atc ttc aaa gag ctg gtg 403
 Val Arg Pro Leu Pro Arg Ser Leu Asn Asn Ile Phe Lys Glu Leu Val
 90 95 100
 agt gat gtc gcc tct tta gcc gat tgg gcg tca gag cag ggg gcc ttg 451
 Ser Asp Val Gly Ser Leu Gly Asp Ser Ala Ser Glu Gln Gly Ala Leu
 105 110 115
 gac tta ggt att aac gcg ccg gcc tct gtc gct gcc aca caa gtt gcc 499
 Asp Leu Gly Ile Asn Ala Pro Gly Ser Val Ala Gly Thr Gln Val Ala
 120 125 130
 ttg ccc gcg gac gcc gac ctc cgt gca tgg agc aac caa gcc gtc gca 547
 Leu Pro Ala Asp Gly Asp Leu Arg Ala Trp Ser Asn Gln Gly Val Ala
 135 140 145
 ttg ttc aac cgc gta ctc acc gtc cac cca gcc cag gcc gga agc cac 595
 Leu Phe Asn Arg Val Leu Thr Val His Pro Gly Gln Ala Gly Ser His
 150 155 160 165
 aag ggt aaa gcc tgg gaa gcg gta acc gaa cag gcg att aaa gcc ttg 643
 Lys Gly Lys Gly Trp Glu Ala Val Thr Glu Gln Ala Ile Lys Ala Leu

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170	175	180	
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Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu Trp Gly Lys Gln Ala			
185	190	195	
caa gag gta cag aaa ttc ctt gga gat acg ccg tgt atc tgc tca gtg			739
Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro Cys Ile Cys Ser Val			
200	205	210	
cac cca tca cgg ctg tgg gcg tgg aga ggc ttt ttt ggc tct aag cct			787
His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe Phe Gly Ser Lys Pro			
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ttt agt cgt gcg aac gaa atc tta agc agc ctg ggt gcc acc gag atc			835
Phe Ser Arg Ala Asn Glu Ile Leu Ser Ser Leu Gly Ala Thr Glu Ile			
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Asp Trp Ser Leu			

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<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

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Ser Trp Lys Pro Val Leu Lys Pro Val Glu Asp Ala Ile Arg Lys Leu
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Gly Val Phe Leu Ala Glu Glu Glu Phe Leu Pro Pro Val Asp Asp Val
35 40 45

Phe Arg Ala Phe Ser Tyr Pro Phe Asp Ala Val Lys Val Leu Ile Met
50 55 60

Gly Gln Asp Pro Tyr Pro Thr Pro Gly His Ala Met Gly Leu Ser Phe
65 70 75 80

Ser Thr Gln Pro Asp Val Arg Pro Leu Pro Arg Ser Leu Asn Asn Ile
85 90 95

Phe Lys Glu Leu Val Ser Asp Val Gly Ser Leu Gly Asp Ser Ala Ser
100 105 110

Glu Gln Gly Ala Leu Asp Leu Gly Ile Asn Ala Pro Gly Ser Val Ala
115 120 125

Gly Thr Gln Val Ala Leu Pro Ala Asp Gly Asp Leu Arg Ala Trp Ser
130 135 140

Asn Gln Gly Val Ala Leu Phe Asn Arg Val Leu Thr Val His Pro Gly
145 150 155 160

Gln Ala Gly Ser His Lys Gly Lys Gly Trp Glu Ala Val Thr Glu Gln
165 170 175

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Ala Ile Lys Ala Leu Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu
180 185 190

Trp Gly Lys Gln Ala Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro
195 200 205

Cys Ile Cys Ser Val His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe
210 215 220

Phe Gly Ser Lys Pro Phe Ser Arg Ala Asn Glu Ile Leu Ser Ser Leu
225 230 235 240

Gly Ala Thr Glu Ile Asp Trp Ser Leu
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<210> 27

<211> 1203

<212> DN

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (101) \dots (1180)$

<223> RXN00484

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cgtcacatgg aatcgacgct atcatcaacc gttatgtgaa gtg gat gcc act ctc 115
Val Asp Ala Thr Leu
1 5

aaa aag aat ctc cgt gat aaa ggg att gaa gtg cat agc cac cca ggt 163
Lys Lys Asn Leu Arg Asp Lys Gly Ile Glu Val His Ser His Pro Gly
10 15 20

ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act ccc 211
Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr Pro
25 30 35

tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc aga 259
 Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala Arg
 40 45 50

gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct cac 307
Val His Ala Tyr Glu Thr Val Lys Asn Asn Val Pro Val Pro Ser His
55 60 65

cta aca gga cca gag gat gta gag ctg ccc atc cta gaa atg gag caa 355
Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile Leu Glu Met Glu Gln
70 75 80 85

cct ttt tgg tca aca acg tta gtt aag gag tgt gct ccc ggt gaa aaa 403
Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys Ala Pro Gly Glu Lys
90 95 100

aat gct tgc gaa aaa ctc ttt gat ttt ttg gaa cat cta cag gac tac 451
Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu His Leu Gln Asp Tyr
105 110 115

ccg caa gct cga gac agc tta gcc cga tcc gct aca agt aaa tta tct 499
 Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala Thr Ser Lys Leu Ser
 120 125 130

gct cat cta agg ttt ggt gag atc agc atc cac cgc gtg tgg gca gag 547
 Ala His Leu Arg Phe Gly Glu Ile Ser Ile His Arg Val Trp Ala Glu
 135 140 145

act gca gca ata gac tct gaa gga act gag tta ttt ctt aaa gaa ctt 595
 Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu Phe Leu Lys Glu Leu
 150 155 160 165

ctc tgg aga gat ttt gcg tgg cat cga ctt tat gcc ctg cca cac atg 643
 Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr Ala Leu Pro His Met
 170 175 180

gac acg caa aac gtt cgt atg caa ttt aat cgt ttc gga tgg tcc tgg 691
 Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg Phe Gly Trp Ser Trp
 185 190 195

gat ccg agt gaa aaa gat aaa ctt aac act cca tcc acc cct ctt atc 739
 Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro Ser Thr Pro Leu Ile
 200 205 210

ccc acc aaa gct gac caa ttc cat gag gat tta gca gca tgg cgt gca 787
 Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu Ala Ala Trp Arg Ala
 215 220 225

gga aaa aca gga att ccg ctg gtc gat gca gcc atg cga gaa tta tgg 835
 Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly Met Arg Glu Leu Trp
 230 235 240 245

gcc acc ggg tca atg cac aat cgc gtc aga atg gta gta gct agt ttt 883
 Ala Thr Gly Ser Met His Asn Arg Val Arg Met Val Val Ala Ser Phe
 250 255 260

tta acc aag aat ctc cag atc cat tgg cgt cat gcc gaa gaa tgg ttt 931
 Leu Thr Lys Asn Leu Gln Ile His Trp Arg His Gly Glu Glu Trp Phe
 265 270 275

tgg gaa act ctc gta gat gct gat cca gct tct aat gct ttc aac tgg 979
 Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser Asn Ala Phe Asn Trp
 280 285 290

caa tgg gct gcg ggt agc gga gat gac gct tgc cct tat ttc cgt att 1027
 Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser Pro Tyr Phe Arg Ile
 295 300 305

ttt aat ccg gtc acc caa gcg aaa aaa ttt gat cca gat gaa act tat 1075
 Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr Tyr
 310 315 320 325

att cgt cgc tgg gta ccc gaa tat gga aca tca tat ccg gat ccc 1123
 Ile Arg Arg Val Pro Glu Tyr Gly Thr Pro Ser Tyr Pro Asp Pro
 330 335 340

atc gtc gat ctg aaa gaa tcc cgt caa att gct tta gac gcc tac tct 1171
 Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala Leu Asp Ala Tyr Ser
 345 350 355

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Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser
275 280 285

Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser
290 295 300

Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp
305 310 315 320

Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro
325 330 335

Ser Tyr Pro Asp Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala
340 345 350

Leu Asp Ala Tyr Ser Ala Ile Lys
355 360

<210> 29

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> FRXA00484

<400> 29

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tgccactctc aaaaagaatc tccgtgataa agggattgaa gtg cat agc cac cca 115
Val His Ser His Pro
1 5

ggt ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act 163
Gly Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr
10 15 20

ccc tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc 211
Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala
25 30 35

aga gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct 259
Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn Val Pro Val Pro Ser
40 45 50

cac cta aca gga cca gag gat gta gag ctg ccc atc cta gaa atg gag 307
His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile Leu Glu Met Glu
55 60 65

caa cct ttt tgg tca aca acg tta gtt aag gag tgt gct ccc ggt gaa 355
Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys Ala Pro Gly Glu
70 75 80 85

aaa aat gct tcg gaa aaa ctc ttt gat ttt ttg gaa cat cta cag gac 403
Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu His Leu Gln Asp
90 95 100

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tac ccg caa gct cga gac agc tta gcc cga tcc gct aca agt aaa tta 451
 Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala Thr Ser Lys Leu
 105 110 115

tct gct cat cta agg ttt ggt gag atc agc atc cac cgc gtg tgg gca 499
 Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile His Arg Val Trp Ala
 120 125 130

gag act gca gca ata gac tct gaa gga act gag tta ttt ctt aaa gaa 547
 Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu Phe Leu Lys Glu
 135 140 145

ctt ctc tgg aga gat ttt gcg tgg cat cga ctt tat gcc ctg cca cac 595
 Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr Ala Leu Pro His
 150 155 160 165

atg gac acg caa aac gtt cgt atg caa ttt aat cgt ttc gga tgg tcc 643
 Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg Phe Gly Trp Ser
 170 175 180

tgg gat ccg agt gaa aaa gat aaa ctt aac act cca tcc acc cct ctt 691
 Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro Ser Thr Pro Leu
 185 190 195

atc ccc acc aaa gct gac caa ttc cat gag gat tta gca gca tgg cgt 739
 Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu Ala Ala Trp Arg
 200 205 210

gca gga aaa aca gga att ccg ctg gtc gat gca gcc atg cga gaa tta 787
 Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly Met Arg Glu Leu
 215 220 225

tgg gcc acc ggg tca atg cac aat cgc gtc aga atg gta gta gct agt 835
 Trp Ala Thr Gly Ser Met His Asn Arg Val Arg Met Val Val Ala Ser
 230 235 240 245

ttt tta acc aag aat ctc cag atc cat tgg cgt cat gcc gaa gaa tgg 883
 Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg His Gly Glu Glu Trp
 250 255 260

ttt tgg gaa act ctc gta gat gct gat cca gct tct aat gct ttc aac 931
 Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser Asn Ala Phe Asn
 265 270 275

tgg caa tgg gct gcg ggt agc gga gat gac gct tgc cct tat ttc cgt 979
 Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser Pro Tyr Phe Arg
 280 285 290

att ttt aat ccg gtc acc caa gcg aaa aaa ttt gat cca gat gaa act 1027
 Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr
 295 300 305

tat att cgt cgc tgg gta ccc gaa tat gga aca cca tca tat ccg gat 1075
 Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro Ser Tyr Pro Asp
 310 315 320 325

ccc atc gtc gat ctg aaa gaa tcc cgt caa att gct tta gac gcc tac 1123
 Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala Leu Asp Ala Tyr
 330 335 340

tct gcg att aag tgagtttaacg cgcagctttt aaa 1158

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Ser Ala Ile Lys
345

<210> 30

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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20 25 30

Ala Trp Glu Val Ala Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn
35 40 45

Val Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro
50 55 60

Ile Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu
65 70 75 80

Cys Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu
85 90 95

Glu His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser
100 105 110

Ala Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile
115 120 125

His Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu
130 135 140

Leu Phe Leu Lys Glu Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu
145 150 155 160

Tyr Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn
165 170 175

Arg Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr
180 185 190

Pro Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp
195 200 205

Leu Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala
210 215 220

Gly Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg
225 230 235 240

Met Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg
245 250 255

His Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala
260 265 270

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Ser Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala
 275 280 285

Ser Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe
 290 295 300

Asp Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr
 305 310 315 320

Pro Ser Tyr Pro Asp Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile
 325 330 335

Ala Leu Asp Ala Tyr Ser Ala Ile Lys
 340 345

<210> 31
 <211> 1002
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 <213> *Corynebacterium glutamicum*

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 <222> (101)..(979)
 <223> RXA02476

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 Met Ser Phe Thr Ala
 1 5

ttt caa aca gcc ctg ctc gtg tgg ttt aga gca aat gcc cgc gat ctt 163
 Phe Gln Thr Ala Leu Leu Val Trp Phe Arg Ala Asn Ala Arg Asp Leu
 10 15 20

gcg tgg cgt gat ccc aat act tca gca tgg gga att ctc ctt tca gag 211
 Ala Trp Arg Asp Pro Asn Thr Ser Ala Trp Gly Ile Leu Leu Ser Glu
 25 30 35

gtg atg agc caa caa act ccc gtc gcg cga gtc gag ccg att tgg cgt 259
 Val Met Ser Gln Gln Thr Pro Val Ala Arg Val Glu Pro Ile Trp Arg
 40 45 50

gag tgg atg gaa aaa tgg ccc act ccg gaa gat ttc gcg aat gcg agc 307
 Glu Trp Met Glu Lys Trp Pro Thr Pro Glu Asp Phe Ala Asn Ala Ser
 55 60 65

acc gat gag att ttg cgg tgg tgg ggc aag ttg ggc tat cca cgt agg 355
 Thr Asp Glu Ile Leu Arg Ser Trp Gly Lys Leu Gly Tyr Pro Arg Arg
 70 75 80 85

gcg ctg agg ttg aag gaa tgt gcg gag gtg atc gtc gaa aag cat gcc 403
 Ala Leu Arg Leu Lys Glu Cys Ala Glu Val Ile Val Glu Lys His Ala
 90 95 100

ggc gag gtg ccg gat acg gtg gag gcg ctg ctc gcg ttg ccg ggg atc 451
 Gly Glu Val Pro Asp Thr Val Glu Ala Leu Leu Ala Leu Pro Gly Ile
 105 110 115

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Val Pro Val Val Asp Thr Asn Val Arg Arg Val Tyr Gln Arg Ala Val	
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gcc gga cgt tac ctt gcg ggg cct gcg aaa aag caa gag ctt atc gac	595
Ala Gly Arg Tyr Leu Ala Gly Pro Ala Lys Lys Gln Glu Leu Ile Asp	
150	155
gtc tcc ctt ctc ctt ccc aac act cac gcc cca gaa ttc tct gcc gca	643
Val Ser Leu Leu Leu Pro Asn Thr His Ala Pro Glu Phe Ser Ala Ala	
170	175
ata atg gag ttg ggt gct ctt atc tgc acg gcc act tcc cca aag tgt	691
Ile Met Glu Leu Gly Ala Leu Ile Cys Thr Ala Thr Ser Pro Lys Cys	
185	190
gac acc tgc cca ctg ctt gac cag tgt caa tgg caa aaa ctt gcc tgt	739
Asp Thr Cys Pro Leu Leu Asp Gln Cys Thr Gln Trp Gln Lys Leu Gly Cys	
200	205
ccc tcc ccg agt gaa gag gag ctg gct tca gcg aaa aag cgt gtg cag	787
Pro Ser Pro Ser Glu Glu Glu Leu Ala Ser Ala Lys Lys Arg Val Gln	
215	220
aaa ttt gtg gga acc gac cga caa gtc cgt gcc cta atc atg gac gta	835
Lys Phe Val Gly Thr Asp Arg Gln Val Arg Gly Leu Ile Met Asp Val	
230	235
ctg cgc aat gcc acc gca cct gtc cca cta tcc gcg att gat gtc gtg	883
Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser Ala Ile Asp Val Val	
250	255
tgg cct gac gat gcc caa cgc tcc cgg gcg ctg ttt tgc ctc att gag	931
Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu Phe Ser Leu Ile Glu	
265	270
gac gga ctc gcg gaa caa aat gag gcg ggt tat ttc cac ctg cca cgg	979
Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr Phe His Leu Pro Arg	
280	285
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Ile Leu Leu Ser Glu Val Met Ser Gln Gln Thr Pro Val Ala Arg Val	
35 40 45	

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(868)
<223> RXA00102

<400> 33
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gtg Val	ctg Leu	gaa Glu	acc Thr	tcc Ser	ctg Leu	cgt Arg	gtg Val	cca Pro	tca Ser	gtg Val	gca Ala	ctt Leu	cac His	gat Asp	ttc Phe	211
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acc Thr	ggt Gly	caa Gln	acc Thr	gtc Val	aac Asn	cgc Arg	gta Val	tgg Trp	ccc Pro	tac Tyr	gga Gly	aaa Lys	cac His	ctc Leu	ttc Phe	259
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				70			75				80				85	
acc Thr	gcg Ala	agg Arg	gta Val	gtg Val	ctt Leu	gtg Val	ctg Leu	tcg Ser	gaa Glu	aac Asn	atc Ile	gag Glu	gtg Val	gtg Val	ggg Gly	403
				90					95					100		
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				105				110					115			
gag Glu	atc Ile	gct Ala	tac Tyr	ctc Leu	ggc Gly	ccc Pro	gac Asp	gtc Val	ctt Leu	gcc Ala	gaa Glu	gaa Glu	ttc Phe	gac Asp	atc Ile	499
				120			125					130				
aac Asn	acc Thr	gca Ala	cgc Arg	aac Asn	aat Asn	att Ile	gca Ala	tcg Ser	aac Asn	cct Pro	tcc Ser	cga Arg	aca Thr	att Ile	ggc Gly	547
				135			140					145				
gaa Glu	gcc Ala	ctc Leu	ctc Leu	gac Leu	caa Gln	tcc Ser	aac Asn	ctc Leu	gct Ala	gga Gly	gta Val	ggc Gly	aac Asn	gaa Glu	tac Tyr	595
					155					160				165		
cgc Arg	gct Ala	gag Glu	atc Ile	tgc Cys	ttc Phe	ctc Leu	atg Met	ggc Gly	gtc Val	cac His	ccg Pro	gcg Ala	aca Thr	caa Gln	gta Val	643
				170				175						180		
gga Gly	tac Tyr	gtt Val	gac Asp	gtc Val	gaa Glu	aag Lys	gct Ala	ctg Leu	aag Lys	att Ile	acc Thr	cga Arg	aga Arg	ctc Leu	atg Met	691
				185				190					195			
tgg Trp	gaa Glu	aat Asn	cga Arg	aat Asn	tcg Ser	ccg Pro	att Ile	cga Arg	gtg Val	acc Thr	acc Thr	ggg Gly	gtt Val	cga Arg	cgc Arg	739
				200			205						210			
gcc Ala	ggg Gly	gaa Glu	tcc Ser	acc Thr	tat Tyr	gtg Val	ttt Phe	ggg Gly	cgt Arg	aac Asn	aat Asn	aaa Lys	ccg Pro	tgc Cys	agg Arg	787
				215		220						225				

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aga tgc cga acc cca atc gtg aaa gcc gag ttg ggg gag cga ata atc 835
 Arg Cys Arg Thr Pro Ile Val Lys Ala Glu Leu Gly Glu Arg Ile Ile
 230 235 240 245

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 Trp Trp Cys Pro Arg Cys Gln Pro Leu Asn Ser
 250 255

caa 891

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<212> PRT

<213> Corynebacterium glutamicum

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Ala Leu His Asp Phe Thr Gly Gln Thr Val Asn Arg Val Trp Pro Tyr
 35 40 45

Gly Lys His Leu Phe Met Gln Phe Gly Glu Glu Ile Leu His Thr His
 50 55 60

Leu Lys Met Glu Gly Thr Trp Ala Val His Arg Lys Gly Asp Arg Trp
 65 70 75 80

Arg Lys Pro Gly His Thr Ala Arg Val Val Leu Val Leu Ser Glu Asn
 85 90 95

Ile Glu Val Val Gly His Ser Leu Gly Phe Val Arg Val Phe Pro Ala
 100 105 110

Asn Arg Tyr Ser Glu Glu Ile Ala Tyr Leu Gly Pro Asp Val Leu Ala
 115 120 125

Glu Glu Phe Asp Ile Asn Thr Ala Arg Asn Asn Ile Ala Ser Asn Pro
 130 135 140

Ser Arg Thr Ile Gly Glu Ala Leu Leu Asp Gln Ser Asn Leu Ala Gly
 145 150 155 160

Val Gly Asn Glu Tyr Arg Ala Glu Ile Cys Phe Leu Met Gly Val His
 165 170 175

Pro Ala Thr Gln Val Gly Tyr Val Asp Val Glu Lys Ala Leu Lys Ile
 180 185 190

Thr Arg Arg Leu Met Trp Glu Asn Arg Asn Ser Pro Ile Arg Val Thr
 195 200 205

Thr Gly Val Arg Arg Ala Gly Glu Ser Thr Tyr Val Phe Gly Arg Asn
 210 215 220

Asn Lys Pro Cys Arg Arg Cys Arg Thr Pro Ile Val Lys Ala Glu Leu

002230.6920360

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                Met Pro Glu Gly His
                1                5

gtg att cat cga cta gct ggg gaa ctc acc aag aat ttt ggc gat acc 163
Val Ile His Arg Leu Ala Gly Glu Leu Thr Lys Asn Phe Gly Asp Thr
                10                15                20

att ttg gac gcc act tca cct caa gga cgc ttt act tct gaa gcg gcg 211
Ile Leu Asp Ala Thr Ser Pro Gln Gly Arg Phe Thr Ser Glu Ala Ala
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atc atc aac ggt cac cgc atc gcg gtt gcg gag gct tac ggc aag cac 259
Ile Ile Asn Gly His Arg Ile Ala Val Ala Glu Ala Tyr Gly Lys His
                40                45                50

ctg ttc gtc gag ttc gat gcg gat cac cct gag cac att ttg tat atc 307
Leu Phe Val Glu Phe Asp Ala Asp His Pro Glu His Ile Leu Tyr Ile
                55                60                65

cat ttg ggg ctg att ggc acg ttg cag ttt gaa cct gcg gaa gaa acc 355
His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro Ala Glu Glu Thr
                70                75                80                85

cgc ggg cag att cgc ctg cac ctt tcc gac ggg gag atc gca gct aat 403
Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu Ile Ala Ala Asn
                90                95                100

ttg cgc gga ccc caa tgg tgc agg ttg atc acc gat gca gag cgc acc 451
Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp Ala Glu Arg Thr
                105                110                115

cag gcc att gga aaa ttg ggc gct gat ccg att cgc gat gat gcc gat 499
Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg Asp Asp Ala Asp
                120                125                130

ccg gaa cca att cgg att aag gtg cag cgc tca ggg cga agc att ggt 547
Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly Arg Ser Ile Gly
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cgt gcg gag aca ctt ttc cgc ctg ggg att tca ccg ttc acc att gga 643
 Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser Pro Phe Thr Ile Gly
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aaa gac atc acc acg gca cag ttc cga tcc att tgg gcg gat ctt gtt 691
 Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile Trp Ala Asp Leu Val
 185 190 195

ggg ttg atg aaa gac ggt gtt gtg act ggt cgg att gat act gtg cgc 739
 Gly Leu Met Lys Asp Gly Val Val Thr Thr Gly Arg Ile Asp Thr Val Arg
 200 205 210

ccg gaa cac aca ccg gag gcg atg ggt agg cca ccg cgg aaa gat gat 787
 Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro Pro Arg Lys Asp Asp
 215 220 225

cac ggc ggt gag gtt tac acc tat cgg cga acc ggt caa gag tgc ttt 835
 His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr Gly Gln Glu Cys Phe
 230 235 240 245

ctg tgc gca act ccc atc aag gag cag gtc atg gag ggt cgc aac tta 883
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 Phe Trp Cys Pro Gly Cys Gln Arg
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Thr Ser Glu Ala Ala Ile Ile Asn Gly His Arg Ile Ala Val Ala Glu
 35 40 45

Ala Tyr Gly Lys His Leu Phe Val Glu Phe Asp Ala Asp His Pro Glu
 50 55 60

His Ile Leu Tyr Ile His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu
 65 70 75 80

Pro Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly
 85 90 95

Glu Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr
 100 105 110

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Asp Ala Glu Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile
 115 120 125
 Arg Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser
 130 135 140
 Gly Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly
 145 150 155 160
 Val Gly Asn Ile Tyr Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser
 165 170 175
 Pro Phe Thr Ile Gly Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile
 180 185 190
 Trp Ala Asp Leu Val Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg
 195 200 205
 Ile Asp Thr Val Arg Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro
 210 215 220
 Pro Arg Lys Asp Asp His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr
 225 230 235 240
 Gly Gln Glu Cys Phe Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met
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 Glu Gly Arg Asn Leu Phe Trp Cys Pro Gly Cys Gln Arg
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 gcg gaa gaa acc cgc ggg cag att cgc ctg cac ctt tcc gac ggg gag 96
 Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu
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 atc gca gct aat ttg cgc gga ccc caa tgg tgc agg ttg atc acc gat 144
 Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp
 35 40 45
 gca gag cgc acc cag gcc att gga aaa ttg ggc gct gat ccg att cgc 192
 Ala Glu Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg
 50 55 60
 gat gat gcc gat ccg gaa cca att cgg att aag gtg cag cgc tca ggg 240
 Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly
 65 70 75 80

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Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly Val	
85	95
gga aat atc tac cgt gcg gag aca ctt ttc cgc ctg ggg att tca ccg	336
Gly Asn Ile Tyr Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser Pro	
100	110
ttc acc att gga aaa gac atc acc acg gca cag ttc cga tcc att tgg	384
Phe Thr Ile Gly Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile Trp	
115	125
gcg gat ctt gtt ggg ttg atg aaa gac ggt gtt gtg act ggt cgg att	432
Ala Asp Leu Val Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg Ile	
130	140
gat act gtg cgc ccg gaa cac aca ccg gag gcg atg ggt agg cca ccg	480
Asp Thr Val Arg Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro Pro	
145	155
cgg aaa gat gat cac gcc ggt gag gtt tac acc tat cgg cga acc ggt	528
Arg Lys Asp Asp His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr Gly	
165	175
caa gag tgc ttt ctg tgc gca act ccc atc aag gag cag gtc atg gag	576
Gln Glu Cys Phe Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met Glu	
180	190
ggt cgc aac tta ttt tgg tgt ccc gcc tgc caa cgc tagacagatt	622
Gly Arg Asn Leu Phe Trp Cys Pro Gly Cys Gln Arg	
195	200
caccttttgc tgt	635
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<p><400> 38</p> <p>His Phe Val Tyr His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro</p> <p>1 5 10 15</p>	
<p>Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu</p> <p>20 25 30</p>	
<p>Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp</p> <p>35 40 45</p>	
<p>Ala Glu Ala Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg</p> <p>50 55 60</p>	
<p>Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly</p> <p>65 70 75 80</p>	
<p>Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly Val</p> <p>85 90 95</p>	
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 Ala Ala Arg Asn Gln Leu Gly Gly Gly Pro Glu Ile Glu Ala Asn Ile
 35 40 45
 Ala Gly Leu Arg Val Ser Ala Ala Lys Arg Arg Gly Lys Phe Leu Trp
 50 55 60
 Leu Glu Leu Ile Asp Ala Pro Ser Gly Glu Thr Arg Pro Asp Leu Gly
 65 70 75 80
 Leu Leu Val His Leu Gly Met Ser Gly Gln Met Leu Ile Lys Glu Pro
 85 90 95
 Asp Ala Pro Ile Ser Pro His Leu Arg Ala Lys Val Glu Leu Asp Asn
 100 105 110
 Gly Asp Glu Val Trp Phe Val Asp Gln Arg Thr Phe Gly Tyr Trp Trp
 115 120 125
 Leu Gly Asp Leu Val Asp Gly Val Pro Glu Arg Val Ser His Ile Ala
 130 135 140
 Thr Asp Val Leu Asp Glu Ser Ala Asp Phe Ser Ala Ile Ala Arg Asn
 145 150 155 160
 Leu Lys Ser Arg Lys Ser Glu Ile Lys Arg Leu Leu Leu Asn Gln Glu
 165 170 175
 Ile Val Ser Gly Ile Gly Asn Ile Tyr Ala Asp Glu Met Leu Trp Gln
 180 185 190
 Ala Lys Ile His Pro Leu Gln Arg Ala Asp Arg Leu Ser Leu Ala Arg
 195 200 205
 Leu Glu Glu Leu Leu Gln Ala Gly Lys Asp Val Met Thr Lys Ala Leu
 210 215 220
 Ala Gln Gly Gly Thr Ser Phe Asp Ala Leu Tyr Val Asn Val Asn Gly
 225 230 235 240
 Asn Ser Gly Tyr Phe Ala Leu Ser Leu Asn Ala Tyr Ala Gln Thr Gly
 245 250 255
 Glu Pro Cys Gly Arg Cys Gly Thr Leu Ile Ile Arg Glu Ser Phe Met
 260 265 270
 Asn Arg Gly Ser His Tyr Cys Pro Asn Cys Gln Lys Arg Arg
 275 280 285

<210> 41
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1879)
 <223> RXA01596

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Figure 1 *Diagram illustrating the experimental design. The study was conducted in two phases. Phase 1 involved a pre-test to determine the appropriate number of items for the questionnaire. Phase 2 involved the main study, which was conducted in two waves. Wave 1 involved the collection of data from 100 participants. Wave 2 involved the collection of data from 100 participants. The data from both waves were then analyzed to determine the effect of the intervention on the dependent variables.*

Glu Asp Ala Glu Leu Val	Glu Gln Ile Arg Arg Leu Gln Asp Val Asp	
215	220	225
acc ctg cgg gag caa gct gca acc gca ttg gct gcg att gat ggt gcc	835	
Thr Leu Arg Glu Gln Ala Ala Thr Ala Leu Ala Ile Asp Gly Ala		
230	235	245
ggc tct ctc agc gac gcc atg ggt ggt tcc ggc ggc ttt gat gaa tcc	883	
Gly Ser Leu Ser Asp Ala Met Gly Gly Ser Gly Gly Phe Asp Glu Ser		
250	255	260
cag gag tca gcc tct gac cag ctc ggc cag gcg gag tcc gcg ctg gca	931	
Gln Glu Ser Ala Ser Asp Gln Leu Gly Gln Ala Glu Ser Ala Leu Ala		
265	270	275
ggc agt gat gac tca aag ctg aaa gat att gcc gtt cag ctt gcg gaa	979	
Gly Ser Asp Asp Ser Lys Leu Lys Asp Ile Ala Val Gln Leu Ala Glu		
280	285	290
atc acc agc cag ctc agc caa gtg tcc atg gaa ttg ggc ggg ttc ctc	1027	
Ile Thr Ser Gln Leu Ser Gln Val Ser Met Glu Leu Gly Gly Phe Leu		
295	300	305
tct gat ctc ccc gca gac ccc caa gca ctc gat gac atg ctc acc cgc	1075	
Ser Asp Leu Pro Ala Asp Pro Gln Ala Leu Asp Asp Met Leu Thr Arg		
310	315	325
caa cag caa ttg aaa ctg ctc acg cgt aaa tac gct gca gat att gac	1123	
Gln Gln Gln Leu Lys Leu Leu Thr Arg Lys Tyr Ala Ala Asp Ile Asp		
330	335	340
ggc gtg att gag tgg cag cgg aaa gcc caa atc cgc cta gac agc att	1171	
Gly Val Ile Glu Trp Gln Arg Lys Ala Gln Ile Arg Leu Asp Ser Ile		
345	350	355
gac att tcc tcc gaa gcg ctt gac aag ctg aaa gaa gac gcg aaa aag	1219	
Asp Ile Ser Ser Glu Ala Leu Asp Lys Leu Lys Glu Asp Ala Lys Lys		
360	365	370
gcg cag gcc tcc atg atg cgt gcc gct aag aag ctt tca gct gtc cgt	1267	
Ala Gln Ala Ser Met Met Arg Ala Ala Lys Lys Leu Ser Ala Val Arg		
375	380	385
gca aag gca gca acc aag ttg ggg aca act gtc acc gag gag ctt cag	1315	
Ala Lys Ala Ala Thr Lys Leu Gly Thr Thr Thr Glu Thr Glu Leu Gln		
390	395	400
ggc ctg gcc atg caa aaa gcc cgc ttt gag gtt gct ttg acc tcc att	1363	
Gly Leu Ala Met Gln Lys Ala Arg Phe Glu Val Ala Leu Thr Ser Ile		
410	415	420
gag gcg tgc gcc agc ggt atc gac cag gtg gaa ttc cag ctc gca gca	1411	
Glu Ala Cys Ala Ser Gly Ile Asp Gln Val Glu Phe Gln Leu Ala Ala		
425	430	435
aat gcc ttt gca cag cct cgt cca ctt gca tcc tct gcg tct ggt ggt	1459	
Asn Ala Phe Ala Gln Pro Arg Pro Leu Ala Ser Ser Ala Ser Gly Gly		
440	445	450
gaa ctt tcc cgc gtt atg ttg gcg ctc gag gtg atc ttg gct gct gga	1507	
Glu Leu Ser Arg Val Met Leu Ala Leu Glu Val Ile Leu Ala Ala Gly		

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gga cgc gca gcg gtg gaa atc ggt cgc cgc ctg gcc cgc ctt gcc acc Gly Arg Ala Ala Val Glu Ile Gly Arg Arg Leu Ala Arg Leu Ala Thr 490 495 500			1603
aaa aac caa gtc atc gtg gtc acc cat ctc cca cag gtc gct gct tac Lys Asn Gln Val Ile Val Thr Thr His Leu Pro Gln Val Ala Ala Tyr 505 510 515			1651
gcc gac acg cac ctg cac gtt gcc aag aat gta gga gaa gcc tcc gtg Ala Asp Thr His Leu His Val Ala Lys Asn Val Gly Glu Ala Ser Val 520 525 530			1699
acc tca gga gtg gag tca ctg acc ttc gac cga cgc gtg gaa gag ctc Thr Ser Gly Val Glu Ser Leu Thr Phe Asp Arg Arg Val Glu Glu Leu 535 540 545			1747
tcc cgc atg ctc gct ggc ctc gac gac acc gcc acc ggc cga gcc cac Ser Arg Met Leu Ala Gly Leu Asp Asp Thr Ala Thr Gly Arg Ala His 550 555 560 565			1795
gca acg gag ctg ctc gag cgt gca cag cgt gaa aag gaa gat att aac Ala Thr Glu Leu Leu Glu Arg Ala Gln Arg Glu Lys Glu Asp Ile Asn 570 575 580			1843
gag gag cga gta gaa cca ctt ctc gcc gcc agt gca taagagtttt Glu Glu Arg Val Glu Pro Leu Leu Ala Ala Ser Ala 585 590			1889
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Ser Ala Glu Phe Ser Ser Gly Leu Thr Val Leu Thr Gly Glu Thr Gly 20 25 30			
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Arg Ala Asp Ala Ser Arg Val Arg Thr Gly Ser Pro Gln Ala Val Val 50 55 60			
Glu Gly Arg Phe Val Thr Gln Gly Val Pro Cys Asp Ile Val Glu Arg 65 70 75 80			
Ala Thr Gly Ile Val Ser Asn Ala Gly Gly Ala Ala Asp Glu Asn Gly 85 90 95			

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Glu Phe Leu Ala Val Arg Ser Val Gly Ala Asn Gly Arg Ser Lys Ala
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 His Leu Gly Gly Arg Ser Val Pro Ala Ala Thr Leu Ser Glu Phe Ser
 115 120 125
 Asp Glu Leu Leu Thr Ile His Gly Gln Asn Asp Gln Leu Arg Leu Leu
 130 135 140
 Ser Pro Glu Arg Gln Leu Glu Ala Leu Asp Arg Phe Asp Pro Glu Leu
 145 150 155 160
 Ala Gln Leu Arg Lys Asn Tyr Asn Ala Lys Tyr Leu Thr Trp Lys Ser
 165 170 175
 Leu Asp Lys Asp Leu Gln Lys Arg Leu Ser Ser Arg Arg Glu Leu Ala
 180 185 190
 Gln Glu Val Asp Arg Leu Gln Phe Ala Ile Asn Glu Ile Glu Glu Val
 195 200 205
 Ser Pro Gln Pro Gly Glu Asp Ala Glu Leu Val Glu Gln Ile Arg Arg
 210 215 220
 Leu Gln Asp Val Asp Thr Leu Arg Glu Gln Ala Ala Thr Ala Leu Ala
 225 230 235 240
 Ala Ile Asp Gly Ala Gly Ser Leu Ser Asp Ala Met Gly Gly Ser Gly
 245 250 255
 Gly Phe Asp Glu Ser Gln Glu Ser Ala Ser Asp Gln Leu Gly Gln Ala
 260 265 270
 Glu Ser Ala Leu Ala Gly Ser Asp Ser Lys Leu Lys Asp Ile Ala
 275 280 285
 Val Gln Leu Ala Glu Ile Thr Ser Gln Leu Ser Gln Val Ser Met Glu
 290 295 300
 Leu Gly Gly Phe Leu Ser Asp Leu Pro Ala Asp Pro Gln Ala Leu Asp
 305 310 315 320
 Asp Met Leu Thr Arg Gln Gln Gln Leu Lys Leu Leu Thr Arg Lys Tyr
 325 330 335
 Ala Ala Asp Ile Asp Gly Val Ile Glu Trp Gln Arg Lys Ala Gln Ile
 340 345 350
 Arg Leu Asp Ser Ile Asp Ile Ser Ser Glu Ala Leu Asp Lys Leu Lys
 355 360 365
 Glu Asp Ala Lys Lys Ala Gln Ala Ser Met Met Arg Ala Ala Lys Lys
 370 375 380
 Leu Ser Ala Val Arg Ala Lys Ala Ala Thr Lys Leu Gly Thr Thr Val
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 Thr Glu Glu Leu Gln Gly Leu Ala Met Gln Lys Ala Arg Phe Glu Val
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Phe Gln Leu Ala Ala Asn Ala Phe Ala Gln Pro Arg Pro Leu Ala Ser
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Ile Leu Ala Ala Gly Thr Thr Gly Thr Thr Leu Val Phe Asp Glu Val
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Asp Ala Gly Val Gly Gly Arg Ala Ala Val Glu Ile Gly Arg Arg Leu
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Ala Arg Leu Ala Thr Lys Asn Gln Val Ile Val Val Thr His Leu Pro
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Gln Val Ala Ala Tyr Ala Asp Thr His Leu His Val Ala Lys Asn Val
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Gly Glu Ala Ser Val Thr Ser Gly Val Glu Ser Leu Thr Phe Asp Arg
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Arg Val Glu Glu Leu Ser Arg Met Leu Ala Gly Leu Asp Asp Thr Ala
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Lys Glu Asp Ile Asn Glu Glu Arg Val Glu Pro Leu Leu Ala Ala Ser
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Met Ser Met Ser Asn 5
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Asn Asp Phe Glu His Glu Ser His Asp Val Ser Ala Lys Gln Ile Phe 20
10 15 20

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Gly Leu Ala Phe Pro Ala Leu Gly Val Leu Ala Ala Met Pro Leu Tyr 35
25 30 35

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 40 45 50

gct gcg ttg ggc gca gca aca aca att caa gct caa gtg aca aca cag 307
 Ala Ala Leu Gly Ala Ala Thr Thr Ile Gln Ala Gln Val Thr Thr Gln
 55 60 65

ctg aca ttc ttg tcc tat gga act acc gcg aga tca tcg aga att ttc 355
 Leu Thr Phe Leu Ser Tyr Gly Thr Thr Ala Arg Ser Ser Arg Ile Phe
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gga atg ggt gat cgc cgg gga gca att gcc gaa ggt gtg caa gca acc 403
 Gly Met Gly Asp Arg Arg Gly Ala Ile Ala Glu Gly Val Gln Ala Thr
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 Trp Val Ala Leu Phe Val Gly Leu Gly Ile Leu Thr Leu Met Leu Ile
 105 110 115

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 Gly Ala Pro Thr Phe Ala Leu Trp Leu Ser Gly Asp Glu Ala Leu Ala
 120 125 130

caa gaa gca ggg cat tgg ctc cgg gtc gct gct ttt gcg gtg cca cta 547
 Gln Glu Ala Gly His Trp Leu Arg Val Ala Ala Phe Ala Val Pro Leu
 135 140 145

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 Ile Leu Met Ile Met Ala Gly Asn Gly Trp Leu Arg Gly Ile Gln Asn
 150 155 160 165

acc aag ctg cca ctc tat ttc acc ttg gcg gga gtc atc ccc ggc gcg 643
 Thr Lys Leu Pro Leu Tyr Phe Thr Leu Ala Gly Val Ile Pro Gly Ala
 170 175 180

atc ttg att ccg ata ttc gtg gct aag ttt gga ctt gtg ggc tct gcc 691
 Ile Leu Ile Pro Ile Phe Val Ala Lys Phe Gly Leu Val Gly Ser Ala
 185 190 195

tgg gca aac ctc att gca gaa gca att act gct tcg ctg ttt ttg ggt 739
 Trp Ala Asn Leu Ile Ala Glu Ala Ile Thr Ala Ser Leu Phe Leu Gly
 200 205 210

gca ttg atc aag cac cac gaa ggt tcg tgg aag ccg agc tgg acg gtg 787
 Ala Leu Ile Lys His His Glu Gly Ser Trp Lys Pro Ser Trp Thr Val
 215 220 225

atg aaa aat cag ttg gtt ctt gga cgt gat ttg atc atg ccg tca atg 835
 Met Lys Asn Gln Leu Val Leu Gly Arg Asp Leu Ile Met Arg Ser Met
 230 235 240 245

tcg ttc cag gtt gct ttt ctt tcc gcg gcc gct gtg gct gca cga ttt 883
 Ser Phe Gln Val Ala Phe Leu Ser Ala Ala Ala Val Ala Ala Arg Phe
 250 255 260

ggc acg gca tcc ttg gcg gcc cac cag gtg ttg ctt cag ctg tgg aat 931
 Gly Thr Ala Ser Leu Ala Ala His Gln Val Leu Leu Gln Leu Trp Asn
 265 270 275

ttc atc aca ttg gtg ctg gat tct cta gct atc gcg gcg cag acc tta 979

00602039 062300

Phe Ile Thr Leu Val Leu Asp Ser Leu Ala Ile Ala Ala Gln Thr Leu
 280 285 290
 act ggt gca gcc ctg ggc gct gga act gcg aag gtc gcc cgc agg gtg 1027
 Thr Gly Ala Ala Leu Gly Ala Gly Thr Ala Lys Val Ala Arg Arg Val
 295 300 305
 ggt aat cag gtg att aag tac tct ctg att ttc gct ggt ggc tta ggt 1075
 Gly Asn Gln Val Ile Lys Tyr Ser Leu Ile Phe Ala Gly Gly Leu Gly
 310 315 320 325
 ttg gtg ttc gtg gtc tta cac tcg tgg att ccg cgt att ttc act cag 1123
 Leu Val Phe Val Val Leu His Ser Trp Ile Pro Arg Ile Phe Thr Gln
 330 335 340
 gac gcc gac gtt tta gat gcg att gct tcc ccg tgg tgg atc atg gtc 1171
 Asp Ala Asp Val Leu Asp Ala Ile Ala Ser Pro Trp Trp Ile Met Val
 345 350 355
 gcg atg atc att ttg ggt ggc att gtc ttt gct att gat ggt gtg ctg 1219
 Ala Met Ile Ile Leu Gly Gly Ile Val Phe Ala Ile Asp Gly Val Leu
 360 365 370
 ttg ggt gct gct gac gcg gtg ttc ctc cga aat gcc tct atc ttg gcg 1267
 Leu Gly Ala Ala Asp Ala Val Phe Leu Arg Asn Ala Ser Ile Leu Ala
 375 380 385
 gtt gtg gtc gga ttc tta cca ggc gtc tgg att tcc tat gca tta gat 1315
 Val Val Val Gly Phe Leu Pro Gly Val Trp Ile Ser Tyr Ala Leu Asp
 390 395 400 405
 gca ggg ctg aca ggc gtg tgg tgt ggt ttg ctg gcg ttt att ctg atc 1363
 Ala Gly Leu Thr Gly Val Trp Cys Gly Leu Leu Ala Phe Ile Leu Ile
 410 415 420
 cga cta ttt gcg gtg att tgg cgg ttt aag tct atg aag tgg gcg cgt 1411
 Arg Leu Phe Ala Val Ile Trp Arg Phe Lys Ser Met Lys Trp Ala Arg
 425 430 435
 tagcttcggc gcgtggcaaa cca 1434

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 <213> *Corynebacterium glutamicum*

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 20 25 30
 Ala Met Pro Leu Tyr Leu Leu Leu Asp Thr Ala Val Val Gly Thr Leu
 35 40 45
 Gly Gly Phe Glu Leu Ala Ala Leu Gly Ala Ala Thr Thr Ile Gln Ala
 50 55 60
 Gln Val Thr Thr Gln Leu Thr Phe Leu Ser Tyr Gly Thr Thr Ala Arg

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65	70	75	80
Ser Ser Arg Ile Phe Gly Met Gly Asp Arg Arg Gly Ala Ile Ala Glu	85	90	95
Gly Val Gln Ala Thr Trp Val Ala Leu Phe Val Gly Leu Gly Ile Leu	100	105	110
Thr Leu Met Leu Ile Gly Ala Pro Thr Phe Ala Leu Trp Leu Ser Gly	115	120	125
Asp Glu Ala Leu Ala Gln Glu Ala Gly His Trp Leu Arg Val Ala Ala	130	135	140
Phe Ala Val Pro Leu Ile Leu Met Ile Met Ala Gly Asn Gly Trp Leu	145	150	155
Arg Gly Ile Gln Asn Thr Lys Leu Pro Leu Tyr Phe Thr Leu Ala Gly	165	170	175
Val Ile Pro Gly Ala Ile Leu Ile Pro Ile Phe Val Ala Lys Phe Gly	180	185	190
Leu Val Gly Ser Ala Trp Ala Asn Leu Ile Ala Glu Ala Ile Thr Ala	195	200	205
Ser Leu Phe Leu Gly Ala Leu Ile Lys His His Glu Gly Ser Trp Lys	210	215	220
Pro Ser Trp Thr Val Met Lys Asn Gln Leu Val Leu Gly Arg Asp Leu	225	230	235
Ile Met Arg Ser Met Ser Phe Gln Val Ala Phe Leu Ser Ala Ala Ala	245	250	255
Val Ala Ala Arg Phe Gly Thr Ala Ser Leu Ala Ala His Gln Val Leu	260	265	270
Leu Gln Leu Trp Asn Phe Ile Thr Leu Val Leu Asp Ser Leu Ala Ile	275	280	285
Ala Ala Gln Thr Leu Thr Gly Ala Ala Leu Gly Ala Gly Thr Ala Lys	290	295	300
Val Ala Arg Arg Val Gly Asn Gln Val Ile Lys Tyr Ser Leu Ile Phe	305	310	315
Ala Gly Gly Leu Gly Leu Val Phe Val Val Leu His Ser Trp Ile Pro	325	330	335
Arg Ile Phe Thr Gln Asp Ala Asp Val Leu Asp Ala Ile Ala Ser Pro	340	345	350
Trp Trp Ile Met Val Ala Met Ile Ile Leu Gly Gly Ile Val Phe Ala	355	360	365
Ile Asp Gly Val Leu Leu Gly Ala Ala Asp Ala Val Phe Leu Arg Asn	370	375	380
Ala Ser Ile Leu Ala Val Val Val Gly Phe Leu Pro Gly Val Trp Ile	385	390	395
			400

00602839 062300

Ser Tyr Ala Leu Asp Ala Gly Leu Thr Gly Val Trp Cys Gly Leu Leu
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Ala Phe Ile Leu Ile Arg Leu Phe Ala Val Ile Trp Arg Phe Lys Ser
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Met Lys Trp Ala Arg
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<210> 45

<211> 702

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(679)

<223> RXA02671

<400> 45

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agaatgctcc gtggcatcaa aaaccgcttc ggtgccaccg atg aag tcg ggc tgc 115
Met Lys Ser Gly Cys
1 5

ttc gaa caa caa tcc gac ggc atc aaa gaa gtc ccc gat ccc tcc gga 163
Phe Glu Gln Gln Ser Asp Gly Ile Lys Glu Val Pro Asp Pro Ser Gly
10 15 20

ctc ttc ctc tcc cac cgc ggc tct acc cca gac ggc acc gcg gtc acc 211
Leu Phe Leu Ser His Arg Gly Ser Thr Pro Asp Gly Thr Ala Val Thr
25 30 35

gtc gcc atg gat ggc gtg cgc ccg cta tta gcg gag gtt caa agc ttg 259
Val Ala Met Asp Gly Val Arg Pro Leu Leu Ala Glu Val Gln Ser Leu
40 45 50

ctt gtc gac gcc ccc tcc aag aat cca cgc agg gtc gtc acg ggc ctc 307
Leu Val Asp Ala Pro Ser Lys Asn Pro Arg Arg Val Val Thr Gly Leu
55 60 65

gac gcc aat cgg gtc ccc atg gtc ctt gcg gtg tta tcc gca cgc gcc 355
Asp Ala Asn Arg Val Pro Met Val Leu Ala Val Leu Ser Ala Arg Ala
70 75 80 85

gga cgc caa acc caa gga aaa gac gct tac gtg gca acc gtt ggt ggc 403
Gly Arg Gln Thr Gln Gly Lys Asp Ala Tyr Val Ala Thr Val Gly Gly
90 95 100

atg aaa gtt ggc gaa cca gca aca gac ctc gct gtc gcg ctc gct act 451
Met Lys Val Gly Glu Pro Ala Thr Asp Leu Ala Val Ala Leu Ala Thr
105 110 115

gcc tcg gct tta gcc aag aaa cca cta cca gat aaa aca gtg gta ctc 499
Ala Ser Ala Leu Ala Lys Lys Pro Leu Pro Asp Lys Thr Val Val Leu
120 125 130

ggc gaa gtc ggc ttg gcc gga gaa atc cgt cgc gtc ccc aac gtt gat 547

002290-622300

Gly Glu Val Gly Leu Ala Gly Glu Ile Arg Arg Val Pro Asn Val Asp
 135 140 145

cgc aga cta gcc gag gcg gaa cgt tta ggt tat gaa aaa gca gtc atc 595
 Arg Arg Leu Ala Glu Ala Glu Arg Leu Gly Tyr Glu Lys Ala Val Ile
 150 155 160 165

ccc gga ggc tca gcc atc aaa caa aca agc ctg aga gtc atc gaa gct 643
 Pro Gly Gly Ser Gly Ile Lys Gln Thr Ser Leu Arg Val Ile Glu Ala
 170 175 180

tca aca ctt gcc gaa gca ctt gca gca gta agc tta taaagcatga 689
 Ser Thr Leu Ala Glu Ala Leu Ala Val Ser Leu
 185 190

caccaacaac cac 702

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 <213> Corynebacterium glutamicum

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 20 25 30

Gly Thr Ala Val Thr Val Ala Met Asp Gly Val Arg Pro Leu Leu Ala
 35 40 45

Glu Val Gln Ser Leu Leu Val Asp Ala Pro Ser Lys Asn Pro Arg Arg
 50 55 60

Val Val Thr Gly Leu Asp Ala Asn Arg Val Pro Met Val Leu Ala Val
 65 70 75 80

Leu Ser Ala Arg Ala Gly Arg Gln Thr Gln Gly Lys Asp Ala Tyr Val
 85 90 95

Ala Thr Val Gly Gly Met Lys Val Gly Glu Pro Ala Thr Asp Leu Ala
 100 105 110

Val Ala Leu Ala Thr Ala Ser Ala Leu Ala Lys Lys Pro Leu Pro Asp
 115 120 125

Lys Thr Val Val Leu Gly Glu Val Gly Leu Ala Gly Glu Ile Arg Arg
 130 135 140

Val Pro Asn Val Asp Arg Arg Leu Ala Glu Ala Glu Arg Leu Gly Tyr
 145 150 155 160

Glu Lys Ala Val Ile Pro Gly Gly Ser Gly Ile Lys Gln Thr Ser Leu
 165 170 175

Arg Val Ile Glu Ala Ser Thr Leu Ala Glu Ala Leu Ala Val Ser
 180 185 190

Leu

096028330 0622300

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aac ttc ctc ggc ggc gcc gag caa aag gca																	ctg	gtc	gcc	cag	gct	cga	163	
Asn	Phe	Leu	Gly	Leu	Ala	Glu	Gln	Lys	Ala	Leu	Val	Ala	Gln	Ala	Arg									
														10			20							
gac ctt gcg cgt gaa gtt gtg ggc aca ccg																	ttg	gcg	atg	gtc	cga	ccc	211	
Asp	Leu	Ala	Arg	Glu	Val	Val	Gly	Thr	Pro	Leu	Ala	Met	Val	Arg	Pro									
														25			35							
aag ctg aaa agt ggt cag atg agt gtc cat atg																	ttg	cat	tta	gga	aag	259		
Lys	Leu	Lys	Ser	Gly	Gln	Met	Ser	Val	His	Met	Leu	His	Leu	Gly	Lys									
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Tyr	Trp	Ala	Ser	Asn	Pro	Tyr	Arg	Tyr	Val	Asp	Val	Val	Asp	Gly	Phe									
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cca gtg cca cca ctg ccg gat tct ttc gtg gac																	ttg	gca	cac	cga	gca	355		
Pro	Val	Pro	Pro	Leu	Pro	Asp	Ser	Phe	Val	Asp	Leu	Ala	His	Arg	Ala									
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ttg ctg tct gca gga tct tta agc aat tca ctt																	cag	tct	tggt	tcg	gag	403		
Leu	Leu	Ser	Ala	Gly	Ser	Leu	Ser	Asn	Ser	Leu	Gln	Ser	Trp	Ser	Glu									
														90			100							
gca tat cga gca gaa gcg gca ttg gtg aat																	tac	tac	tcg	cca	gat	gct	451	
Ala	Tyr	Arg	Ala	Glu	Ala	Ala	Leu	Val	Asn	Tyr	Tyr	Ser	Pro	Asp	Ala									
														105			115							
tca atg ggc atg cac caa gac gct aat gaa																	gaa	tcg	gaa	gcc	cct	gtg	499	
Ser	Met	Gly	Met	His	Gln	Asp	Ala	Asn	Glu	Glu	Ser	Glu	Ala	Pro	Val									
														120			130							
atc tcc cta tcg atc ggt gat acc gga atc																	ttt	cga	ctg	ggc	ggc	act	547	
Ile	Ser	Leu	Ser	Ile	Gly	Asp	Thr	Gly	Ile	Phe	Arg	Leu	Gly	Gly	Thr									
														135			145							
cta aac cgc aat aaa ccg tgg aca gat atc																	cca	cta	atg	agt	ggt	gat	595	
Leu	Asn	Arg	Asn	Lys	Pro	Trp	Thr	Asp	Ile	Pro	Leu	Met	Ser	Gly	Asp									
														150			160							
ctc atc gtt ttc qqa ggt gca aac aqg																	caa	gca	ttt	cat	ggc	att	ccc	643

Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala Phe His Gly Ile Pro
 170 175 180
 tct att gag gcc aat act gca cct gca gga tgc ggg ttg aaa gaa ggg 691
 Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys Gly Leu Lys Glu Gly
 185 190 195
 gaa tca aca tca cga tcc gcc aac ttg cac tat aaa act cca ggt aga 739
 Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr Lys Thr Pro Gly Arg
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 ggt atg tct cgg ggg tgaaatagcc ccgcaatgtc cca 777
 Gly Met Ser Arg Gly
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Ala Met Val Arg Pro Lys Leu Lys Ser Gly Gln Met Ser Val His Met
 35 40 45
 Leu His Leu Gly Lys Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp
 50 55 60
 Val Val Asp Gly Phe Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp
 65 70 75 80
 Leu Ala His Arg Ala Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu
 85 90 95
 Gln Ser Trp Ser Glu Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr
 100 105 110
 Tyr Ser Pro Asp Ala Ser Met Gly Met His Gln Asp Ala Asn Glu Glu
 115 120 125
 Ser Glu Ala Pro Val Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe
 130 135 140
 Arg Leu Gly Gly Thr Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro
 145 150 155 160
 Leu Met Ser Gly Asp Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala
 165 170 175
 Phe His Gly Ile Pro Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys
 180 185 190
 Gly Leu Lys Glu Gly Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr
 195 200 205

00602639.062300

Lys Thr Pro Gly Arg Gly Met Ser Arg Gly
210 215

<210> 49

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(754)

<223> FRXA02291

<400> 49

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Val Val His Leu Pro
1 5

aac ttc ctc ggc ttg gcc gag caa aag gca ctg gtc gcc cag gct cga 163
Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu Val Ala Gln Ala Arg
10 15 20

gac ctt gcg cgt gaa gtt gtg gcc aca ccg ttg gcg atg gtc cga ccc 211
Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu Ala Met Val Arg Pro
25 30 35

aag ctg aaa agt ggt cag atg agt gtc cat atg ttg cat tta gga aag 259
Lys Leu Lys Ser Gly Gln Met Ser Val His Met Leu His Leu Gly Lys
40 45 50

tac tgg gca tcc aat cct tat cgc tat gtg gat gtc gtt gat ggt ttt 307
Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp Val Val Asp Gly Phe
55 60 65

cca gtg cca cca ctg ccg gat tct ttc gtg gac ttg gca cac cga gca 355
Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp Leu Ala His Arg Ala
70 75 80 85

ttg ctg tct gca gga tct tta agc aat tca ctt cag tct tgg tgg gag 403
Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu Gln Ser Trp Ser Glu
90 95 100

gca tat cga gca gaa gcg gca ttg gtg aat tac tac tgg cca gat gct 451
Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr Tyr Ser Pro Asp Ala
105 110 115

tca atg ggc atg cac caa gac gct aat gaa gaa tgg gaa gcc cct gtg 499
Ser Met Gly Met His Gln Asp Ala Asn Glu Glu Ser Glu Ala Pro Val
120 125 130

atc tcc cta tgg atc ggt gat acc gga atc ttt cga ctg gcc gcc act 547
Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe Arg Leu Gly Gly Thr
135 140 145

cta aac cgc aat aaa ccg tgg aca gat atc cca cta atg agt ggt gat 595
Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro Leu Met Ser Gly Asp
150 155 160 165

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ctc atc gtt ttc gga ggt gca aac agg caa gca ttt cat ggc att ccc 643
Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala Phe His Gly Ile Pro
170 175 180

tct att gag gcc aat act gca cct gca gga tgc ggg ttg aaa gaa ggg 691
Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys Gly Leu Lys Glu Gly
185 190 195

gaa tca aca tca cga tcc gcc aac ttg cac tat aaa act cca ggt aga 739
Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr Lys Thr Pro Gly Arg
200 205 210

ggt atg tct cgg ggg tgaaatagcc cgcgaatgtc cca 777
Gly Met Ser Arg Gly
215

<210> 50

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

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Val Ala Gln Ala Arg Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu
20 25 30

Ala Met Val Arg Pro Lys Leu Lys Ser Gly Gln Met Ser Val His Met
35 40 45

Leu His Leu Gly Lys Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp
50 55 60

Val Val Asp Gly Phe Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp
65 70 75 80

Leu Ala His Arg Ala Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu
85 90 95

Gln Ser Trp Ser Glu Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr
100 105 110

Tyr Ser Pro Asp Ala Ser Met Gly Met His Gln Asp Ala Asn Glu Glu
115 120 125






Ser Glu Ala Pro Val Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe
130 135 140

Arg Leu Gly Gly Thr Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro
145 150 155 160

Leu Met Ser Gly Asp Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala
165 170 175

Phe His Gly Ile Pro Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys
180 185 190

Gly Leu Lys Glu Gly Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr
195 200 205

				
$\text{CH}_3\text{CH}_2\text{Cl}_2$	CH_3CHCl_2	$\text{CH}_3\text{CHClCH}_2\text{Cl}$	$\text{CH}_3\text{CCl}_2\text{CH}_3$	$\text{CH}_2\text{ClCHClCH}_2\text{Cl}$
1,2-DCE	1,1-DCE	1,1,2-TCE	1,1,1-TCE	1,1,2,2-TCF

Lys Thr Pro Gly Arg Gly Met Ser Arg Gly
 210 215

<210> 51
 <211> 1274
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (70)..(1251)
 <223> RXN01733

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 Met His Ile Arg Ser Leu Glu Leu Arg Asp Tyr Arg Ser Trp
 1 5 10

cct gaa ctc aaa gtg gat ttg gaa cct gga att aca gtt ttt atc ggc 159
 Pro Glu Leu Lys Val Asp Leu Glu Pro Gly Ile Thr Val Phe Ile Gly
 15 20 25 30

cgc aac ggt ttt ggt aaa acc aac atc gtc gag gcc atc ggc tat ctt 207
 Arg Asn Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu
 35 40 45

gcg cat ttg tca tgc cat cgg gtg tcc tct gat gcg cca ttg gtg cgg 255
 Ala His Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg
 50 55 60

gcg cac gct gaa aac gcc cga gtt tgc gcg gtt gct gtt aat caa ggc 303
 Ala His Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly
 65 70 75

cga gaa ttg gca gct cac ttg ctg atc aaa ccc cat gct gcg aat cag 351
 Arg Glu Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln
 80 85 90

gca agt ttg aat cgc aca aaa gtc agg act ccc cgg gag ctg ctt ggt 399
 Ala Ser Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly
 95 100 105 110

gtg gtg aaa acg gtg ctg ttt gcg cgg gaa gat ttg gca tta gtc aaa 447
 Val Val Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys
 115 120 125

ggc gag cca gca gaa cgt cgc cgc tat tta gat gac att att gcc act 495
 Gly Glu Pro Ala Glu Arg Arg Arg Tyr Leu Asp Asp Ile Ile Ala Thr
 130 135 140

cgc cag cct cgg atg gcg ggg gtc aag gcc gac tac gac aag gtg ctg 543
 Arg Gln Pro Arg Met Ala Gly Val Lys Ala Asp Tyr Asp Lys Val Leu
 145 150 155

aaa caa agg aac gcc ctg ctc aag acc gcc acc att gcg ctt cgt cga 591
 Lys Gln Arg Asn Ala Leu Leu Lys Thr Ala Thr Ile Ala Leu Arg Arg
 160 165 170

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ggt tac ggc acc gag gaa ggc gca gct gcg ctg agt act ttg gat acc 639
 Gly Tyr Gly Thr Glu Glu Gly Ala Ala Ala Leu Ser Thr Leu Asp Thr
 175 180 185 190

tgg gat ggc cag ttg gca cgc ctg ggt gct gaa gtg atg gca gcc aga 687
 Trp Asp Gly Gln Leu Ala Arg Leu Gly Ala Glu Val Met Ala Ala Arg
 195 200 205

ttt gcc ctg ctc aat gag ttg ggg ccg aaa atc tat gag gct tac acc 735
 Phe Ala Leu Leu Asn Glu Leu Gly Pro Lys Ile Tyr Glu Ala Tyr Thr
 210 215 220

acg atc gcc ccg gaa tcc ccg cca gct gcg gtg aat tac aaa acc acc 783
 Thr Ile Ala Pro Glu Ser Arg Pro Ala Ala Val Asn Tyr Lys Thr Thr
 225 230 235

atc gat caa ggc ctg tcg cag ttt tcc gaa ttc gat gcc gcc atc atc 831
 Ile Asp Gln Gly Leu Ser Gln Phe Ser Glu Phe Asp Ala Gly Ile Ile
 240 245 250

gaa gcc acg ctg ctg aca gaa ttg gca gcg aaa cgt caa cga gaa atc 879
 Glu Ala Thr Leu Leu Thr Glu Leu Ala Ala Lys Arg Gln Arg Glu Ile
 255 260 265 270

gaa cgc ggc tca agc ctg gtc gcc ccc cac cgc gat gat gtc gat tta 927
 Glu Arg Gly Ser Ser Leu Val Gly Pro His Arg Asp Asp Val Asp Leu
 275 280 285

atg ctc ggc gat cag ccc gcc aaa ggc ttt gcc agc cac gcc gag acc 975
 Met Leu Gly Asp Gln Pro Ala Lys Gly Phe Ala Ser His Gly Glu Thr
 290 295 300

tgg tct ttc gcg ctt tca ctg cga att gca gaa ttt aac ctg ctg aaa 1023
 Trp Ser Phe Ala Leu Ser Leu Arg Ile Ala Glu Phe Asn Leu Leu Lys
 305 310 315

tcc gat ggc acc gac ccg atc ctc atc ttg gat gat gtg ttt tcc gag 1071
 Ser Asp Gly Thr Asp Pro Ile Leu Ile Leu Asp Asp Val Phe Ser Glu
 320 325 330

ctc gac gcc ggc cgt cgc gaa aaa ctc gtg ggc ata gcg caa gag gtg 1119
 Leu Asp Ala Gly Arg Arg Glu Lys Leu Val Gly Ile Ala Gln Glu Val
 335 340 345 350

gaa cag gtg ctc atc acc gct gca gtc cac gac gat ctg ccg gag aat 1167
 Glu Gln Val Leu Ile Thr Ala Ala Val His Asp Asp Leu Pro Glu Asn
 355 360 365

ctc aag aaa gtg ctc act gcg cag cac acc gtc acc gtc caa gac acc 1215
 Leu Lys Lys Val Leu Thr Ala Gln His Thr Val Thr Val Gln Asp Thr
 370 375 380

ggc acc ggg ccg att tca ctc ctg gat gtg caa cca tgacagatcc 1261
 Gly Thr Gly Arg Ile Ser Leu Leu Asp Val Gln Pro
 385 390

aattgagcag gca 1274

<211> 394
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 52
 Met His Ile Arg Ser Leu Glu Leu Arg Asp Tyr Arg Ser Trp Pro Glu
 1 5 10 15
 Leu Lys Val Asp Leu Glu Pro Gly Ile Thr Val Phe Ile Gly Arg Asn
 20 25 30
 Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu Ala His
 35 40 45
 Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg Ala His
 50 55 60
 Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly Arg Glu
 65 70 75 80
 Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln Ala Ser
 85 90 95
 Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly Val Val
 100 105 110
 Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys Gly Glu
 115 120 125
 Pro Ala Glu Arg Arg Arg Tyr Leu Asp Asp Ile Ile Ala Thr Arg Gln
 130 135 140
 Pro Arg Met Ala Gly Val Lys Ala Asp Tyr Asp Lys Val Leu Lys Gln
 145 150 155 160
 Arg Asn Ala Leu Leu Lys Thr Ala Thr Ile Ala Leu Arg Arg Gly Tyr
 165 170 175
 Gly Thr Glu Glu Gly Ala Ala Leu Ser Thr Leu Asp Thr Trp Asp
 180 185 190
 Gly Gln Leu Ala Arg Leu Gly Ala Glu Val Met Ala Ala Arg Phe Ala
 195 200 205
 Leu Leu Asn Glu Leu Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile
 210 215 220
 Ala Pro Glu Ser Arg Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp
 225 230 235 240
 Gln Gly Leu Ser Gln Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala
 245 250 255
 Thr Leu Leu Thr Glu Leu Ala Ala Lys Arg Gln Arg Glu Ile Glu Arg
 260 265 270
 Gly Ser Ser Leu Val Gly Pro His Arg Asp Asp Val Asp Leu Met Leu
 275 280 285
 Gly Asp Gln Pro Ala Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser
 290 295 300

00602300 00602300 00602300

Phe Ala Leu Ser Leu Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp
305 310 315 320

Gly Thr Asp Pro Ile Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp
325 330 335

Ala Gly Arg Arg Glu Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln
340 345 350

Val Leu Ile Thr Ala Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys
355 360 365

Lys Val Leu Thr Ala Gln His Thr Val Thr Val Gln Asp Thr Gly Thr
370 375 380

Gly Arg Ile Ser Leu Leu Asp Val Gln Pro
385 390

<210> 53

<211> 566

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(543)

<223> FRXA01733

<400> 53

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Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile Ala Pro Glu Ser Arg
1 5 10 15

cca gct gcg gtg aat tac aaa acc acc atc gat caa ggc ctg tcg cag 96
Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp Gln Gly Leu Ser Gln
20 25 30

ttt tcc gaa ttc gat gcc ggc atc atc gaa gcc acg ctg ctg aca gaa 144
Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala Thr Leu Leu Thr Glu
35 40 45

ttg gca gcg aaa cgt caa cga gaa atc gaa cgc ggc tca agc ctg gtc 192
Leu Ala Ala Lys Arg Gln Arg Glu Ile Glu Arg Gly Ser Ser Leu Val
50 55 60

ggc ccc cac cgc gat gat gtc gat tta atg ctc ggc gat cag ccc gcc 240
Gly Pro His Arg Asp Asp Val Asp Leu Met Leu Gly Asp Gln Pro Ala
65 70 75 80

aaa ggc ttt gcc agc cac ggc gag acc tgg tct ttc gcg ctt tca ctg 288
Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser Phe Ala Leu Ser Leu
85 90 95

cga att gca gaa ttt aac ctg ctg aaa tcc gat gcc acc gac ccg atc 336
Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp Gly Thr Asp Pro Ile
100 105 110

ctc atc ttg gat gat gtg ttt tcc gag ctc gac gcc ggc cgt cgc gaa 384
Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp Ala Gly Arg Arg Glu

00602830 062300

115	120	125	
aaa ctc gtg ggc ata gcg caa gag gtg gaa cag gtg ctc atc acc gct			432
Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln Val Leu Ile Thr Ala			
130	135	140	
gca gtc cac gac gat ctg ccg gag aat ctc aag aaa gtg ctc act gcg			480
Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys Lys Val Leu Thr Ala			
145	150	155	160
cag cac acc gtc acc gtc caa gac acc ggc acc ggg cgg att tca ctc			528
Gln His Thr Val Thr Val Gln Asp Thr Gly Thr Gly Arg Ile Ser Leu			
165	170	175	
ctg gat gtg caa cca tgacagatcc aattgagcag gca			566
Leu Asp Val Gln Pro			
180			

<210> 54

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile Ala Pro Glu Ser Arg		
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Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp Gln Gly Leu Ser Gln		
20	25	30

Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala Thr Leu Leu Thr Glu		
35	40	45

Leu Ala Ala Lys Arg Gln Arg Glu Ile Glu Arg Gly Ser Ser Leu Val		
50	55	60

Gly Pro His Arg Asp Asp Val Asp Leu Met Leu Gly Asp Gln Pro Ala		
65	70	75

Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser Phe Ala Leu Ser Leu		
85	90	95

Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp Gly Thr Asp Pro Ile		
100	105	110

Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp Ala Gly Arg Arg Glu		
115	120	125

Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln Val Leu Ile Thr Ala		
130	135	140

Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys Lys Val Leu Thr Ala		
145	150	155

Gln His Thr Val Thr Val Gln Asp Thr Gly Thr Gly Arg Ile Ser Leu		
165	170	175

Leu Asp Val Gln Pro
180

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 <211> 777
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(754)
 <223> RXA01252

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 ttccttgtcc aatttttagt tcagataggt agtctaagac gtg ttt gaa ggc cca 115
 Val Phe Glu Gly Pro
 1 5
 ctc cag gat ctc atc gac gaa ctt tct cgt ctc ccc ggc gtc ggc ccc 163
 Leu Gln Asp Leu Ile Asp Glu Leu Ser Arg Leu Pro Gly Val Gly Pro
 10 15 20
 aaa agt gcc caa cgc atc gca ttt cac ctg ctc aac gta gat cct tcc 211
 Lys Ser Ala Gln Arg Ile Ala Phe His Leu Leu Asn Val Asp Pro Ser
 25 30 35
 gac att acc cgc ctt cag gaa gcc ctc gga ggc gtg cgt gat ggc gtc 259
 Asp Ile Thr Arg Leu Gln Glu Ala Leu Gly Gly Val Arg Asp Gly Val
 40 45 50
 caa ttc tgc cgc atc tgc tgc aac att tcc cgc gaa gaa gtc tgt cgc 307
 Gln Phe Cys Arg Ile Cys Cys Asn Ile Ser Arg Glu Glu Val Cys Arg
 55 60 65
 atc tgc tcc gac tcc gga cgt gac ggc gga aca atc tgt gtc gtc gaa 355
 Ile Cys Ser Asp Ser Gly Arg Asp Gly Gly Thr Ile Cys Val Val Glu
 70 75 80 85
 gaa cca aaa gac atc caa gtt atc gag cgc acc ggc gaa ttc tcc ggc 403
 Glu Pro Lys Asp Ile Gln Val Ile Glu Arg Thr Gly Glu Phe Ser Gly
 90 95 100
 cgc tac cac gtc ctc ggc ggc gcc ctc gac ccg ctg gcc aac atc ggc 451
 Arg Tyr His Val Leu Gly Gly Ala Leu Asp Pro Leu Ala Asn Ile Gly
 105 110 115
 ccc cgc gaa ctc aac att tcc acg ctc ctg cag cgc atc ggc ggc gtc 499
 Pro Arg Glu Leu Asn Ile Ser Thr Leu Leu Gln Arg Ile Gly Gly Val
 120 125 130
 ctg cca gac cgt gag ctc gca gat tcc acg cct gaa aat aag ctt ttc 547
 Leu Pro Asp Arg Glu Leu Ala Asp Ser Thr Pro Glu Asn Lys Leu Phe
 135 140 145
 gac gcc acc ccc acc gtc cgc gaa gtc atc ctc gca aca gac ccc aac 595
 Asp Ala Thr Pro Thr Val Arg Glu Val Ile Leu Ala Thr Asp Pro Asn
 150 155 160 165
 acc gaa ggc gaa gcc acc gcc tca tac ctc ggc cgc ctc ttg aaa gac 643
 Thr Glu Gly Glu Ala Thr Ala Ser Tyr Leu Gly Arg Leu Leu Lys Asp
 170 175 180

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ttc cca gat ctg gta att tcc cgc ctc gca tcc gga atg cca cta ggc 691
Phe Pro Asp Leu Val Ile Ser Arg Leu Ala Ser Gly Met Pro Leu Gly
185 190 195

ggc gac ctc gaa ttc gtc gac gaa ctc act ctc tcc cga gca ttg agt 739
Gly Asp Leu Glu Phe Val Asp Glu Leu Thr Leu Ser Arg Ala Leu Ser
200 205 210

ggc cgc ctg cag atc tagccctcc ttacaggct ggc 777
Gly Arg Leu Gln Ile
215

<210> 56

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 56

Val Phe Glu Gly Pro Leu Gln Asp Leu Ile Asp Glu Leu Ser Arg Leu
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Pro Gly Val Gly Pro Lys Ser Ala Gln Arg Ile Ala Phe His Leu Leu
20 25 30

Asn Val Asp Pro Ser Asp Ile Thr Arg Leu Gln Glu Ala Leu Gly Gly
35 40 45

Val Arg Asp Gly Val Gln Phe Cys Arg Ile Cys Cys Asn Ile Ser Arg
50 55 60

Glu Glu Val Cys Arg Ile Cys Ser Asp Ser Gly Arg Asp Gly Gly Thr
65 70 75 80

Ile Cys Val Val Glu Glu Pro Lys Asp Ile Gln Val Ile Glu Arg Thr
85 90 95

Gly Glu Phe Ser Gly Arg Tyr His Val Leu Gly Gly Ala Leu Asp Pro
100 105 110

Leu Ala Asn Ile Gly Pro Arg Glu Leu Asn Ile Ser Thr Leu Leu Gln
115 120 125

Arg Ile Gly Gly Val Leu Pro Asp Arg Glu Leu Ala Asp Ser Thr Pro
130 135 140

Glu Asn Lys Leu Phe Asp Ala Thr Pro Thr Val Arg Glu Val Ile Leu
145 150 155 160

Ala Thr Asp Pro Asn Thr Glu Gly Glu Ala Thr Ala Ser Tyr Leu Gly
165 170 175

Arg Leu Leu Lys Asp Phe Pro Asp Leu Val Ile Ser Arg Leu Ala Ser
180 185 190

Gly Met Pro Leu Gly Gly Asp Leu Glu Phe Val Asp Glu Leu Thr Leu
195 200 205

Ser Arg Ala Leu Ser Gly Arg Leu Gln Ile
210 215

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<210> 57
<211> 1002
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(979)
<223> RXAQ1878
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atagtagaaa tctggcatcc aataggtaga ttgggatgct	atg gaa gaa ccc tca Met Glu Glu Pro Ser 1 5	115
ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag		163
Gly Ala Gln Leu Leu 10	Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys 20	
ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat		211
Leu Asp Val Thr 25	Pro Thr Lys Lys Leu 30	
ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat		211
Leu Asp Val Thr 25	Pro Thr Lys Lys Leu 30	
ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac		259
Pro Asn Thr Val Arg Arg Ile Val Ala Ala Glu Leu Thr Pro Asn		
gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc		307
Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala		
ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt		355
Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg		
ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt		403
Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu		
gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa		451
Ala His Lys Lys Ser Ile Val Leu Lys Asp Ala Met Lys Val Gln Gln		
tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac		499
Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr		
aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc		547
Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr		
atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg		595
Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu		
gct gcg gat cca gga tgc aag att tat ggt gtg cct agc gtg aag gcg		643
Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala		

170 175 180
 tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc 691
 Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val
 185 190 195
 ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739
 Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg
 200 205 210
 gaa gac acc cgc tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787
 Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp
 215 220 225
 ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct 835
 Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala
 230 235 240 245
 gcg ctt tct gga cac tac ggt tct gcc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
 250 255 260
 cgg gcc gct gat att gat cca acg ctt cgt gcc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275
 act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys
 280 285 290
 tgaaaattac cgctaaggcg tgg 1002

 <210> 58
 <211> 293
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 58
 Met Glu Glu Pro Ser Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg
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 Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln
 20 25 30
 Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala
 35 40 45
 Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60
 Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80
 Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95
 Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110
 Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val

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115 120 125
 Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140
 Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160
 Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175
 Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190
 Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205
 Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220
 Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240
 Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255
 Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
 260 265 270
 Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
 275 280 285
 Gln Lys Asp Glu Lys
 290
 <210> 59
 <211> 872
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (1)..(849)
 <223> RXA01556
 <400> 59
 aac atc cgc ttt gag acc ctc aac atc atg gga cct gcg cgt cgc atc 48
 Asn Ile Arg Phe Glu Thr Leu Asn Ile Met Gly Pro Ala Arg Arg Ile
 1 5 10 15
 cac ctg ggt cac gtg tgg aat gat cgc ctg acc ttt gaa tac agt cgc 96
 His Leu Gly His Val Trp Asn Asp Arg Leu Thr Phe Glu Tyr Ser Arg
 20 25 30
 tcg ctg ttc ggt aaa gag acc ctg tcg cca gac atc gcg cgc ctg ttc 144
 Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe
 35 40 45
 acc gac cgc gtt ccc acc cct ccg ctg cca gct ccg cgt aaa gcg cgc 192
 Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg

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50	55	60	
gca gtg gcg cag gtg	ctg gtg tcc aac cct gcg gat	cag acc agt ttg	240
Ala Val Ala Gln Val	Leu Val Ser Asn Pro	Ala Asp Gln Thr Ser Leu	
65	70	80	
gaa gaa ttt gcg gag atc	caa ggc gtt tcg gcg cgt act	ttg cag cgc	288
Glu Glu Phe Ala Glu Ile	Gln Gly Val Ser Ala Arg Thr	Leu Gln Arg	
85	90	95	
cag ttc ctc aaa tcc acg ggc	tat tca ttc agc gaa tgg	cgt gct gcg	336
Gln Phe Leu Lys Ser Thr	Gly Tyr Ser Phe Ser Glu Trp	Arg Ala Ala	
100	105	110	
cag cgc gtc tgc gtc gcc	gcg agc ctg ctg gcc cac	gac ttc agc att	384
Gln Arg Val Cys Val Ala	Ala Ser Leu Leu Ala His	Asp Phe Ser Ile	
115	120	125	
tca gtg gtt gcg aac ctc	gtc ggg ttc gcc gcg acc	agc agc ttg acc	432
Ser Val Val Ala Asn Leu	Val Gly Phe Ala Ala Thr	Ser Ser Ser Leu Thr	
130	135	140	
aga gct ttt cga cgc cac	acc ggt gca act ccg tcc	acc ttt act act	480
Arg Ala Phe Arg Arg His	Thr Gly Ala Thr Pro Ser	Thr Phe Thr Thr	
145	150	155	160
gga cag atc ggc atg ggc	tcc gca ggt cac oca oca	cgc atc cca gca	528
Gly Gln Ile Gly Met Gly	Ser Ala Gly His Pro Pro	Arg Ile Pro Ala	
165	170	175	
acc acc acg ttt gcc	gaa gcg cat cag gac	cag cag ctg tgg att tac	576
Thr Thr Thr Phe Ala	Glu Ala His Gln Asp	Gln Gln Leu Trp Ile Tyr	
180	185	190	
agc gga acc gca acc	gtc acc acc ccc ggc	tac tgc cga ttc atg gga	624
Ser Gly Thr Ala Thr Val	Thr Thr Pro Gly Tyr Cys	Arg Phe Met Gly	
195	200	205	
caa ggt gac atg gtg	acc atc cct gcc ggc	acc caa acc cgc att gac	672
Gln Gly Asp Met Val Thr	Ile Pro Ala Gly Thr	Gln Thr Arg Ile Asp	
210	215	220	
gtg gca gcc gga tcc	atc gca ttc cca gtc	cca gtt gga ctc gac gaa	720
Val Ala Ala Gly Ser	Ile Ala Phe Pro Val Pro	Val Gly Leu Asp Glu	
225	230	235	240
tgg gga atg gac cta	acc cgc gtc gtg gct gtt	aat aac cag cag cca	768
Trp Gly Met Asp Leu Thr	Arg Val Val Ala Val Asn	Asn Gln Gln Pro	
245	250	255	
aag cca ctg acc att	ttg gaa cag tct gaa tgg	tcc aag ctc agc gaa	816
Lys Pro Leu Thr Ile	Leu Glu Gln Ser Glu Trp	Ser Lys Leu Ser Glu	
260	265	270	
gaa ctt ctg aac act	cct gta cct gta caa atg	tgaaggtagt aaaggtgtga	869
Glu Leu Leu Asn Thr	Pro Val Pro Val Gln Met		
275	280		
aaa			872

006290.6880960

0609

<400>	60
Asn Ile Arg Phe Glu Thr Leu Asn Ile Met Gly Pro Ala Arg Arg Ile	
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Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe	
35 40 45	
Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg	
50 55 60	
Ala Val Ala Gln Val Leu Val Ser Asn Pro Ala Asp Gln Thr Ser Leu	
65 70 75 80	
Glu Glu Phe Ala Glu Ile Gln Gly Val Ser Ala Arg Thr Leu Gln Arg	
85 90 95	
Gln Phe Leu Lys Ser Thr Gly Tyr Ser Phe Ser Glu Trp Arg Ala Ala	
100 105 110	
Gln Arg Val Cys Val Ala Ala Ser Leu Leu Ala His Asp Phe Ser Ile	
115 120 125	
Ser Val Val Ala Asn Leu Val Gly Phe Ala Ala Thr Ser Ser Leu Thr	
130 135 140	
Arg Ala Phe Arg Arg His Thr Gly Ala Thr Pro Ser Thr Phe Thr Thr	
145 150 155 160	
Gly Gln Ile Gly Met Gly Ser Ala Gly His Pro Pro Arg Ile Pro Ala	
165 170 175	
Thr Thr Thr Phe Ala Glu Ala His Gln Asp Gln Gln Leu Trp Ile Tyr	
180 185 190	
Ser Gly Thr Ala Thr Val Thr Thr Pro Gly Tyr Cys Arg Phe Met Gly	
195 200 205	
Gln Gly Asp Met Val Thr Ile Pro Ala Gly Thr Gln Thr Arg Ile Asp	
210 215 220	
Val Ala Ala Gly Ser Ile Ala Phe Pro Val Pro Val Gly Leu Asp Glu	
225 230 235	
Trp Gly Met Asp Leu Thr Arg Val Val Ala Val Asn Asn Gln Gln Pro	
245 250 255	
Lys Pro Leu Thr Ile Leu Glu Gln Ser Glu Trp Ser Lys Leu Ser Glu	
260 265 270	
Glu Leu Leu Asn Thr Pro Val Pro Val Gln Met	
275 280	

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 <211> 516
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(493)
 <223> RXA00053

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 gttagcattg ggtttctgac cagtagttct gaggagaatc gtg aag aaa cgc atc 115
 Val Lys Lys Arg Ile
 1 5
 aat gta acc ggc gcc gtc cta gtc aag gaa aac cgt atc ctt gca gca 163
 Asn Val Thr Gly Ala Val Leu Val Lys Glu Asn Arg Ile Leu Ala Ala
 10 15 20
 caa cgt ggt cca gag atg tca ctt ccc gga tat tgg gag ttt ccg gga 211
 Gln Arg Gly Pro Glu Met Ser Leu Pro Gly Tyr Trp Glu Phe Pro Gly
 25 30 35
 gga aag atc gag cag gcc gaa act cca gaa gct tca ctt gca cga gag 259
 Gly Lys Ile Glu Gln Gly Glu Thr Pro Glu Ala Ser Leu Ala Arg Glu
 40 45 50
 ctc aaa gaa gaa ttg ctt tgc gac gcc acc gta ggc gaa cac ctc acc 307
 Leu Lys Glu Glu Leu Leu Cys Asp Ala Thr Val Gly Glu His Leu Thr
 55 60 65
 act aca gag cac gag tac gac ttt gga atc gtc gtg ctt tcc acc tac 355
 Thr Thr Glu His Glu Tyr Asp Phe Gly Ile Val Val Leu Ser Thr Tyr
 70 75 80 85
 ttc tgc aca cta aat gat gca gag cct caa ttg acc gag cat gct gag 403
 Phe Cys Thr Leu Asn Asp Ala Glu Pro Gln Leu Thr Glu His Ala Glu
 90 95 100
 atc cgc tgg gtg gca cca cac gaa ttg gaa tct ttg gag tgg gca cct 451
 Ile Arg Trp Val Ala Pro His Glu Leu Glu Ser Leu Glu Trp Ala Pro
 105 110 115
 gct gat att cct gcg gtg aaa ctt ctc gtc gag cag ctt gct 493
 Ala Asp Ile Pro Ala Val Lys Leu Leu Val Glu Gln Leu Ala
 120 125 130
 taatgagccc attcgattca aag 516

<210> 62
 <211> 131
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 62
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 1 5 10 15

005602030 00560300

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      20                      25                      30
Trp Glu Phe Pro Gly Gly Lys Ile Glu Gln Gly Glu Thr Pro Glu Ala
      35                      40                      45
Ser Leu Ala Arg Glu Leu Lys Glu Glu Leu Leu Cys Asp Ala Thr Val
      50                      55                      60
Gly Glu His Leu Thr Thr Thr Glu His Glu Tyr Asp Phe Gly Ile Val
      65                      70                      75                      80
Val Leu Ser Thr Tyr Phe Cys Thr Leu Asn Asp Ala Glu Pro Gln Leu
      85                      90                      95
Thr Glu His Ala Glu Ile Arg Trp Val Ala Pro His Glu Leu Glu Ser
      100                     105                     110
Leu Glu Trp Ala Pro Ala Asp Ile Pro Ala Val Lys Leu Leu Val Glu
      115                     120                     125
Gln Leu Ala
      130

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<210> 63
<211> 624
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(601)
<223> RXA00280

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                                         Val Asp Thr Met Lys
                                         1                      5
ggc gac ggc gat gga tgg gca gca gca ccc aat ggc ggg gca gta tgg 163
Gly Asp Gly Asp Gly Trp Ala Ala Ala Pro Asn Gly Gly Ala Val Trp
                        10                      15                      20
ggc aaa aac gga gca gca gga ttg ttg ttg gta gca gat aaa caa atg 211
Gly Lys Asn Gly Ala Ala Gly Leu Leu Leu Val Ala Asp Lys Lys Gln Met
                        25                      30                      35
ctc atg cag cac cga gcc gca tgg acc aac aac ggc gac acc tgg gca 259
Leu Met Gln His Arg Ala Ala Trp Thr Asn Asn Gly Asp Thr Trp Ala
                        40                      45                      50
ctc cct gga ggc gca cga gac tca cat gaa acc gca gcg gaa tca gcc 307
Leu Pro Gly Gly Ala Arg Asp Ser His Glu Thr Ala Ala Glu Ser Ala
                        55                      60                      65
ctg cgt gaa gca ttt gaa gaa act gga atc ctg ccc gac gac gtg gaa 355
Leu Arg Glu Ala Phe Glu Glu Thr Gly Ile Leu Pro Asp Asp Val Glu
                        70                      75                      80                      85

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002290.6220960

gtt tta gat tca ata gtc acc gca ggc cct ttt ccc gcc gat cca gaa 403
 Val Leu Asp Ser Ile Val Thr Ala Gly Pro Phe Pro Ala Asp Pro Glu
 90 95 100

cgc cca gaa ctt gcc ggc aac tgg acc tac acc acg gtc atc gca cga 451
 Arg Pro Glu Leu Ala Gly Asn Trp Thr Tyr Thr Thr Val Ile Ala Arg
 105 110 115

act aaa acc ggc gaa acc cta gat acc acc gct aat gaa gaa tcc ctc 499
 Thr Lys Thr Gly Glu Thr Leu Asp Thr Thr Ala Asn Glu Glu Ser Leu
 120 125 130

gaa cta cgg tgg gta gat atc gca gcg gtt gac tct ttg gct ttg atg 547
 Glu Leu Arg Trp Val Asp Ile Ala Ala Val Asp Ser Leu Ala Leu Met
 135 140 145

cca gca ttc gcc aaa gcg tgg ccc tct tta aga aag cta ctg aac aca 595
 Pro Ala Phe Ala Lys Ala Trp Pro Ser Leu Arg Lys Leu Leu Asn Thr
 150 155 160 165

aca gag taggtttatg cgacactggt gcg 624
 Thr Glu

<210> 64
 <211> 167
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 64
 Val Asp Thr Met Lys Gly Asp Gly Asp Gly Trp Ala Ala Ala Pro Asn
 1 5 10 15
 Gly Gly Ala Val Trp Gly Lys Asn Gly Ala Ala Gly Leu Leu Val
 20 25 30
 Ala Asp Lys Gln Met Leu Met Gln His Arg Ala Ala Trp Thr Asn Asn
 35 40 45
 Gly Asp Thr Trp Ala Leu Pro Gly Gly Ala Arg Asp Ser His Glu Thr
 50 55 60
 Ala Ala Glu Ser Ala Leu Arg Glu Ala Phe Glu Glu Thr Gly Ile Leu
 65 70 75 80
 Pro Asp Asp Val Glu Val Leu Asp Ser Ile Val Thr Ala Gly Pro Phe
 85 90 95
 Pro Ala Asp Pro Glu Arg Pro Glu Leu Ala Gly Asn Trp Thr Tyr Thr
 100 105 110
 Thr Val Ile Ala Arg Thr Lys Thr Gly Glu Thr Leu Asp Thr Thr Ala
 115 120 125
 Asn Glu Glu Ser Leu Glu Leu Arg Trp Val Asp Ile Ala Ala Val Asp
 130 135 140
 Ser Leu Ala Leu Met Pro Ala Phe Ala Lys Ala Trp Pro Ser Leu Arg
 145 150 155 160

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Lys Leu Leu Asn Thr Thr Glu
165

<210> 65
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXA00333

<400> 65
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cctgggagtc aaagattacc aattggagag gttttgctgc atg gcg gtt cca gag 115
Met Ala Val Pro Glu
1 5
ttc att gtt agt ttg cgg gag aag gtc ggt cag gat ccg ttg tgg ttg 163
Phe Ile Val Ser Leu Arg Glu Lys Val Gly Gln Asp Pro Leu Trp Leu
10 15 20
ccg gct gta act gcg gtt gtt att cgt gat gtt cct ccg ggg tct cct 211
Pro Ala Val Thr Ala Val Val Ile Arg Asp Val Pro Pro Gly Ser Pro
25 30 35
ttc cat gtg gtt ccg gat gtg ttg ttg gtc aag cgc gct gat act ggt 259
Phe His Val Val Pro Asp Val Leu Leu Val Lys Arg Ala Asp Thr Gly
40 45 50
gag tgg act cca ccg acc ggt att tgt gat ccg gat gag cag cct cat 307
Glu Trp Thr Pro Pro Thr Gly Ile Cys Asp Pro Asp Glu Gln Pro His
55 60 65
gtg act gcg gtg cgt gaa gtc aag gag gaa acc ggc ctt gat gtc agc 355
Val Thr Ala Val Arg Glu Val Lys Glu Glu Thr Gly Leu Asp Val Ser
70 75 80 85
gtt gag gcg ttg ctt ggc gtg ggc gcg gtg ggg cct gtg acc tat caa 403
Val Glu Ala Leu Leu Gly Val Gly Ala Val Gly Pro Val Thr Tyr Gln
90 95 100
aat ggt gat gtg gcg agc tac atg gat acg acc atg cgt tgc gtt gtt 451
Asn Gly Asp Val Ala Ser Tyr Met Asp Thr Thr Met Arg Cys Val Val
105 110 115
tct ggt gat tcc gat gag cct cac gtc ggc gat gac gag aac gtg gat 499
Ser Gly Asp Ser Asp Glu Pro His Val Gly Asp Asp Glu Asn Val Asp
120 125 130
gtt gca tgg ttc ccg att tct aag atg cct gtc act aat cag cgt ttc 547
Val Ala Trp Phe Pro Ile Ser Lys Met Pro Val Thr Asn Gln Arg Phe
135 140 145
cgc atg gtc atc gct gat gcg gtg gca cag ttg aag cat ccg caa ggt 595
Arg Met Val Ile Ala Asp Ala Val Ala Gln Leu Lys His Pro Gln Gly
150 155 160 165

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tat aag ccc cgc atg gga tat gag aaa agg aat gca cga tgagtattga 644
Tyr Lys Pro Arg Met Gly Tyr Glu Lys Arg Asn Ala Arg
170 175

atttccggtta ggt 657

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<210> 66
<211> 178
<212> PRT
<213> Corynebacterium glutamicum
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<400> 66
Met Ala Val Pro Glu Phe Ile Val Ser Leu Arg Glu Lys Val Gly Gln
  1           5           10          15
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Asp Pro Leu Trp Leu Pro Ala Val Thr Ala Val Val Ile Arg Asp Val
20 25 30

Pro Pro Gly Ser Pro Phe His Val Val Pro Asp Val Leu Leu Val Lys
35 40 45

Arg Ala Asp Thr Gly Glu Trp Thr Pro Pro Thr Gly Ile Cys Asp Pro
50 55 60

Asp Glu Gln Pro His Val Thr Ala Val Arg Glu Val Lys Glu Glu Thr
65 70 75 80

Gly Leu Asp Val Ser Val Glu Ala Leu Leu Gly Val Gly Ala Val Gly
85 90 95

Pro Val Thr Tyr Gln Asn Gly Asp Val Ala Ser Tyr Met Asp Thr Thr
100 105 110

Met Arg Cys Val Val Ser Gly Asp Ser Asp Glu Pro His Val Gly Asp
115 120 125

Asp Glu Asn Val Asp Val Ala Trp Phe Pro Ile Ser Lys Met Pro Val
130 135 140

Thr Asn Gln Arg Phe Arg Met Val Ile Ala Asp Ala Val Ala Gln Leu
145 150 155 160

Lys His Pro Gln Gly Tyr Lys Pro Arg Met Gly Tyr Glu Lys Arg Asn
165 170 175

Ala Arg

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<210> 67
<211> 741
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(718)
<223> RXA02110
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06908

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accctaaggt gggtttcttgc ccgcttcacc tgaaatccag atg gcc gta tcc acg																115
Met Ala Val Ser Thr																5
atc atc ttc gcg ctg cgc ccc ggc ccc cag gat ctc ccc agc ctg tgg																163
Ile Ile Phe Ala Leu Arg Pro Gly Pro Gln Asp Leu Pro Ser Leu Trp																20
gcc ccc ttc gtt ccg cgc acc cgc gaa cca cat tta aat aaa tgg gca																211
Ala Pro Phe Val Pro Arg Thr Arg Glu Pro His Leu Asn Lys Trp Ala																35
ctg ccc ggc ggt tgg ctg cca cca cat gaa gaa ctt gaa gat gct gct																259
Leu Pro Gly Gly Trp Leu Pro Pro His Glu Glu Leu Glu Asp Ala Ala																40
gcc cgc aca ctc gca gaa acc acc ggc ctg cac ccc agc tat cta gaa																307
Ala Arg Thr Leu Ala Glu Thr Thr Gly Leu His Pro Ser Tyr Leu Glu																55
cag ctc tac act ttc gga aaa gtc gac cgc tcc cca acc gga cgc gtg																355
Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser Pro Thr Gly Arg Val																70 75 80 85
atc tct gtg gtg tat tgg gca ctt gtc cga gcc gat gaa gcg ttg aaa																403
Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala Asp Glu Ala Leu Lys																90 95 100
gcc atc cca gga gaa aac gtc cag tgg ttt ccc gcc gat cat ctc cct																451
Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro Ala Asp His Leu Pro																105 110 115
gag ctg gca ttt gac cac aat aac atc gtc aaa tat gca cta gaa cga																499
Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys Tyr Ala Leu Glu Arg																120 125 130
ctt cgc acc aag gtg gaa tac tcc gaa atc gcc cac tcc ttc ctc gga																547
Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala His Ser Phe Leu Gly																135 140 145
gaa acc ttc acc atc gcc cag ctt cga tcc gtg cat gag gca gtc ctt																595
Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val His Glu Ala Val Leu																150 155 160 165
gga cac aaa ctc gat gcc gcc aac ttc cga aga tcc gtg gcc acc tcg																643
Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg Ser Val Ala Thr Ser																170 175 180
ccc gat ctg atc gac acc ggc gaa gtg ctt gcg gga aca ccg cac cgc																691
Pro Asp Leu Ile Asp Thr Gly Glu Val Leu Ala Gly Thr Pro His Arg																185 190 195
cca ccc aaa ctg ttc aga ttc caa aga taaattctga cgctcatccc																738
Pro Pro Lys Leu Phe Arg Phe Gln Arg																200 205
aac																741

<210> 68
 <211> 206
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 68
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 1 5 10 15
 Leu Pro Ser Leu Trp Ala Pro Phe Val Pro Arg Thr Arg Glu Pro His
 20 25 30
 Leu Asn Lys Trp Ala Leu Pro Gly Gly Trp Leu Pro Pro His Glu Glu
 35 40 45
 Leu Glu Asp Ala Ala Ala Arg Thr Leu Ala Glu Thr Thr Gly Leu His
 50 55 60
 Pro Ser Tyr Leu Glu Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser
 65 70 75 80
 Pro Thr Gly Arg Val Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala
 85 90 95
 Asp Glu Ala Leu Lys Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro
 100 105 110
 Ala Asp His Leu Pro Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys
 115 120 125
 Tyr Ala Leu Glu Arg Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala
 130 135 140
 His Ser Phe Leu Gly Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val
 145 150 155 160
 His Glu Ala Val Leu Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg
 165 170 175
 Ser Val Ala Thr Ser Pro Asp Leu Ile Asp Thr Gly Glu Val Leu Ala
 180 185 190
 Gly Thr Pro His Arg Pro Pro Lys Leu Phe Arg Phe Gln Arg
 195 200 205

<210> 69
 <211> 522
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(499)
 <223> RXA02290

<400> 69
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Val Asp Leu Asn Ala
 1 5
 ctt ttt gag atc ttg acg ttg gta gtt ttc caa gtg ggt gtc acc tgg 163
 Leu Phe Glu Ile Leu Thr Leu Val Val Phe Gln Val Gly Val Thr Trp
 10 15 20
 cat gct gtg ctg tcc aaa cgg gaa ggg ttc cgt caa gca ttc gcc caa 211
 His Ala Val Leu Ser Lys Arg Glu Gly Phe Arg Gln Ala Phe Ala Gln
 25 30 35
 ttc gat gtt gca aaa gta gcc gcc ttc aat gag gac gac gtg gaa cgc 259
 Phe Asp Val Ala Lys Val Ala Ala Phe Asn Glu Asp Asp Val Glu Arg
 40 45 50
 cta ctt gat gat cta cag att ttt aga aac cga aga aaa atc aac gct 307
 Leu Leu Asp Asp Leu Gln Ile Phe Arg Asn Arg Arg Lys Ile Asn Ala
 55 60 65
 gcc atc acc aat gcc aaa gcg ttg ctg gag tta aac gat gaa aca ggc 355
 Ala Ile Thr Asn Ala Lys Ala Leu Leu Glu Leu Asn Asp Glu Thr Gly
 70 75 80 85
 acc ttt gac tca att att gcc gac cac tca act gac gcc aca gcc atg 403
 Thr Phe Asp Ser Ile Ile Ala Asp His Ser Thr Asp Ala Thr Ala Met
 90 95 100
 gtg aag cat ctc aaa gcc ttg ggc ttt acc cat atc gga ctg acc tcc 451
 Val Lys His Leu Lys Ala Leu Gly Phe Thr His Ile Gly Leu Thr Ser
 105 110 115
 ttg agc atc ctc cag cag gcc att ggg gtc aca gag ctg aag gct gcc 499
 Leu Ser Ile Leu Gln Gln Ala Ile Gly Val Thr Glu Leu Lys Ala Ala
 120 125 130
 taagatatataa ctccgatgac aac 522

 <210> 70
 <211> 133
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 70
 Val Asp Leu Asn Ala Leu Phe Glu Ile Leu Thr Leu Val Val Phe Gln
 1 5 10 15
 Val Gly Val Thr Trp His Ala Val Leu Ser Lys Arg Glu Gly Phe Arg
 20 25 30
 Gln Ala Phe Ala Gln Phe Asp Val Ala Lys Val Ala Ala Phe Asn Glu
 35 40 45
 Asp Asp Val Glu Arg Leu Leu Asp Asp Leu Gln Ile Phe Arg Asn Arg
 50 55 60
 Arg Lys Ile Asn Ala Ala Ile Thr Asn Ala Lys Ala Leu Leu Glu Leu
 65 70 75 80
 Asn Asp Glu Thr Gly Thr Phe Asp Ser Ile Ile Ala Asp His Ser Thr
 85 90 95

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Asp Ala Thr Ala Met Val Lys His Leu Lys Ala Leu Gly Phe Thr His
100 105 110

Ile Gly Leu Thr Ser Leu Ser Ile Leu Gln Gln Ala Ile Gly Val Thr
115 120 125

Glu Leu Lys Ala Ala
130

<210> 71

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(688)

<223> RXA02557

<400> 71

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ttgggggatat ccgagagccc ggccgcccga aggagaatcc atg agt tca tta atc 115
Met Ser Ser Leu Ile
1 5

gtt gcc acg gac gcc ctc agt cgc ccg agt tgg gct gcg caa gat ccc 163
Val Gly Thr Asp Gly Leu Ser Arg Pro Ser Trp Ala Ala Gln Asp Pro
10 15 20

ctg atg cgc gat tat tac gac acc gag tgg gga atg ccg att cgc gat 211
Leu Met Arg Asp Tyr Tyr Asp Thr Glu Trp Gly Met Pro Ile Arg Asp
25 30 35

gaa cag gga tta ttc gaa aga gtt agt ctg gaa gct ttt caa tcc ggg 259
Glu Gln Gly Leu Phe Glu Arg Val Ser Leu Glu Ala Phe Gln Ser Gly
40 45 50

ctg tcc tgg gcg acg att ttg cgc aag cgc gat agt ttc cgc gca gct 307
Leu Ser Trp Ala Thr Ile Leu Arg Lys Arg Asp Ser Phe Arg Ala Ala
55 60 65

ttc tct cag ttt gat ccg gaa tta gtc gca aaa ttc acc gat gct gac 355
Phe Ser Gln Phe Asp Pro Glu Leu Val Ala Lys Phe Thr Asp Ala Asp
70 75 80 85

atc gaa cgc ctc atg gag gac gcc gcc atc gtg cgc aac aaa cgt aaa 403
Ile Glu Arg Leu Met Glu Asp Ala Gly Ile Val Arg Asn Lys Arg Lys
90 95 100

att ttg gcc acc att aac aac gcc aaa gcc acc ctt caa ttg cgt gag 451
Ile Leu Ala Thr Ile Asn Asn Ala Lys Ala Thr Leu Gln Leu Arg Glu
105 110 115

aag ggt gcc ttg gtg gaa ttt gta tgg ggt ttc aaa ccg att gat acc 499
Lys Gly Gly Leu Val Glu Phe Val Trp Gly Phe Lys Pro Ile Asp Thr
120 125 130

cca cag ccg gag acc ctg gag gag att ccg acg cag tcc ccg gag tca 547

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<210> 72
<211> 196
<212> PRT
<213> Corynebacterium glutamicum
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[illegible]

75

195

<210> 73
 <211> 110
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(87)
 <223> RXA02130

<400> 73
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 Met Thr Ser Asp Leu Gln Ser Arg Arg Leu Gly Leu Thr Ala Thr
 1 5 10 15
 ctc gtg cgc gaa gac gga cga gaa ggc gat gtc tca gcc tgatcgggcc 97
 Leu Val Arg Glu Asp Gly Arg Glu Gly Asp Val Ser Ala
 20 25
 caagcggttac gac 110

<210> 74
 <211> 29
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 74
 Met Thr Ser Asp Leu Gln Ser Arg Arg Leu Gly Leu Thr Ala Thr
 1 5 10 15
 Leu Val Arg Glu Asp Gly Arg Glu Gly Asp Val Ser Ala
 20 25

<210> 75
 <211> 2472
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2449)
 <223> RXA02742

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 ttcgaacagt ccagaatagc cctgacctag acttagagct atg tcc gaa caa aga 115
 Met Ser Glu Gln Arg
 1 5
 ctc gat cag ctt gag cga cgg ctt tct gaa ctg gaa cgg gag atc gcc 163
 Leu Asp Gln Leu Glu Arg Arg Leu Ser Glu Leu Glu Arg Glu Ile Ala
 10 15 20
 gcg att cgt cag gag atc cgc cag gaa cgc cta gtg ctt ccg gaa ccg 211
 Ala Ile Arg Gln Glu Ile Arg Gln Glu Arg Leu Val Leu Pro Glu Pro

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25										30										35																
gaa Glu	cct Pro	gtg Val	aaa Lys	gtt Val	gat Asp	aca Thr	gtc Ala	atc Ile	gcc Ala	acc Thr	gaa Glu	gcg Ala	acc Thr	gga Gly	gtc Val	259																				
40																45										50										
aat Asn	gca Ala	tcg Ser	tcg Ser	ggt Gly	ccg Pro	gag Glu	gcg Ala	aag Lys	atc Ile	gct Ala	ttg Leu	ttc Phe	atg Met	gag Glu	agg Arg	307																				
55																60										65										
ttt Phe	agt Ser	ggt Gly	cgc Arg	cac His	gat Asp	gtg Val	tat Tyr	gcg Ala	cgg Arg	cgc Arg	tgg Trp	acc Thr	agc Ser	aga Arg	aaa Lys	355																				
70																75										80										
acg Thr	ggc Gly	aaa Lys	agt Ser	gga Gly	tgg Trp	tcg Ser	ccg Pro	gct Thr	act Thr	cgc Arg	cag Gln	ggt Gly	ttt Phe	tac Tyr	tca Ser	403																				
90																95										100										
aaa Lys	gac Asp	acc Thr	aca Thr	ccg Pro	aag Lys	gac Asp	tat Tyr	ctc Leu	ccc Pro	ttc Phe	acc Thr	gtt Val	gac Asp	acc Thr	gtc Val	451																				
105																110										115										
aat Asn	gcg Ala	cat His	ctg Leu	cgc Arg	ccg Arg	ggc Gly	ggc Gly	gac Asp	cat His	atc Ile	ggt Gly	ctc Leu	tat Tyr	gtg Val	atg Met	499																				
120																125										130										
gtc Val	ccc Pro	atc Ile	gac Asp	acg Thr	tcg Cys	aaa Lys	ctt Leu	ctc Leu	gcc Ala	tgc Cys	gat Asp	ttc Phe	gac Asp	gat Asp	ggc Gly	547																				
135																140										145										
acc Thr	tgg Trp	aag Lys	caa Gln	gat Asp	gcg Ala	gcc Ala	gct Ala	ttc Phe	gtg Val	tca Ser	gcc Ala	tgc Cys	acc Thr	gac Asp	cac His	595																				
150																155										160										
gga Gly	atc Ile	gat Asp	gcg Ala	ttg Leu	gct Ala	gaa Glu	att Ile	tct Ser	cga Arg	tcc Ser	gac Asp	gac Asp	ggc Gly	gcc Ala	ccc Pro	643																				
170																175										180										
gtg Val	tgg Trp	ata Ile	ttt Phe	ttc Phe	gat Asp	acc Thr	cca Pro	atc Ile	tcc Ser	gcg Ala	atg Met	ctg Leu	gct Ala	cgg Arg	cgc Arg	691																				
185																190										195										
cta Leu	ggt Gly	ttt Phe	gcc Ala	atg Met	ctc Leu	cgc Arg	caa Gln	gcc Ala	atg Met	aac Asn	tcc Ser	cgc Arg	cct Pro	gac Asp	atg Met	739																				
200																205										210										
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215																220										225										
acg Thr	cgc Arg	gca Ala	aac Asn	gga Gly	agc Ser	gca Ser	cgg Arg	ctg Leu	gga Gly	aat Asn	ttg Leu	atc Ile	gcg Ala	ctg Leu	ccc Pro	835																				
230																235										240										
ctc Leu	aac Asn	ggc Gly	gac Asp	tgt Cys	cga Arg	gcc Ala	cgc Arg	aac Asn	acc Thr	gcc Ala	gtc Val	ttc Phe	gcc Ala	gat Asp	tcg Ser	883																				
250																255										260										
gaa Glu	acg Thr	tgg Trp	gtt Val	ccc Pro	ttc Phe	gaa Glu	gat Asp	cct Pro	ttc Phe	gca Ala	gcg Ala	ctc Leu	gcg Ala	gcc Ala	atc Ile	931																				
265																270										275										

acg cca cta gcc acc gaa aaa atc gag cag atc ctt gcc acc acg cag 979
 Thr Pro Leu Ala Thr Glu Lys Ile Glu Gln Ile Leu Ala Thr Thr Gln
 280 285 290

gaa aaa ttt ggc ccc gaa ccc gaa cac atc aaa cgc ccc acc cgc gcc 1027
 Glu Lys Phe Gly Pro Glu Pro Glu His Ile Lys Arg Pro Thr Arg Ala
 295 300 305

gaa ctc aaa cag gtt aaa gcc aac ggc gaa acc atc aaa ctc acc atc 1075
 Glu Leu Lys Gln Val Lys Ala Asn Gly Glu Thr Ile Lys Leu Thr Ile
 310 315 320 325

acc aac gag ctg agc gtc ccc acc gaa agg tta ccc gcg gcc gtc atc 1123
 Thr Asn Glu Leu Ser Val Pro Thr Glu Arg Leu Pro Ala Ala Val Ile
 330 335 340

gcg gag att aaa cac cgg gcg gta atc cca aac cct gag ttt tat cgt 1171
 Ala Glu Ile Lys His Arg Ala Val Ile Pro Asn Pro Glu Phe Tyr Arg
 345 350 355

cga caa gcg caa aga ttt tgc acc ttc ggc gtg cgg cgc atc gtc atc 1219
 Arg Gln Ala Gln Arg Phe Ser Thr Phe Gly Val Pro Arg Ile Val Ile
 360 365 370

cgc ttc gcc cag gcc gag cag cgc ttg ctg ctc cca cgc ggg ctt gtc 1267
 Arg Phe Ala Gln Ala Glu Gln Arg Leu Leu Leu Pro Arg Gly Leu Val
 375 380 385

gac gac acc ctc cgg atc ctc acc ctc gcc ggg tac aaa gtc agc gtc 1315
 Asp Asp Thr Leu Arg Ile Leu Thr Leu Ala Gly Tyr Lys Val Ser Val
 390 395 400 405

atc tgg cct cgg caa act cgg aaa acc atc gac gcg tct ttc gag gcc 1363
 Ile Trp Pro Arg Gln Thr Arg Lys Thr Ile Asp Ala Ser Phe Glu Gly
 410 415 420

gaa ttg cga tcc atg caa caa gag gga atc gac tgg ctc aaa gcc caa 1411
 Glu Leu Arg Ser Met Gln Gln Glu Gly Ile Asp Ser Leu Lys Gly Gln
 425 430 435

cgc acc ggc gta ttg gta gca cgg cgg ggc gct gga aaa aca gtg atg 1459
 Arg Thr Gly Val Leu Val Ala Pro Pro Gly Ala Gly Lys Thr Val Met
 440 445 450

gcc tgt gca ctc atc gcg aac aga aaa atc ccc acc gca gtg ata gtc 1507
 Ala Cys Ala Leu Ile Ala Asn Arg Lys Ile Pro Thr Ala Val Ile Val
 455 460 465

aac cgt gca gaa ttg att tcc caa tgg cgg gat cgt ctc gcg caa tac 1555
 Asn Arg Ala Glu Leu Ile Ser Gln Trp Arg Asp Arg Leu Ala Gln Tyr
 470 475 480 485

ctg agc atc gac gca gac tcc atc gga cag atc ggc gcg ggc cga cgc 1603
 Leu Ser Ile Asp Ala Asp Ser Ile Gly Gln Ile Gly Ala Gly Arg Arg
 490 495 500

aaa acc acc gga att atc gat ctc atc acc gtc caa tcc ttg agc cgt 1651
 Lys Thr Thr Gly Ile Ile Asp Leu Ile Thr Val Gln Ser Leu Ser Arg
 505 510 515

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aaa gat tcc gat ccg aaa att ttg gaa caa tac ggc caa atc atc gtc 1699
 Lys Asp Ser Asp Pro Lys Ile Leu Glu Gln Tyr Gly Gln Ile Ile Val
 520 525 530

gac gag tgc cac aac atc gca gcc cca ggc gcc gaa gcc gca ttg aac 1747
 Asp Glu Cys His Asn Ile Ala Ala Pro Gly Ala Glu Ala Ala Leu Asn
 535 540 545

cag gtc aag gcc ccc tac tgg ctg ggt cta acc gcc acg ccg ttt cgt 1795
 Gln Val Lys Ala Pro Tyr Trp Leu Gly Leu Thr Ala Thr Pro Phe Arg
 550 555 560 565

tca gac cac atg gat gaa atc atc acc atg cag tgc ggt cct gtg cgc 1843
 Ser Asp His Met Asp Glu Ile Ile Thr Met Gln Cys Gly Pro Val Arg
 570 575 580

cac cgc atg gaa gtg gca aca gac aat gaa cag cgc ttg att cac atc 1891
 His Arg Met Glu Val Ala Thr Asp Asn Glu Gln Arg Leu Ile His Ile
 585 590 595

cac gaa acc tct ttc gac tct gag gaa acc acc gaa atc cag gat ctc 1939
 His Glu Thr Ser Phe Asp Ser Glu Glu Thr Thr Glu Ile Gln Asp Leu
 600 605 610

tac aat gag ctc gcg gtc gat tct gcc cga aat gcg caa atc act gcc 1987
 Tyr Asn Glu Leu Ala Val Asp Ser Ala Arg Asn Ala Gln Ile Thr Ala
 615 620 625

gaa gtg cac aaa gcg ctt gaa gct ggc gac cga tgt cta gtt ttg gtc 2035
 Glu Val His Lys Ala Leu Glu Ala Gly Asp Arg Cys Leu Val Leu Val
 630 635 640 645

aac cga att gca gcc ctt gaa gca ctg acc agc agt att acc gaa tct 2083
 Asn Arg Ile Ala Ala Leu Glu Ala Leu Thr Ser Ser Ile Thr Glu Ser
 650 655 660

ggc gat cac act gtc tta gtg atg cat ggc cgc caa acc caa gag gag 2131
 Gly Asp His Thr Val Leu Val Met His Gly Arg Gln Thr Gln Glu Glu
 665 670 675

cga gtt cac ctt cgt gcg caa ctt gcc tca ttg agt gaa aag cag gat 2179
 Arg Val His Leu Arg Ala Gln Leu Ala Ser Leu Ser Glu Lys Gln Asp
 680 685 690

ccg ttt gta ctg gtc gcg atg aat aaa gtc gcc ggc gaa ggc ctt gac 2227
 Pro Phe Val Leu Val Ala Met Asn Lys Val Ala Glu Gly Leu Asp
 695 700 705

atc ccc agc ctc aac acg ctg ttt ttg gca gcg ccg gtg tcc ttc aag 2275
 Ile Pro Ser Leu Asn Thr Leu Phe Leu Ala Ala Pro Val Ser Phe Lys
 710 715 720 725

ggg ctg gtg att cag caa atc ggc cga gtt act cgc gca acc ggt gat 2323
 Gly Leu Val Ile Gln Gln Ile Gly Arg Val Thr Arg Ala Thr Gly Asp
 730 735 740

caa aac gct cct ccg gtg act gcc acg gtc cat gat ttt gtt gat tcc 2371
 Gln Asn Ala Pro Pro Val Thr Ala Thr Val His Asp Phe Val Asp Ser
 745 750 755

aag att ccg aca ctc aaa cgc atg cac ggt cgc cga ttg cgg gct atg 2419

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Lys Ile Pro Thr Leu Lys Arg Met His Gly Arg Arg Leu Arg Ala Met
760 765 770

caa aag gaa gga ttc gct gtt tcc gag cct tgaggaggac cagaccaaac 2469
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cag 2472

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<211> 783

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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35 40 45

Glu Ala Thr Gly Val Asn Ala Ser Ser Gly Pro Glu Ala Lys Ile Ala
50 55 60

Leu Phe Met Glu Arg Phe Ser Gly Arg His Asp Val Tyr Ala Arg Arg
65 70 75 80

Trp Thr Ser Arg Lys Thr Gly Lys Ser Gly Trp Ser Pro Ala Thr Arg
85 90 95

Gln Gly Phe Tyr Ser Lys Asp Thr Thr Pro Lys Asp Tyr Leu Pro Phe
100 105 110

Thr Val Asp Thr Val Asn Ala His Leu Arg Arg Gly Gly Asp His Ile
115 120 125

Gly Leu Tyr Val Met Val Pro Ile Asp Thr Cys Lys Leu Leu Ala Cys
130 135 140

Asp Phe Asp Asp Gly Thr Trp Lys Gln Asp Ala Ala Ala Phe Val Ser
145 150 155 160

Ala Cys Thr Asp His Gly Ile Asp Ala Leu Ala Glu Ile Ser Arg Ser
165 170 175

Asp Asp Gly Ala Pro Val Trp Ile Phe Phe Asp Thr Pro Ile Ser Ala
180 185 190

Met Leu Ala Arg Arg Leu Gly Phe Ala Met Leu Arg Gln Ala Met Asn
195 200 205

Ser Arg Pro Asp Met Asp Met Ser Ser Tyr Asp Arg Phe Phe Pro Ala
210 215 220

Gln Asp Thr Ile Ala Thr Arg Ala Asn Gly Ser Ala Arg Leu Gly Asn
225 230 235 240

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Leu Ile Ala Leu Pro Leu Asn Gly Asp Cys Arg Ala Arg Asn Thr Ala
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 Val Phe Ala Asp Ser Glu Thr Trp Val Pro Phe Glu Asp Pro Phe Ala
 260 265 270
 Ala Leu Ala Ala Ile Thr Pro Leu Ala Thr Glu Lys Ile Glu Gln Ile
 275 280 285
 Leu Ala Thr Thr Gln Glu Lys Phe Gly Pro Glu Pro Glu His Ile Lys
 290 295 300
 Arg Pro Thr Arg Ala Glu Leu Lys Gln Val Lys Ala Asn Gly Glu Thr
 305 310 315 320
 Ile Lys Leu Thr Ile Thr Asn Glu Leu Ser Val Pro Thr Glu Arg Leu
 325 330 335
 Pro Ala Ala Val Ile Ala Glu Ile Lys His Arg Ala Val Ile Pro Asn
 340 345 350
 Pro Glu Phe Tyr Arg Arg Gln Ala Gln Arg Phe Ser Thr Phe Gly Val
 355 360 365
 Pro Arg Ile Val Ile Arg Phe Ala Gln Ala Glu Gln Arg Leu Leu Leu
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 Pro Arg Gly Leu Val Asp Asp Thr Leu Arg Ile Leu Thr Leu Ala Gly
 385 390 395 400
 Tyr Lys Val Ser Val Ile Trp Pro Arg Gln Thr Arg Lys Thr Ile Asp
 405 410 415
 Ala Ser Phe Glu Gly Glu Leu Arg Ser Met Gln Gln Glu Gly Ile Asp
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 Ser Leu Lys Gly Gln Arg Thr Gly Val Leu Val Ala Pro Pro Gly Ala
 435 440 445
 Gly Lys Thr Val Met Ala Cys Ala Leu Ile Ala Asn Arg Lys Ile Pro
 450 455 460
 Thr Ala Val Ile Val Asn Arg Ala Glu Leu Ile Ser Gln Trp Arg Asp
 465 470 475 480
 Arg Leu Ala Gln Tyr Leu Ser Ile Asp Ala Asp Ser Ile Gly Gln Ile
 485 490 495
 Gly Ala Gly Arg Arg Lys Thr Thr Gly Ile Ile Asp Leu Ile Thr Val
 500 505 510
 Gln Ser Leu Ser Arg Lys Asp Ser Asp Pro Lys Ile Leu Glu Gln Tyr
 515 520 525
 Gly Gln Ile Ile Val Asp Glu Cys His Asn Ile Ala Ala Pro Gly Ala
 530 535 540
 Glu Ala Ala Leu Asn Gln Val Lys Ala Pro Tyr Trp Leu Gly Leu Thr
 545 550 555 560
 Ala Thr Pro Phe Arg Ser Asp His Met Asp Glu Ile Ile Thr Met Gln

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565										570					575						
Cys	Gly	Pro	Val	Arg	His	Arg	Met	Glu	Val	Ala	Thr	Asp	Asn	Glu	Gln						
580										585					590						
Arg	Leu	Ile	His	Ile	His	Glu	Thr	Ser	Phe	Asp	Ser	Glu	Glu	Thr	Thr						
595										600					605						
Glu	Ile	Gln	Asp	Leu	Tyr	Asn	Glu	Leu	Ala	Val	Asp	Ser	Ala	Arg	Asn						
610										615					620						
Ala	Gln	Ile	Thr	Ala	Glu	Val	His	Lys	Ala	Leu	Glu	Ala	Gly	Asp	Arg						
625										630					635						
Cys	Leu	Val	Leu	Val	Asn	Arg	Ile	Ala	Ala	Leu	Glu	Ala	Leu	Thr	Ser						
645										650					655						
Ser	Ile	Thr	Glu	Ser	Gly	Asp	His	Thr	Val	Leu	Val	Met	His	Gly	Arg						
660										665					670						
Gln	Thr	Gln	Glu	Glu	Arg	Val	His	Leu	Arg	Ala	Gln	Leu	Ala	Ser	Leu						
675										680					685						
Ser	Glu	Lys	Gln	Asp	Pro	Phe	Val	Leu	Val	Ala	Met	Asn	Lys	Val	Ala						
690										695					700						
Gly	Glu	Gly	Leu	Asp	Ile	Pro	Ser	Leu	Asn	Thr	Leu	Phe	Leu	Ala	Ala						
705										710					715						
Pro	Val	Ser	Phe	Lys	Gly	Leu	Val	Ile	Gln	Gln	Ile	Gly	Arg	Val	Thr						
725										730					735						
Arg	Ala	Thr	Gly	Asp	Gln	Asn	Ala	Pro	Pro	Val	Thr	Ala	Thr	Val	His						
740										745					750						
Asp	Phe	Val	Asp	Ser	Lys	Ile	Pro	Thr	Leu	Lys	Arg	Met	His	Gly	Arg						
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Arg	Leu	Arg	Ala	Met	Gln	Lys	Glu	Gly	Phe	Ala	Val	Ser	Glu	Pro							
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<213> Corynebacterium glutamicum
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<223> RXA02445
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                                     Val Glu Pro Phe Glu
                                     1           5
tta gag aaa gac ctt gag cgt ctt agg aaa aac gga aaa gac gat gaa 163
Leu Glu Lys Asp Leu Glu Arg Leu Arg Lys Asn Gly Lys Asp Asp Glu

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	10	15	20	
acc gta gaa gtg aaa tct tgg ggt cgg tta cct tta agc aaa gga tca	211			
Thr Val Glu Val Lys Ser Trp Gly Arg Leu Pro Leu Ser Lys Gly Ser	25	30	35	
aaa agc ttc tgg gaa tca tta agc gca ttc gca aac acc aac ggt gga	259			
Lys Ser Phe Trp Glu Ser Leu Ser Ala Phe Ala Asn Thr Asn Gly Gly	40	45	50	
tac atc cta ttg ggg cta agc gaa cca gat ttc act cca gtt gaa gga	307			
Tyr Ile Leu Leu Gly Leu Ser Glu Pro Asp Phe Thr Pro Val Glu Gly	55	60	65	
ttt gat tca cag gcg agt atc cag ttc att cgt gca ggt tta aat cca	355			
Phe Asp Ser Gln Ala Ser Ile Gln Phe Ile Arg Ala Gly Leu Asn Pro	70	75	80	85
caa gat cgc gac gcc caa aaa gtg gaa cca gtg ccc cat cat gaa att	403			
Gln Asp Arg Asp Ala Gln Lys Val Glu Pro Val Pro His His Glu Ile	90	95	100	
cat gaa atg act gtt gat ggt gct gaa gtt gtt tta gtt tca gtc tca	451			
His Glu Met Thr Val Asp Gly Ala Glu Val Val Leu Val Ser Val Ser	105	110	115	
cgg ttg tca gtg aac ggg ccc tgt tat tat ctt ccc gtc gga atc act	499			
Pro Leu Ser Val Asn Gly Pro Cys Tyr Tyr Leu Pro Val Gly Ile Thr	120	125	130	
aat ggc agc ttc aaa cgc gtt ggc gat gaa gac cgg aag ctc agt cat	547			
Asn Gly Ser Phe Lys Arg Val Gly Asp Glu Asp Arg Lys Leu Ser His	135	140	145	
ctt gaa att tac gag ctc caa aat agg ttt gtt caa acc aaa aca gat	595			
Leu Glu Ile Tyr Glu Leu Gln Asn Arg Phe Val Gln Thr Lys Thr Asp	150	155	160	165
aga aat cca gtt cca gat tca agc att gac gat ctc aac aat cag ctc	643			
Arg Asn Pro Val Pro Asp Ser Ser Ile Asp Asp Leu Asn Asn Gln Leu	170	175	180	
gcg gcg tca ttt aag cag cgc cta att gag tca aat agt cgc tcc ctt	691			
Ala Ala Ser Phe Lys Gln Arg Leu Ile Glu Ser Asn Ser Arg Ser Leu	185	190	195	
gga aca gac gat aac tgg tta ctg cgc aaa aat atc act aca tca aag	739			
Gly Thr Asp Asn Trp Leu Leu Arg Lys Asn Ile Thr Thr Ser Lys	200	205	210	
gga gaa ctg acg att gct ggc tta ctg gct ctc gga agc tat cct caa	787			
Gly Glu Leu Thr Ile Ala Gly Leu Leu Ala Leu Gly Ser Tyr Pro Gln	215	220	225	
cag ttt ttc ccc cga gtg atc att gat gtt gcc gta cat cca ggt ctg	835			
Gln Phe Phe Pro Arg Val Ile Ile Asp Val Ala Val His Pro Gly Leu	230	235	240	245
cat aag tca cca atc ggt acc tca att cgt ttt gaa gac cga aaa atc	883			
His Lys Ser Pro Ile Gly Thr Ser Ile Arg Phe Glu Asp Arg Lys Ile	250	255	260	

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Cys	gag	gga	aat	ctc	ctc	gag	atg	gtt	caa	gag	gct	atg	tct	gcc	atc	931
Glu	Gly	Asn	Leu	Leu	Glu	Met	Val	Gln	Glu	Ala	Met	Ser	Ala	Ile		
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aaa	cga	aac	cta	cgt	gta	cgc	cgc	gtc	gtt	gaa	gga	ctc	tca	ggt	aaa	979
Lys	Arg	Asn	Leu	Arg	Val	Arg	Arg	Val	Val	Glu	Gly	Leu	Ser	Gly	Lys	
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gat	gtt	cta	gaa	atc	cca	gaa	gaa	gtt	ttg	aga	gag	gct	cta	gca	aac	1027
Asp	Val	Leu	Glu	Ile	Pro	Glu	Glu	Val	Leu	Arg	Glu	Ala	Leu	Ala	Asn	
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gcc	gta	ctt	cac	cgt	gat	tat	tct	gag	cta	gct	caa	aat	gaa	gca	att	1075
Ala	Val	Leu	His	Arg	Asp	Tyr	Ser	Glu	Leu	Ala	Gln	Asn	Glu	Ala	Ile	
		310			315					320					325	
cat	gta	gac	atc	tat	aag	gat	cga	gtt	gag	atc	acg	agt	cca	ggt	gga	1123
His	Val	Asp	Ile	Tyr	Lys	Asp	Arg	Val	Glu	Ile	Thr	Ser	Pro	Gly	Gly	
				330					335					340		
tta	ccc	aat	ggt	aaa	cgc	cca	gag	tca	ata	ctg	gac	gga	tac	tct	gaa	1171
Leu	Pro	Asn	Gly	Lys	Arg	Pro	Glu	Ser	Ile	Leu	Asp	Gly	Tyr	Ser	Glu	
			345				350					355				
cca	aga	aat	cgt	gtg	ctt	tca	aga	atc	cta	atg	gat	att	cca	tgg	aca	1219
Pro	Arg	Asn	Arg	Val	Leu	Ser	Arg	Ile	Leu	Met	Asp	Ile	Pro	Trp	Thr	
		360					365									
cat	gaa	gta	caa	gga	gta	ctt	gct	gaa	agc	aac	ggt	act	ggc	gtt	ccc	1267
His	Glu	Val	Gln	Gly	Val	Leu	Ala	Glu	Ser	Asn	Gly	Thr	Gly	Val	Pro	
		375				380					385					
cga	atg	ttc	aat	ttg	atg	cgt	gaa	cgc	gga	ctt	ccg	gta	ccg	aat	ttt	1315
Arg	Met	Phe	Asn	Leu	Met	Arg	Glu	Ala	Gly	Leu	Pro	Val	Pro	Asn	Phe	
					395				400					405		
aaq	att	gat	att	tct	agc	gtc	act	gtc	gaa	ctc	agc	cgt	cac	ggt	ctt	1363
Lys	Ile	Asp	Ile	Ser	Ser	Val	Thr	Val	Glu	Leu	Ser	Arg	His	Gly	Leu	
				410					415					420		
cta	gat	gcc	caa	aca	agt	gaa	tgg	ctt	gta	gaa	aaa	ctc	gga	tca	gat	1411
Leu	Asp	Ala	Gln	Thr	Ser	Glu	Trp	Leu	Val	Glu	Lys	Leu	Gly	Ser	Asp	
			425				430						435			
ttt	tct	aac	aca	caa	ggc	att	gct	ctt	gtt	ctc	gca	aaa	gaa	ctt	gga	1459
Phe	Ser	Asn	Thr	Gln	Gly	Ile	Ala	Leu	Val	Leu	Ala	Lys	Glu	Leu	Gly	
			440			445						450				
gcg	gta	acg	tct	cga	gat	ctc	cgc	aat	caa	act	ggt	cat	gat	tca	gaa	1507
Ala	Val	Thr	Ser	Arg	Asp	Leu	Arg	Asn	Gln	Thr	Gly	His	Asp	Ser	Glu	
			455			460					465					

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Leu Asn Asn Gln Leu Ala Ala Ser Phe Lys Gln Arg Leu Ile Glu Ser
180 185 190

[illegible]

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515 520 525

Lys Thr Ala Ser Ser Leu Arg Pro Leu Leu Arg Gly Leu Val Glu Ala
530 535 540

Gly Leu Val Val Ala Thr Ala Pro Pro Ser Ser Arg Asn Arg Ala Tyr
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Leu Lys Ala

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<223> RXA00927

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Met Ser Asp Val Glu
1 5

aga aca gag ttt gaa att ccg gga gga att cca cct cgt cga aac ggt 163
Arg Thr Glu Phe Glu Ile Pro Gly Gly Ile Pro Arg Arg Asn Gly
10 15 20

ggt caa ggc cgt gca gct gat acc aac gta gat gcg aac ctg aag cct 211
Gly Gln Gly Arg Ala Ala Asp Thr Asn Val Asp Ala Asn Leu Lys Pro
25 30 35

gat gaa tac gat gcg gaa gta aca ctt cgt ccg aag tct ttg act gag 259
Asp Glu Tyr Asp Ala Glu Val Thr Leu Arg Pro Lys Ser Leu Thr Glu
40 45 50

ttt atc ggc cag ccg aag gtg cgc gat cag ctt agt ttg gtg ctt acc 307
Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu Ser Leu Val Leu Thr
55 60 65

ggt gcg aaa aac cgt ggt gtg gtt ccc gat cac gtg ttg ttg tct ggc 355
Gly Ala Lys Asn Arg Gly Val Val Pro Asp His Val Leu Leu Ser Gly
70 75 80 85

cct cct ggc ctg ggt aag acc acc atg gcg atg att atc gcc cag gag 403
Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met Ile Ile Ala Gln Glu
90 95 100

ttg ggc acc agt ttg cgt atg acc tca ggc cca gcc ttg gaa cgc gca 451
Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro Ala Leu Glu Arg Ala
105 110 115

ggc gat ctg gct gcc atg ctg tcc aac ctc atg gaa ggg gac gtg ctg 499
Gly Asp Leu Ala Ala Met Leu Ser Asn Leu Met Glu Gly Asp Val Leu
120 125 130

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 135 140 145

tac atg gcg atg gaa gat ttc cgg atc gat gtc atc gtc ggt aag ggt 595
 Tyr Met Ala Met Glu Asp Phe Arg Ile Asp Val Ile Val Gly Lys Gly
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cct ggc gct acc tca atc ccg ctg gag atc cca ccc ttt acc ctg gtt 643
 Pro Gly Ala Thr Ser Ile Pro Leu Glu Ile Pro Phe Thr Leu Val
 170 175 180

ggt gca acc acc agg tcg ggc atg ctg acc ggc cca ctg cgt gac cgt 691
 Gly Ala Thr Thr Arg Ser Gly Met Leu Thr Gly Pro Leu Arg Asp Arg
 185 190 195

ttc ggt ttt acc gcg cag atg gaa ttc tac gat gtg cct gat ctg acc 739
 Phe Gly Phe Thr Ala Gln Met Glu Phe Tyr Asp Val Pro Asp Leu Thr
 200 205 210

aaa gtg gtg aaa cga aca gct aag atc ctg gat gtc gga atc gac aac 787
 Lys Val Val Lys Arg Thr Ala Lys Ile Leu Asp Val Gly Ile Asp Asn
 215 220 225

gat gcc gcc gtg gaa att gcc tcg cgg tct cgt ggt act cct cgt att 835
 Asp Ala Ala Val Glu Ile Ala Ser Arg Ser Arg Gly Thr Pro Arg Ile
 230 235 240 245

gct aac cga ctg ctt cgt cga gtc cgt gac ttc gct gaa gtt cat gcg 883
 Ala Asn Arg Leu Leu Arg Arg Val Arg Asp Phe Ala Glu Val His Ala
 250 255 260

gat ggt cac atc acg atg ggt gct gcc aat gct gcg ctg att gta ttc 931
 Asp Gly His Ile Thr Met Gly Ala Ala Asn Ala Ala Leu Ile Val Phe
 265 270 275

gat gtc gat gaa gtc gga ctg gat cgc ctg gat agg gca gtg ctt gat 979
 Asp Val Asp Glu Val Gly Leu Asp Arg Leu Asp Arg Ala Val Leu Asp
 280 285 290

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 Ala Leu Ile Arg Gly His Gly Gly Gly Pro Val Gly Val Asn Thr Leu
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gcg gtt gca gtt ggt gaa gaa ccc gcc act gtg gaa gaa gta tgc gag 1075
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 Pro Tyr Leu Val Arg Ala Gly Met Ile Ala Arg Thr Gly Arg Gly Arg
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00602030 062300

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 <213> *Corynebacterium glutamicum*

<400> 80

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Ala Asn Leu Lys Pro Asp Glu Tyr Asp Ala Glu Val Thr Leu Arg Pro
          35           40           45

Lys Ser Leu Thr Glu Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu
          50           55           60

Ser Leu Val Leu Thr Gly Ala Lys Asn Arg Gly Val Val Pro Asp His
          65           70           75           80

Val Leu Leu Ser Gly Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met
          85           90           95

Ile Ile Ala Gln Glu Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro
          100          105          110

Ala Leu Glu Arg Ala Gly Asp Leu Ala Ala Met Leu Ser Asn Leu Met
          115          120          125

Glu Gly Asp Val Leu Phe Ile Asp Glu Ile His Arg Ile Ala Arg Pro
          130          135          140

Ala Glu Glu Met Leu Tyr Met Ala Met Glu Asp Phe Arg Ile Asp Val
          145          150          155          160

Ile Val Gly Lys Gly Pro Gly Ala Thr Ser Ile Pro Leu Glu Ile Pro
          165          170          175

Pro Phe Thr Leu Val Gly Ala Thr Thr Arg Ser Gly Met Leu Thr Gly
          180          185          190

Pro Leu Arg Asp Arg Phe Gly Phe Thr Ala Gln Met Glu Phe Tyr Asp
          195          200          205

Val Pro Asp Leu Thr Lys Val Val Lys Arg Thr Ala Lys Ile Leu Asp
          210          215          220

Val Gly Ile Asp Asn Asp Ala Ala Val Glu Ile Ala Ser Arg Ser Arg
          225          230          235          240

Gly Thr Pro Arg Ile Ala Asn Arg Leu Leu Arg Arg Val Arg Asp Phe
          245          250          255

Ala Glu Val His Ala Asp Gly His Ile Thr Met Gly Ala Ala Asn Ala
          260          265          270

Ala Leu Ile Val Phe Asp Val Asp Glu Val Gly Leu Asp Arg Leu Asp
          275          280          285

Arg Ala Val Leu Asp Ala Leu Ile Arg Gly His Gly Gly Gly Pro Val

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Ser Gly Ala Leu Arg Ala Ala Leu Ala Lys Leu Ser Gly Lys
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gaa ttt gaa cgc tca att att cgc gag cgc caa gca gaa ggt att gcc 547

060320Z FEB 60

Glu Phe Glu Arg Ser Ile Ile Arg Glu Arg Gln Ala Glu Gly Ile Ala
 135 140 145

ctg gca aaa aag gcc ggc aag tat gca ggt cgc cca aaa gcc ctc gac 595
 Leu Ala Lys Lys Ala Gly Lys Tyr Ala Gly Arg Pro Lys Ala Leu Asp
 150 155 160

aag gaa caa ata caa gaa gca aaa gat atg atc gct caa ggt gaa aca 643
 Lys Glu Gln Ile Gln Glu Ala Lys Asp Met Ile Ala Gln Gly Glu Thr
 170 175 180

aaa tct gct gtc gcc aag cat ttt ggt att aat cgc tgc acc ttg tac 691
 Lys Ser Ala Val Ala Lys His Phe Gly Ile Asn Arg Ser Thr Leu Tyr
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 20 25 30

Gln Arg Glu Ala Val Asn His Ser Gly His Ile Asp Arg Glu Phe Thr
 35 40 45

Asp Glu Leu Ser Gly Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp
 50 55 60

Cys Ile Asn Tyr Leu Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile
 65 70 75 80

Asp Arg Leu Ala Arg Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg
 85 90 95

Ile Thr Asp Lys Gly Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr
 100 105 110

Phe Ala Ala Gly Arg Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile
 115 120 125

Leu Gly Ser Phe Ala Glu Phe Glu Arg Ser Ile Ile Arg Glu Arg Gln
 130 135 140

Ala Glu Gly Ile Ala Leu Ala Lys Lys Ala Gly Lys Tyr Ala Gly Arg
 145 150 155 160

Pro Lys Ala Leu Asp Lys Glu Gln Ile Gln Glu Ala Lys Asp Met Ile
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Ala Gln Gly Glu Thr Lys Ser Ala Val Ala Lys His Phe Gly Ile Asn
 180 185 190

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Arg Ser Thr Leu Tyr Glu Tyr Leu Lys Asn Pro Asp
195 200

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ttt aag gaa caa aca act aac ccg aga agt caa cga gtt tct tat ttg 163
Phe Lys Glu Gln Thr Thr Asn Pro Arg Ser Gln Arg Val Ser Tyr Leu
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Arg Val Ser Ser Thr Asp Gln Asn Leu Ala Arg Gln Arg Glu Ala Val
25 30 35
aac cat tcc ggt cat att gat cgt gag ttc aca gat gag ctt tcc ggt 259
Asn His Ser Gly His Ile Asp Arg Glu Phe Thr Asp Glu Leu Ser Gly
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Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp Cys Ile Asn Tyr Leu
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cgc gag gat gat gtt ctt gtc gtc gca tcc att gac cga ctt gca cgc 355
Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile Asp Arg Leu Ala Arg
70 75 80 85
tcg ctg gtt gat tta cgc gtc atc att gac cgc atc aca gac aaa ggc 403
Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg Ile Thr Asp Lys Gly
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gca tcg gtc att ttt ctc aaa gag aat ttg act ttc gct gca ggc cgc 451
Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr Phe Ala Ala Gly Arg
105 110 115
gat gat cct cga gca aac ctc atg ctc ggt att ttg ggc agt ttc gca 499
Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile Leu Gly Ser Phe Ala
120 125 130
gaa ttt gaa cgc tca att att cgc gag cgc caa gca gaa ggt att gcc 547
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Leu
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 Asp Glu Leu Ser Gly Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp
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 Cys Ile Asn Tyr Leu Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile
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 Ile Thr Asp Lys Gly Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr
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 Phe Ala Ala Gly Arg Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile
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Ala	Arg	Phe	Asp	Asp	Asp	Arg	Ile	Arg	Ala	Ile	Glu	Lys	Met	Gly	Lys	
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Phe	Glu	His	Asn	Ser	Leu	Glu	Gln	Arg	Thr	Thr	Gly	Arg	Ala	Leu	Glu	
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Ala	Leu	Arg	Ser	Leu	Lys	Leu	Pro	Val	Tyr	Leu	Leu	Pro	Gly	Asn	His	
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Gly	Val	Thr	Ile	Leu	Ser	Asp	Thr	Thr	Val	His	Gly	Val	Ala	Pro	Gly	
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Leu	Val	Ala	Glu	Ala	Leu	Lys	Asp	Leu	Glu	Pro	Thr	Ser	Asn	Val	Arg	
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atc	gct	gtg	ggg	cac	ggc	caa	gca	gaa	gct	cgc	acc	act	gac	cac	cgg	643
Ile	Ala	Val	Gly	His	Gly	Gln	Ala	Glu	Ala	Arg	Thr	Thr	Asp	His	Arg	
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gct	gac	tta	atc	gat	ctg	aac	act	gtt	gaa	gcc	aaa	ttg	gct	gac	ggg	691
Ala	Asp	Leu	Ile	Asp	Leu	Asn	Thr	Val	Glu	Ala	Lys	Leu	Ala	Asp	Gly	
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Thr	Ile	Asp	Tyr	Leu	Ala	Leu	Gly	Asp	Thr	His	Ser	Ala	Gln	Pro	Val	
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Gly	Thr	Ser	Gly	Lys	Val	Trp	Phe	Ser	Gly	Ala	Pro	Glu	Thr	Thr	Asp	
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ttc	cat	gac	tta	gat	cca	gac	cgt	gtg	ggc	ggt	gag	gtg	aac	tct	ggc	835
Phe	His	Asp	Leu	Asp	Pro	Asp	Arg	Val	Gly	Gly	Glu					

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tcg ggt acc gat gtg gaa gat ttc ttg gat acc ttg cag gca tac cct 979
 Ser Gly Thr Asp Val Glu Asp Phe Leu Asp Thr Leu Gln Ala Tyr Pro
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gat aaa tct cga aca gtc atc aaa tat ggt ctc cgc gga acc atc acc 1027
 Asp Lys Ser Arg Thr Val Ile Lys Tyr Gly Leu Arg Gly Thr Ile Thr
 295 300 305

ctg gaa caa aac agg cgt ttg gaa gaa ggc atc gct ggg tta gaa gat 1075
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 Val Phe Ala Ser Leu Lys Pro Arg Glu Arg Thr Thr Asp Leu Val Leu
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gct gaa gta ttg cga gag ctc gct gac tct gtg gtc aat ggt gca gcg 1219
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ccg gaa gaa gac cgc gat gcg ctc aac cta ttg ttc cga cta agc cgg 1267
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 Glu Lys Met Gly Lys Ile Ala Arg Lys Asn Gln Cys Glu Phe Ile Val
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 Leu Ala Gly Asp Val Phe Glu His Asn Ser Leu Glu Gln Arg Thr Thr
 65 70 75 80
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 Leu Pro Gly Asn His Asp Pro Leu Thr Ala Asp Ser Leu Phe Tyr Arg
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 115 120 125
 Gly Val Ala Pro Gly Val Glu Ile Ile Gly Ala Pro Leu Leu His Lys
 130 135 140
 Met Ala Thr Ser Asp Leu Val Ala Glu Ala Leu Lys Asp Leu Glu Pro
 145 150 155 160
 Thr Ser Asn Val Arg Ile Ala Val Gly His Gly Gln Ala Glu Ala Arg
 165 170 175
 Thr Thr Asp His Arg Ala Asp Leu Ile Asp Leu Asn Thr Val Glu Ala
 180 185 190
 Lys Leu Ala Asp Gly Thr Ile Asp Tyr Leu Ala Leu Gly Asp Thr His
 195 200 205
 Ser Ala Gln Pro Val Gly Thr Ser Gly Lys Val Trp Phe Ser Gly Ala
 210 215 220
 Pro Glu Thr Thr Asp Phe His Asp Leu Asp Pro Asp Arg Val Gly Gly
 225 230 235 240
 Glu Val Asn Ser Gly Lys Val Leu Ile Val Ser Ala Ser Lys Gly Asp
 245 250 255
 Val Ser Val Glu Glu Val Glu Val Gly Lys Trp Thr Phe His Ala Leu
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 Ser Lys Glu Ile Thr Ser Gly Thr Asp Val Glu Asp Phe Leu Asp Thr
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 Leu Gln Ala Tyr Pro Asp Lys Ser Arg Thr Val Ile Lys Tyr Gly Leu
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 Arg Gly Thr Ile Thr Leu Glu Gln Asn Arg Arg Leu Glu Glu Gly Ile
 305 310 315 320
 Ala Gly Leu Glu Asp Val Phe Ala Ser Leu Lys Pro Arg Glu Arg Thr
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 Thr Asp Leu Val Leu Glu Pro Gly Glu Glu Glu Leu Ala Asn Leu Asp
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 Ala Thr Gly Tyr Ala Ala Glu Val Leu Arg Glu Leu Ala Asp Ser Val
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Gly Glu Thr Thr Thr Pro Leu Pro Asp Ser Asp Arg Ala Thr Ala Leu
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Ile His Asp His Ile Thr Lys Ala Gln Glu Ile Thr Ile Ile Thr Asp
55 60 65

Phe Asp Met Asp Gly Ile Ser Ala Gly Val Ile Ala Tyr Ala Gly Leu
70 75 80 85

Ala Glu Leu Gly Ala Gln Val Asn Met Val Val Pro Asp Tyr Arg Gly
90 95 100

Glu Arg Asn Val Thr Ala Ser Asp Ile Asp Arg Ala Leu Glu Leu Tyr
105 110 115

Pro Ala Thr Ser Leu Ile Ile Thr Cys Asp Val Gly Ile Gly Ser His
120 125 130

Glu Gly Ile Ala Arg Ala His Glu Arg Ser Ile Ala Val Leu Val Thr
135 140 145

Asp His His Met Glu Val Glu Pro Cys Gln Ala Asp Val Val Leu Asn
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Pro Asn Arg Ile Asp Ser Asp Tyr Pro Asn Lys Asp Ile Cys Gly Ala
170 175 180

Sln Val Ile Phe Ala Thr Leu Ser Asp Tyr Ala Arg Arg Tyr Arg Ala
185 190 195

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THE 2006

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 215 220 225

aag cag gct att gcg ttg ctt cgg ctt gct atc cca caa gta agt aaa 835
 Lys Gln Ala Ile Ala Leu Leu Arg Leu Ala Ile Pro Gln Val Ser Lys
 230 235 240 245

aac cgt ttc gcc ggt tgg gat acc tat gct gca cgc tct gtt aat cct 883
 Asn Arg Phe Gly Trp Asp Thr Tyr Ala Ala Arg Ser Val Asn Pro
 250 255 260

gat acg tcc aca ctc atg cat att gtc aat gcc agc cag cat gat cac 931
 Asp Thr Ser Thr Leu Met His Ile Val Asn Ala Ser Gln His Asp His
 265 270 275

cgc ttc att gca gcc ttc caa gcc atc tca att ctt ctt ggt gaa ctg 979
 Arg Phe Ile Ala Ala Phe Gln Gly Ile Ser Ile Leu Gly Glu Leu
 280 285 290

att gcg caa aag aag cta gta aac atc gac aat att tct gag tca ttc 1027
 Ile Ala Gln Lys Lys Leu Val Asn Ile Asp Asn Ile Ser Glu Ser Phe
 295 300 305

att ggc ttc act ctt ggt ccg atg ttt aac gct act cgt cgt gtt ggt 1075
 Ile Gly Phe Thr Leu Gly Pro Met Phe Asn Ala Thr Arg Arg Val Gly
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gct gcc gta cac agc tca gat cag ccc tac gcg ccc ttt gtg tgg ctc 1267
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 Arg Glu Ser Asp Val Pro Ala Ile Val Ile Asn Pro Asp Thr Leu Ser
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 Gly Ser Ala Arg Ser Pro Glu Trp Ala Pro Ile Ile Thr Gln Val Asn
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 Thr Leu Ser Ala Gln Gly His Gly Gly Ile His Ala Ala Gly His Glu

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Tyr Ala Cys Gly Met Arg Phe Asp Asn His Asp Ile Val Thr Phe
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gtt gca aca ctc gac gca ctc gat aaa aac acg cca cgg gaa gca cag 1555
Val Ala Thr Leu Asp Ala Leu Asp Lys Asn Thr Pro Arg Glu Ala Gln
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ccg gca gat ctg cat ttg gtt gac att gac cac gcg cgt cct gtg ctt 1603
Pro Ala Asp Leu His Leu Val Asp Ile Asp His Ala Arg Pro Val Leu
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gat aac ccc tca ctc acc caa gag ctc agt acg gtc gat gct gca gtg 1651
Asp Asn Pro Ser Leu Thr Gln Glu Leu Ser Thr Val Asp Ala Ala Val
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Asp Ala Ala Gln Leu Leu Val Leu Ile Asp Gln Leu Asp Gln Leu Gln
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cca ttt gga cat ggt ttt acc tat ccg cgc atc gac gtg acg ttc agg 1747
Pro Phe Gly His Gly Phe Thr Tyr Pro Arg Ile Asp Val Thr Phe Arg
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ccg gca gaa aca gaa ttc aag gtt atg ggt cag cac cat caa cat ctc 1795
Pro Ala Glu Thr Glu Phe Lys Val Met Gly Gln His His Gln His Leu
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aag gtg atc act cac tca ggg ttg acc tta ttg tgg tgg aat aag gct 1843
Lys Val Ile Thr His Ser Gly Leu Thr Leu Leu Trp Trp Asn Lys Ala
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Gln Gln Leu Asp Glu Ile Ala Gln Ser Glu Leu Val Thr Met Ser Val
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<212> PRT

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Ser Thr Ile Asn Thr Gly Glu Thr Thr Pro Leu Pro Asp Ser Asp
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 65 70 75 80
 Ala Tyr Ala Gly Leu Ala Glu Leu Gly Ala Gln Val Asn Met Val Val
 85 90 95
 Pro Asp Tyr Arg Gly Glu Arg Asn Val Thr Ala Ser Asp Ile Asp Arg
 100 105 110
 Ala Leu Glu Leu Tyr Pro Ala Thr Ser Leu Ile Ile Thr Cys Asp Val
 115 120 125
 Gly Ile Gly Ser His Glu Gly Ile Ala Arg Ala His Glu Arg Ser Ile
 130 135 140
 Ala Val Leu Val Thr Asp His His Met Glu Val Glu Pro Cys Gln Ala
 145 150 155 160
 Asp Val Val Leu Asn Pro Asn Arg Ile Asp Ser Asp Tyr Pro Asn Lys
 165 170 175
 Asp Ile Cys Gly Ala Gln Val Ile Phe Ala Thr Leu Ser Asp Tyr Ala
 180 185 190
 Arg Arg Tyr Arg Ala Asp Lys Ile Ile Asp Ile Asn Leu Leu Ala Val
 195 200 205
 Phe Ser Gly Ile Gly Ala Leu Ala Asp Val Met Pro Leu Thr Arg Asp
 210 215 220
 Thr Arg Pro Thr Val Lys Gln Ala Ile Ala Leu Leu Arg Leu Ala Ile
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 Pro Gln Val Ser Lys Asn Arg Phe Gly Gly Trp Asp Thr Tyr Ala Ala
 245 250 255
 Arg Ser Val Asn Pro Asp Thr Ser Thr Leu Met His Ile Val Asn Ala
 260 265 270
 Ser Gln His Asp His Arg Phe Ile Ala Ala Phe Gln Gly Ile Ser Ile
 275 280 285
 Leu Leu Gly Glu Leu Ile Ala Gln Lys Lys Leu Val Asn Ile Asp Asn
 290 295 300
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 Thr Arg Arg Val Gly Gly Asp Met His Asp Ser Phe Leu Val Phe Ala
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 Ala Ala Ile Ser Arg Ile Ile Asp Asn Asn Glu Arg Arg Lys Glu Leu
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Ser Lys Ser Ser Tyr Ala Ala Val His Ser Ser Asp Gln Pro Tyr Ala
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 Pro Phe Val Trp Leu Ser Glu Ala Pro Ser Gly Ile Leu Gly Leu Ile
 385 390 395 400
 Ala Ser Gln Leu Thr Arg Glu Ser Asp Val Pro Ala Ile Val Ile Asn
 405 410 415
 Pro Asp Thr Leu Ser Gly Ser Ala Arg Ser Pro Glu Trp Ala Pro Ile
 420 425 430
 Ile Thr Gln Val Asn Thr Leu Ser Ala Gln Gly His Gly Gly Ile His
 435 440 445
 Ala Ala Gly His Glu Tyr Ala Cys Gly Met Arg Phe Asp Asn His Asp
 450 455 460
 Asp Ile Val Thr Phe Val Ala Thr Leu Asp Ala Leu Asp Lys Asn Thr
 465 470 475 480
 Pro Arg Glu Ala Gln Pro Ala Asp Leu His Leu Val Asp Ile Asp His
 485 490 495
 Ala Arg Pro Val Leu Asp Asn Pro Ser Leu Thr Gln Glu Leu Ser Thr
 500 505 510
 Val Asp Ala Ala Val Asp Ala Ala Gln Leu Leu Val Leu Ile Asp Gln
 515 520 525
 Leu Asp Gln Leu Gln Pro Phe Gly His Gly Phe Thr Tyr Pro Arg Ile
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 Asp Val Thr Phe Arg Pro Ala Glu Thr Glu Phe Lys Val Met Gly Gln
 545 550 555 560
 His His Gln His Leu Lys Val Ile Thr His Ser Gly Leu Thr Leu Leu
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ctt cgg gta atg ggc att gac cca ggt ctt acc cgt tgt ggc tta tct 163
 Leu Arg Val Met Gly Ile Asp Pro Gly Leu Thr Arg Cys Gly Leu Ser 20
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 Val Val Gln Ala Gly Arg Gly Arg Thr Val Tyr Pro Val Ser Val Gly 35
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gtg gtg cgc acc cca cca gat gcg gag ttg gcg gag cgg ttg ctt cgg 259
 Val Val Arg Thr Pro Pro Asp Ala Glu Leu Ala Glu Arg Leu Leu Arg 50
 40 45

ctc agc aaa gca gtg ggt gag tgg atg gat gag tac acc cca gat gtc 307
 Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu Tyr Thr Pro Asp Val 65
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 Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn Val Ser Thr Val Met 85
 70 75 80

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 Asn Thr Ala His Ala Val Gly Val Leu Ile Leu Ala Ala Ala Glu Arg 100
 90 95

gga ttg cca gtt cac atg tac acc ccc agt gag gtg aaa aag gct atc 451
 Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu Val Lys Lys Ala Ile 115
 105 110

tcc ggt aat ggt cgc gct gat aag aaa cag atg acg gtc atg atc act 499
 Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met Thr Val Met Ile Thr 130
 120 125

cga att ctg gcg ctt ggt gag cca ccc aaa cct gct gac gcc gct gat 547
 Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro Ala Asp Ala Ala Asp 145
 135 140

gct tta tcg ttg gcg gtg tgt cac tgc tgg cgg gcg cca atg ctt atg 595
 Ala Leu Ser Leu Ala Val Cys His Cys Trp Arg Ala Pro Met Leu Met 165
 150 155 160

cgg gcg caa tcg cag tac tcc gag caa gag ttg gaa aag cga cgg cgt 643
 Arg Ala Gln Ser Gln Tyr Ser Glu Gln Glu Leu Glu Lys Arg Arg Arg 180
 170 175

gtg cag caa gga aaa ttg ggt aaa gcg aaa tca act tac aat gcg gaa 691
 Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser Thr Tyr Asn Ala Glu 195
 185 190

caa gct caa tcc cat gca tcc gat cct gct aaa gcg gct cat ccc agt 739
 Gln Ala Gln Ser His Ala Ser Asp Pro Ala Lys Ala Ala His Pro Ser 210
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 <213> *Corynebacterium glutamicum*

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 Glu Arg Leu Leu Arg Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu
 50 55 60
 Tyr Thr Pro Asp Val Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn
 65 70 75 80
 Val Ser Thr Val Met Asn Thr Ala His Ala Val Gly Val Leu Ile Leu
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 Ala Ala Ala Glu Arg Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu
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 Val Lys Lys Ala Ile Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met
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 Thr Val Met Ile Thr Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro
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 Glu Lys Arg Arg Arg Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser
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 Val Val Leu Gly Asp Gly Thr Asp Ala Asp Ile Ile Ala Phe Ala Thr
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 Gly Leu Leu Val Asp Ala Thr Thr Gln Pro Glu Gly Asp Ala Pro Glu
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 Thr Asp Pro Ala Leu Pro Phe Leu Met Gln Asp Phe Leu Val Gln Phe
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 Tyr Gly Asp Ala Val Glu Arg Ala Glu Thr Glu Ala Lys Glu Asp Ala
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 Ala Val Ile Glu Arg Arg Gly Val Asp Lys His Ser Phe Glu Glu Ala
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 Ala Pro Val Thr Arg Ala Ser Val Val Pro Arg Glu Ile Leu Val Gln
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 His Lys Leu Lys Arg Val Gly Asp Leu Thr Ala Arg Ser Ala Ala Leu
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 Tyr Arg Val Lys Glu Ala Ala Gly Asp Gly His Ser Asn Asp Val Ala
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 Ser Ile Ala Glu Ile Thr Arg Arg Arg Phe Leu Arg His Asn Gln Asp
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 Lys Leu Ala Val Pro Glu Ala Glu Glu Phe Asp Gly Ser Thr Phe Ser
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 Ser Tyr Ala Arg Met Phe Leu Gly Gln Met Asp Lys Pro Asp Val Asp
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 Asn Arg Asn Pro Arg Ser Thr Val Gly Thr Ile Thr Glu Val Tyr Asp
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 Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly Thr Ala His Cys Pro Val
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Ser	Glu	Lys	Met	Ser	Cys 250	Pro	Asn	Gly	His 255	Ala	Leu	Thr	Val	Asp 260	Glu	
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Leu	Glu	Pro	Arg	Ala	Phe 265	Ser	Phe	Asn 270	Ser	Pro	Tyr	Gly	Ala	Cys 275	Pro	
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Ala	Cys	Asp	Gly	Leu	Gly 280	Val	Arg	Thr 285	Glu	Val	Asp	Ile	Asp	Leu	Ile	
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Ile	Pro	Asp	Pro	Asp	Ala 295	Pro	Ala	Thr	Lys	Ala 300	Val	Gln	Pro	Trp	Asn	
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Ser	Ser	Pro	Asn	His	Ser 310	Tyr	Phe	Glu	Lys 315	Leu	Ile	Glu	Gly	Leu	Ala 320	
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Lys	Ala	Leu	Gly	Phe	Asp 330	Pro	Glu	Thr	Pro 335	Tyr	Ser	Glu	Leu	Thr	Ala 340	
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Pro	Thr	Cys	Lys	Gly	Ala 410	Arg	Leu	Lys	Pro 415	Glu	Ile	Leu	Ala	Val	Arg 420	
cta	gac	tcc	gga	agc	cat	gga	gcg	ttg	tcc	att	gct	gga	cta	acc	gcg	1411
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920 925 930

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00602639-062300

tca

2952

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 Trp Thr Ala Pro Phe Glu Gly Val Met Gly Tyr Phe Asp Arg Lys Leu
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 Pro Gly Arg Ala Lys Arg Val Glu Gly Leu Glu His Leu Asp Lys Leu
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 Val Gln Val Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn Pro
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 Asn Ile Lys Gly Gly Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr Leu
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 Gly Lys Asn Ile Ala Glu Val Leu Gly Met Pro Ile Ser Glu Ala Ala
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 Ser Gly Gly Gly Thr Val Val Ala Glu Gly Thr Pro Glu Gln Val Ala
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atc acg gaa gtc tat gac tac ctg cgt ctt ctg tac gcc cgc gct ggt 144
 Ile Thr Glu Val Tyr Asp Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly
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 Thr Ala His Cys Pro Val Cys Asp Ala Arg Val Glu Arg Gln Thr Pro
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caa atc ctt gcg cct gtg gtg cgt acc cgt aaa ggt gag ttc gtt gat 288
 Gln Ile Leu Ala Pro Val Val Arg Thr Arg Lys Gly Glu Phe Val Asp
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 Leu Phe Ala Asp Leu Ala Ser Gln Gly Tyr Ser Arg Val Arg Val Asp
 100 105 110

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 Gly Glu Val His Gln Leu Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile
 115 120 125

aag cac gat att gat gtt gtg gtt gac cgt ctg cag gta aaa gcc agc 432
 Lys His Asp Ile Asp Val Val Val Asp Arg Leu Gln Val Lys Ala Ser
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 Gln Lys Gln Arg Leu Thr Asp Ser Met Glu Thr Ala Leu Arg Leu Ala
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gat gcc gtg gct gtg ctg gag ttc gtt gcc ctg gag gaa gat gat ccg 528
 Asp Gly Val Ala Val Leu Glu Phe Val Gly Leu Glu Glu Asp Asp Pro
 165 170 175

aat agg ctt cgt cga ttc tct gaa aag atg agc tgc cct aac ggt cac 576
 Asn Arg Leu Arg Arg Phe Ser Glu Lys Met Ser Cys Pro Asn Gly His

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245	250	255	
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275	280	285	
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 820 825 830

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Gln	Ile	Leu	Ala 85	Pro	Val	Val	Arg	Thr 90	Arg	Lys	Gly	Glu	Phe 95	Val	Asp
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Gly	Glu	Val 115	His	Gln	Leu	Ser	Asp 120	Pro	Pro	Lys	Leu	Glu 125	Lys	Gln	Ile
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Gln 145	Lys	Gln	Arg	Leu	Thr 150	Asp	Ser	Met	Glu 155	Thr	Ala	Leu	Arg	Leu	Ala 160
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 740 745 750
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 785 790 795 800
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Glu Lys Val Pro Ala Phe Arg Val Leu Arg Glu Lys Arg Met Leu Asp						
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Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val Gly Lys						
	40				50	
tcg aca ttg ctg gag gct atc gcg atc aat gcg ggc ttc gac aca gca						307
Ser Thr Leu Leu Glu Ala Ile Ala Ile Asn Ala Gly Phe Asp Thr Ala						
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Gly Gly Glu His Thr Gly Lys Phe Lys Pro Ser Asp Asn Pro Leu Gln						
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Thr Val Ala Lys Ala His Lys Gly Lys Glu Pro Met Arg Gly Tyr Phe						
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ctg cgg gcg gaa act cat ttc aac gtc gcg tct gga tat cgc gat gag						451
Leu Arg Ala Glu Thr His Phe Asn Val Ala Ser Gly Tyr Arg Asp Glu						
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gct ccc ggc tgg gtg aac ctt cat cac atg tcg cac ggg gag tcg gtg						499
Ala Pro Gly Trp Val Asn Leu His His Met Ser His Gly Glu Ser Val						
	120				130	
atg cat att gtg cag aat gct ttt gtg ggc aag ggg ctg tat ctg atg						547
Met His Ile Val Gln Asn Ala Phe Val Gly Lys Gly Leu Tyr Leu Met						
	135				145	
gat gag cct gaa gcg ggg cta tcg ttc att cga cag atg gcg att ctg						595
Asp Glu Pro Glu Ala Gly Leu Ser Phe Ile Arg Gln Met Ala Ile Leu						
	150				165	
gcg gag ctt aat ttt ctg gcg gaa agt ggt gcg caa att atc atc gtg						643
Ala Glu Leu Asn Phe Leu Ala Glu Ser Gly Ala Gln Ile Ile Val						
	170				180	
acg cat tcg ccg gtg ttg atg gct att ccg ggt gca gaa att tgg gag						691
Thr His Ser Pro Val Leu Met Ala Ile Pro Gly Ala Glu Ile Trp Glu						
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Phe Ser Ala Ser Gly Glu Leu His Arg Gly Phe Asp Phe Glu Val Thr						
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Thr Ala Phe Arg Ala Leu Arg Asp Phe Phe Phe Pro Glu Glu Ile						
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230 235 240

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Lys Arg Met Leu Asp Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu
35 40 45

Asn Gly Val Gly Lys Ser Thr Leu Leu Glu Ala Ile Ala Ile Asn Ala
50 55 60

Gly Phe Asp Thr Ala Gly Gly Glu His Thr Gly Lys Phe Lys Pro Ser
65 70 75 80

Asp Asn Pro Leu Gln Thr Val Ala Lys Ala His Lys Gly Lys Glu Pro
85 90 95

Met Arg Gly Tyr Phe Leu Arg Ala Glu Thr His Phe Asn Val Ala Ser
100 105 110

Gly Tyr Arg Asp Glu Ala Pro Gly Trp Val Asn Leu His His Met Ser
115 120 125

His Gly Glu Ser Val Met His Ile Val Gln Asn Ala Phe Val Gly Lys
130 135 140

Gly Leu Tyr Leu Met Asp Glu Pro Glu Ala Gly Leu Ser Phe Ile Arg
145 150 155 160

Gln Met Ala Ile Leu Ala Glu Leu Asn Phe Leu Ala Glu Ser Gly Ala
165 170 175

Gln Ile Ile Ile Val Thr His Ser Pro Val Leu Met Ala Ile Pro Gly
180 185 190

Ala Glu Ile Trp Glu Phe Ser Ala Ser Gly Glu Leu His Arg Gly Phe
195 200 205

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Lys Gly Glu Ser

<210> 103

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 Met Ala Phe Ala Ala
 1 5
 gaa cat cct gtc ctg tcc cac tct gag cac cgc ccg gtt ggt gaa atc 163
 Glu His Pro Val Leu Ser His Ser Glu His Arg Pro Val Gly Glu Ile
 10 15 20
 gag cgt agc gat gac aaa ttt gtt gtc gtt agt gaa ttt gag cct gcg 211
 Glu Arg Ser Asp Asp Lys Phe Val Val Val Ser Glu Phe Glu Pro Ala
 25 30 35
 ggt gac cag cct gcg gct att aaa gag ctc gat gag cgc ttg gat cgc 259
 Gly Asp Gln Pro Ala Ala Ile Lys Glu Leu Asp Glu Arg Leu Asp Arg
 40 45 50
 ggt gag cgg gac gtc gtt ttg atg ggt gct act ggt acg ggt aag tcc 307
 Gly Glu Arg Asp Val Val Leu Met Gly Ala Thr Gly Thr Gly Lys Ser
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 gcg act gcg gcg tgg ttg atc gaa aag cag cag cgc ccc gct ttg gtg 355
 Ala Thr Ala Ala Trp Leu Ile Glu Lys Gln Gln Arg Thr Ala Leu Val
 70 75 80 85
 atg gcg ccg aat aag acg ctg gct gcg cag ttg gct aat gaa ttg cgg 403
 Met Ala Pro Asn Lys Thr Leu Ala Ala Gln Leu Ala Asn Glu Leu Arg
 90 95 100
 cag ctg ttg ccc aat aac gcg gtg gag tat ttc gtg tct tat tac gat 451
 Gln Leu Leu Pro Asn Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp
 105 110 115
 tac tac cag cca gaa gcg tat atc gcg cag act gat acc tat att gaa 499
 Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Gln Thr Asp Thr Tyr Ile Glu
 120 125 130
 aag gac tcc tcg att aat gag gat gtg gag cgt ctg cgt cac tcg gcg 547
 Lys Asp Ser Ser Ile Asn Glu Asp Val Glu Arg Leu Arg His Ser Ala
 135 140 145
 acg tcg tct ttg ctg agt agg cga gac gtc gtg gtt gtt agt tcg gtg 595
 Thr Ser Ser Leu Leu Ser Arg Arg Asp Val Val Val Val Ser Ser Val
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 tcg tgt att tat ggc ttg ggc act cca cag tct tat ctt gac cgt tcc 643
 Ser Cys Ile Tyr Gly Leu Gly Thr Pro Gln Ser Tyr Leu Asp Arg Ser
 170 175 180
 gtt gtg ttg aac gtg ggg gag gag atc gac cgc gat cgc ttt ttg cgc 691

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Val	Val	Leu	Asn	Val	Gly	Glu	Glu	Ile	Asp	Arg	Asp	Arg	Phe	Leu	Arg	
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Leu	Leu	Val	Asp	Ile	Gln	Tyr	Glu	Arg	Asn	Asp	Val	Gly	Phe	Thr	Arg	
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ggt	gct	ttc	cgc	gtg	aag	ggc	gat	acc	gtg	gac	atc	atc	ccg	gcc	tat	787
Gly	Ala	Phe	Arg	Val	Lys	Gly	Asp	Thr	Val	Asp	Ile	Ile	Pro	Ala	Tyr	
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gag	gaa	ttg	gcg	gtg	cgc	att	gag	ttt	ttc	ggc	gat	gaa	att	gat	gcg	835
Glu	Glu	Leu	Ala	Val	Arg	Ile	Glu	Phe	Phe	Gly	Asp	Glu	Ile	Asp	Ala	
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ttg	tac	tac	atc	cat	ccc	ctg	act	ggt	gac	acc	atc	cgg	cag	gtg	aat	883
Leu	Tyr	Tyr	Ile	His	Pro	Leu	Thr	Gly	Asp	Thr	Ile	Arg	Gln	Val	Asn	
				250					255					260		
gag	atc	cgt	att	ttc	cca	gct	acg	cac	tat	ggt	gcg	gga	cct	gag	cgg	931
Glu	Ile	Arg	Ile	Phe	Pro	Ala	Thr	His	Tyr	Val	Ala	Gly	Pro	Glu	Arg	
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Met	Glu	Lys	Ala	Val	Ala	Asp	Ile	Lys	Ala	Glu	Leu	Glu	Val	Arg	Leu	
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gct	gat	ttg	gag	aac	cgt	ggc	aag	tta	ttg	gaa	gcg	cag	cgt	ctt	agg	1027
Ala	Asp	Leu	Glu	Asn	Arg	Gly	Lys	Leu	Leu	Glu	Ala	Gln	Arg	Leu	Arg	
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atg	cgt	act	gaa	tat	gac	tta	gaa	atg	atc	gag	cag	ggt	ggt	ttc	tgt	1075
Met	Arg	Thr	Glu	Tyr	Asp	Leu	Glu	Met	Ile	Gln	Val	Gly	Phe	Cys		
		310			315				320					325		
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Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp	Gly	Arg	Gly	Glu	Gly	
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acc	gca	cgc	gcc	acg	ctg	att	gac	tat	ttc	cca	gag	gat	ttc	ctc	acc	1171
Thr	Ala	Pro	Ala	Thr	Leu	Ile	Asp	Tyr	Phe	Pro	Glu	Asp	Phe	Leu	Thr	
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atc	atc	gat	gag	tct	cac	gtg	aca	gtc	ccg	cag	atc	ggc	ggc	atg	ttt	1219
Ile	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln	Ile	Gly	Gly	Met	Phe	
		360					365				370					
gag	ggc	gat	atg	tcc	cgt	aaa	cgt	aac	ctc	gta	gaa	ttc	ggt	ttc	cgc	1267
Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Asn	Leu	Val	Glu	Phe	Gly	Phe	Arg	
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ctg	cca	tcc	gcg	atg	gat	aac	cgc	cca	ttg	acc	tgg	gag	gag			

425					430					435					
aca ggt	ctg	gtg	gat	cca	aag	gtc	acc	gtc	aag	cca	acg	aag	ggg	cag	1459
Thr Gly	Leu	Val	Asp	Pro	Lys	Val	Thr	Val	Lys	Pro	Thr	Lys	Gly	Gln	
	440					445					450				
att gat	gat	ctg	atc	cat	gaa	att	cgc	caa	cgc	acc	gat	aaa	gat	gag	1507
Ile Asp	Asp	Leu	Ile	His	Glu	Ile	Arg	Gln	Arg	Met	Thr	Asp	Lys	Asp	
	455				460					465					
cgc gtt	ttg	gtc	acc	aca	ttg	acc	aag	aaa	atg	gct	gag	gat	ctt	act	1555
Arg Val	Leu	Val	Thr	Thr	Leu	Thr	Lys	Lys	Met	Ala	Glu	Asp	Leu	Thr	
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gat tac	ctg	ctg	gaa	aac	ggc	atc	cgc	gtg	cgc	tac	ctg	cac	tca	gat	1603
Asp Tyr	Leu	Leu	Glu	Asn	Gly	Ile	Arg	Val	Arg	Tyr	Leu	His	Ser	Asp	
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att gat	acc	ttg	cag	cgt	gtg	gaa	ttg	ctg	cgt	cag	ctt	cgc	ctg	ggc	1651
Ile Asp	Thr	Leu	Gln	Arg	Val	Glu	Leu	Leu	Arg	Gln	Leu	Arg	Leu	Gly	
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gaa tac	gat	gtg	ttg	gta	ggc	att	aac	ctg	ctg	cgt	gag	ggc	ctt	gac	1699
Glu Tyr	Asp	Val	Leu	Val	Gly	Ile	Asn	Leu	Leu	Arg	Glu	Gly	Leu	Asp	
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Leu Pro	Glu	Val	Ser	Leu	Val	Ala	Ile	Leu	Asp	Ala	Asp	Lys	Glu	Gly	
	535				540				545						
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Phe Leu	Arg	Ser	Thr	Thr	Ser	Leu	Ile	Gln	Thr	Ile	Gly	Arg	Ala	Ala	
	550			555					560				565		
cga aat	gtg	tcc	ggc	gag	gtc	atc	atg	tac	gcc	gac	aag	atc	act	gat	1843
Arg Asn	Val	Ser	Gly	Glu	Val	Ile	Met	Tyr	Ala	Asp	Lys	Ile	Thr	Asp	
			570					575					580		
tcg atg	cag	tat	gcc	atc	gag	gaa	acc	gat	cga	cgc	cgt	gaa	aag	cag	1891
Ser Met	Gln	Tyr	Ala	Ile	Glu	Glu	Thr	Asp	Arg	Arg	Arg	Glu	Lys	Gln	
		585					590					595			
gtc gct	tat	aac	aag	gaa	cac	ggc	atc	gat	cgc	cag	cgc	ctt	cga	aag	1939
Val Ala	Tyr	Asn	Lys	Glu	His	Gly	Ile	Asp	Pro	Gln	Pro	Leu	Arg	Lys	
	600					605					610				
aaa atc	gcg	gac	atc	ctc	gac	cag	gtc	tat	gac	aat	tcc	gct	gat	gga	1987
Lys Ile	Ala	Asp	Ile	Leu	Asp	Gln	Val	Tyr	Asp	Asn	Ser	Ala	Asp	Gly	
	615				620				625						
gca gga	cct	tct	gcc	tct	ggc	gat	gcg	gca	gtc	gtg	gct	aaa	cct	gac	2035
Ala Gly	Pro	Ser	Ala	Ser	Gly	Asp	Ala	Ala	Val	Val	Ala	Lys	Pro	Asp	
	630			635					640				645		
gtg tct	agc	atg	ccc	gcc	aaa	gaa	gtg	caa	aag	ctt	atc	gac	gac	ctc	2083
Val Ser	Ser	Met	Pro	Ala	Lys	Glu	Val	Gln	Lys	Leu	Ile	Asp	Asp	Leu	
			650					655					660		
agc gct	cag	atg	gct	gcg	gcc	gcg	cgg	gag	ctc	aag	ttc	gag	ctg	gca	2131
Ser Ala	Gln	Met	Ala	Ala	Ala	Ala	Arg	Glu	Leu	Lys	Phe	Glu	Leu	Ala	
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ggg cgt ctg cga gat gag atc ttc gag ctc aag aag gaa ctg aga ggt 2179
 Gly Arg Leu Arg Asp Glu Ile Phe Glu Leu Lys Lys Glu Leu Arg Gly
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<213> Corynebacterium glutamicum

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Glu Phe Glu Pro Ala Gly Asp Gln Pro Ala Ala Ile Lys Glu Leu Asp
 35 40 45

Glu Arg Leu Asp Arg Gly Glu Arg Asp Val Val Leu Met Gly Ala Thr
 50 55 60

Gly Thr Gly Lys Ser Ala Thr Ala Ala Trp Leu Ile Glu Lys Gln Gln
 65 70 75 80

Arg Pro Ala Leu Val Met Ala Pro Asn Lys Thr Leu Ala Ala Gln Leu
 85 90 95

Ala Asn Glu Leu Arg Gln Leu Leu Pro Asn Asn Ala Val Glu Tyr Phe
 100 105 110

Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Gln Thr
 115 120 125

Asp Thr Tyr Ile Glu Lys Asp Ser Ser Ile Asn Glu Asp Val Glu Arg
 130 135 140

Leu Arg His Ser Ala Thr Ser Ser Leu Leu Ser Arg Arg Asp Val Val
 145 150 155 160

Val Val Ser Ser Val Ser Cys Ile Tyr Gly Leu Gly Thr Pro Gln Ser
 165 170 175

Tyr Leu Asp Arg Ser Val Val Leu Asn Val Gly Glu Glu Ile Asp Arg
 180 185 190

Asp Arg Phe Leu Arg Leu Leu Val Asp Ile Gln Tyr Glu Arg Asn Asp
 195 200 205

Val Gly Phe Thr Arg Gly Ala Phe Arg Val Lys Gly Asp Thr Val Asp
 210 215 220

Ile Ile Pro Ala Tyr Glu Glu Leu Ala Val Arg Ile Glu Phe Phe Gly
 225 230 235 240

00602030 062300

Asp Glu Ile Asp Ala Leu Tyr Tyr Ile His Pro Leu Thr Gly Asp Thr
 245 250 255
 Ile Arg Gln Val Asn Glu Ile Arg Ile Phe Pro Ala Thr His Tyr Val
 260 265 270
 Ala Gly Pro Glu Arg Met Glu Lys Ala Val Ala Asp Ile Lys Ala Glu
 275 280 285
 Leu Glu Val Arg Leu Ala Asp Leu Glu Asn Arg Gly Lys Leu Leu Glu
 290 295 300
 Ala Gln Arg Leu Arg Met Arg Thr Glu Tyr Asp Leu Glu Met Ile Glu
 305 310 315 320
 Gln Val Gly Phe Cys Ser Gly Ile Glu Asn Tyr Ser Arg His Ile Asp
 325 330 335
 Gly Arg Gly Glu Gly Thr Ala Pro Ala Thr Leu Ile Asp Tyr Phe Pro
 340 345 350
 Glu Asp Phe Leu Thr Ile Ile Asp Glu Ser His Val Thr Val Pro Gln
 355 360 365
 Ile Gly Gly Met Phe Glu Gly Asp Met Ser Arg Lys Arg Asn Leu Val
 370 375 380
 Glu Phe Gly Phe Arg Leu Pro Ser Ala Met Asp Asn Arg Pro Leu Thr
 385 390 395 400
 Trp Glu Glu Phe Asp Glu Arg Arg Gly Gln Thr Val Phe Met Ser Ala
 405 410 415
 Thr Pro Gly Lys Phe Glu Ile Ala Ala Asp Gly Glu Phe Val Glu
 420 425 430
 Gln Val Ile Arg Pro Thr Gly Leu Val Asp Pro Lys Val Thr Val Lys
 435 440 445
 Pro Thr Lys Gly Gln Ile Asp Asp Leu Ile His Glu Ile Arg Gln Arg
 450 455 460
 Thr Asp Lys Asp Glu Arg Val Leu Val Thr Thr Leu Thr Lys Lys Met
 465 470 475 480
 Ala Glu Asp Leu Thr Asp Tyr Leu Leu Glu Asn Gly Ile Arg Val Arg
 485 490 495
 Tyr Leu His Ser Asp Ile Asp Thr Leu Gln Arg Val Glu Leu Leu Arg
 500 505 510
 Gln Leu Arg Leu Gly Glu Tyr Asp Val Leu Val Gly Ile Asn Leu Leu
 515 520 525
 Arg Glu Gly Leu Asp Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp
 530 535 540
 Ala Asp Lys Glu Gly Phe Leu Arg Ser Thr Thr Ser Leu Ile Gln Thr
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 Met Ala Ala Leu Ala
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 gaa aac tat caa aca ccg gcg ccg agt tcg cag gtg gtg gtg tct gtg 163
 Glu Asn Tyr Gln Thr Pro Ala Pro Ser Ser Gln Val Val Val Ser Val
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 Val Gly His Val Ala Lys Pro Gly Leu Val Thr Leu Ala Glu Gly Ser
 25 30 35
 cgg gtg gct gat gcc ctg gcc att gca ggt gcc ttg cca gac gcc gat 259
 Arg Val Ala Asp Ala Leu Ala Ile Ala Gly Ala Leu Pro Asp Ala Asp
 40 45 50
 ctg acg gcg ctc aac ttg gcg caa ttg ctt gtc gac ggc acc cag atc 307
 Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly Thr Gln Ile
 55 60 65
 cat gtt tta gct atc gcc gag gta caa cct att tcg gtt gat gct gct 355
 His Val Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val Asp Ala Ala
 70 75 80 85
 gcg act tct gct tct ggg ttg att tcc ttg aat acc gcc act gtt gct 403
 Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala Thr Val Ala
 90 95 100
 gat ttg gtg acg ctg cct ggg gtg ggg gag aag aca gcg cag gcg atc 451
 Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Ile
 105 110 115
 att gac ttt cgg gag agc aac ggt ggg ttt agc acc gtg gag gat tta 499
 Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val Glu Asp Leu
 120 125 130
 ctg cag gtc aag ggg att ggg ccc tca aag ttt gag cag atc tct gga 547
 Leu Gln Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln Ile Ser Gly
 135 140 145
 ttg gtg tcc cca tgattgaggt gcgtttggtt ccc 582
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00602639.062300

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Leu Ala Glu Gly Ser Arg Val Ala Asp Ala Leu Ala Ile Ala Gly Ala
35 40 45

Leu Pro Asp Ala Asp Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val
50 55 60

Asp Gly Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile
65 70 75 80

Ser Val Asp Ala Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn
85 90 95

Thr Ala Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys
100 105 110

Thr Ala Gln Ala Ile Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser
115 120 125

Thr Val Glu Asp Leu Leu Gln Val Lys Gly Ile Gly Pro Ser Lys Phe
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Glu Gln Ile Ser Gly Leu Val Ser Pro
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<210> 109

<211> 528

<212> DNA

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<222> (101)..(505)

<223> FRXA02386

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Val Ser Val Val Gly
1 5

cac gtg gct aaa ccc ggc ctg gtc acg ctg gct gag ggc tgc cgg gtg 163
His Val Ala Lys Pro Gly Leu Val Thr Leu Ala Glu Gly Ser Arg Val
10 15 20

gct gat gcc ctg gcc att gca ggt gcc ttg cca gac gcc gat ctg acg 211
Ala Asp Ala Leu Ala Ile Ala Gly Ala Leu Pro Asp Ala Asp Leu Thr
25 30 35

gcg ctg aac ttg gcg caa ttg ctt gtc gac ggc acc cag atc cat gtt 259
Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly Thr Gln Ile His Val

006290-662300

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 Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala Thr Val Ala Asp Leu
 70 75 80 85
 gtg acg ctg cct ggg gtg ggg gag aag aca gcg cag gcg atc att gac 403
 Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Ile Ile Asp
 90 95 100
 ttt cgg gag agc aac ggt ggg ttt agc acc gtg gag gat tta ctg cag 451
 Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val Glu Asp Leu Leu Gln
 105 110 115
 gtc aag ggg att ggg ccc tca aag ttt gag cag atc tct gga ttg gtg 499
 Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln Ile Ser Gly Leu Val
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 Asp Ala Asp Leu Thr Ala Leu Asn Leu Ala Gln Leu Val Asp Gly
 35 40 45
 Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val
 50 55 60
 Asp Ala Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala
 65 70 75 80
 Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala
 85 90 95
 Gln Ala Ile Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val
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 Glu Asp Leu Leu Gln Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln
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 <213> *Corynebacterium glutamicum*

<220>
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 <223> RXN02388

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 Met Ile Glu Val Arg
 1 5
 ttg gtt ccc gtg cgg gct gtg atg tgg atg gct gtc gct cgg ttg att 163
 Leu Val Pro Val Ala Ala Val Met Trp Met Ala Val Ala Ala Leu Ile
 10 15 20
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 Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile Val Gly Ile Ala Ile
 25 30 35
 att gct gct tgt gtg ttt aaa cac tgg ggt caa gct gtg gtg ata gct 259
 Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln Ala Val Val Ile Ala
 40 45 50
 gca ctg ggc gtt ggt gcc gta gtg atg gct cgg ttg aga atc agc agc 307
 Ala Leu Gly Val Gly Ala Val Val Met Ala Ala Leu Arg Ile Ser Ser
 55 60 65
 gcg aag gca ttt gaa gca ccg caa acc tgg gtg ggt acc gca gaa acc 355
 Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val Gly Thr Ala Glu Thr
 70 75 80 85
 atc aag ttt tta gac agc ggt gat caa cta atc ggt ttg aga gta gaa 403
 Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile Gly Leu Arg Val Glu
 90 95 100
 ggc tat cca cgg ccg att cca gtg ttt tac tct ggt agc gac acc att 451
 Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser Gly Ser Asp Thr Ile
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 gag aaa gcc tct ctc att gca gtg tcc ggt cgg att aaa cca gat agt 499
 Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg Ile Lys Pro Asp Ser
 120 125 130
 ttc cct ggg gtg ggt gat ctg acc att tcc act gaa gac att gat cag 547
 Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr Glu Asp Ile Asp Gln
 135 140 145
 ttg gaa ccg acc act ggt tat agc gca tgg gtg aac cag gtg cgt gac 595
 Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val Asn Gln Val Arg Asp
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 ggg ttt tcc caa gcc gtg gaa gaa acc gtg ggg gag tct tcc cgt gga 643
 Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly Glu Ser Ser Arg Gly
 170 175 180

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Leu Ile	Pro Gly 185	Met Val	Leu Gly	Asp Thr 190	Arg Leu	Gln Gly 195	Ser Ile	
gaa gcc	caa acc	tat att	gat acg	ggg ttg	tct cac	ctg tca	gct gtt	739
Glu Ala	Gln Thr 200	Tyr Ile	Asp Thr 205	Gly Leu	Ser His 210	Ser Ala	Val	
agt gga	agc aat	gta gcc	att gtg	gtg tcc	tct gtg	gtg gtg	ttg tcg	787
Ser Gly 215	Ser Asn	Val Ala	Ile Ile 220	Val Val	Ser Ser 225	Val Val	Leu Ser	
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Tyr Phe 230	Leu Thr	Ala Gly 235	Pro Arg	Ile Arg	Val Val 240	Ala Ser	Leu Leu 245	
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Ser Leu	Val Ile 250	Phe Val	Ser Leu	Val Gly 255	Phe Glu	Pro Ser 260	Val Leu	
cgt gct	tcg gtc	aca ggc	atc gtg	ggg ctt	ctg gca	atc atc	aac tct	931
Arg Ala	Ser Val 265	Thr Gly	Ile Val	Gly Leu 270	Leu Ala	Ile Ile 275	Asn Ser	
tct cgg	atg gag	ccg atg	cat ggg	ttg agt	ctt tcg	gtg att	tgc tta	979
Ser Arg 280	Met Glu	Pro Met	His Gly 285	Leu Ser	Leu Ser 290	Val Ile	Cys Leu	
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Leu Phe 295	Tyr Asp	Ser Asn 300	Ala Val	His Thr	Gly Phe 305	Leu Leu	Ser	
cgt gca	gca act	gct ggc	att gtg	atg ctt	caa cca	ctg ctg	tac cgt	1075
Tys Ala 310	Ala Thr	Ala Gly 315	Ile Val	Met Leu 320	Gln Pro	Leu Leu	Tyr Arg 325	
gcc atc	ggt cca	cca ctg	gcg gtg	tgg aaa	gta cca	gac atc	gtg gtg	1123
Ala Ile	Gly Pro 330	Leu Ala	Val Trp	Lys Val 335	Pro Asp	Ile Val 340	Val	
cgc gct	ttc gcg	gtg tcc	att gcc	gct gat	ctg gtg	acc atc	ccg att	1171
Arg Ala	Phe Ala 345	Val Ser	Ile Ala	Ala Asp 350	Leu Val	Thr Ile 355	Pro Ile	
atc gct	ctg atg	gct cgc	caa ata	tcc ctc	gtg gca	gtg ctg	gcc aac	1219
Ile Ala 360	Leu Met	Ala Arg	Gln Ile 365	Ser Leu	Val Ala	Val Leu	Ala Asn	
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Val Leu 375	Val Glu	Leu Ala	Val Pro 380	Pro Gly	Ile Thr 385	Leu Leu	Gly Leu Ile	
gcc gtg	ctg gca	agc ctt	ctt ccc	tgg cca	gtg gaa	tac cca	ctc ttg	1315
Ala Val 390	Leu Ala	Ser Leu 395	Pro Trp	Pro Val 400	Glu Tyr	Pro Leu	Leu 405	
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Lys Ile	Ile Glu 410	Pro Phe	Thr Trp	Trp Ile 415	His His	Val Ala	Lys Trp 420	
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Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile Ser Ala Gly Trp Ala
 425 430 435
 ggg att gcc tgg gcg tgt atg gca gcg gtg tgg gtg gtg att atc 1459
 Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp Val Val Val Ile Ile
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 tac aaa gga tat gtg cgc acc ctt gca gtg tgt tgt gtc tgc ttc ttt 1507
 Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys Cys Val Cys Phe Phe
 455 460 465
 ctt ttc gcc gcg tgg aat aac aga ctg cca gcc caa ata gat ccg aca 1555
 Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala Gln Ile Asp Pro Thr
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 gag ctg cgg ttt gtc atc atc gcc gat gat tct gag ctc act gat gtg 1603
 Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser Glu Leu Thr Asp Val
 490 495 500
 ccc gaa cat gca gaa ttg atc atc gtg gaa gac ccc cac gcc agc atg 1651
 Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp Pro His Gly Ser Met
 505 510 515
 tcc gat cgc ccc atc gtc acc aga gaa gga atc cct gtg ctg tat cca 1699
 Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile Pro Val Leu Tyr Pro
 520 525 530
 tac cgc gat ggg gag gtc agc ctt cat att gat ggc acc cag cat gca 1747
 Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp Gly Thr Gln His Ala
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 gcg gac ggg aga ttt taacgacact tgtggcacga tgg 1785
 Ala Asp Gly Arg Phe
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 <213> *Corynebacterium glutamicum*
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 Val Gly Ile Ala Ile Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln
 35 40 45
 Ala Val Val Ile Ala Ala Leu Gly Val Gly Ala Val Val Met Ala Ala
 50 55 60
 Leu Arg Ile Ser Ser Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val
 65 70 75 80
 Gly Thr Ala Glu Thr Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile
 85 90 95
 Gly Leu Arg Val Glu Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser

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100 105 110
 Gly Ser Asp Thr Ile Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg
 115 120 125
 Ile Lys Pro Asp Ser Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr
 130 135 140
 Glu Asp Ile Asp Gln Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val
 145 150 155 160
 Asn Gln Val Arg Asp Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly
 165 170 175
 Glu Ser Ser Arg Gly Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg
 180 185 190
 Leu Gln Gly Ser Ile Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser
 195 200 205
 His Leu Ser Ala Val Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser
 210 215 220
 Val Val Val Leu Ser Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val
 225 230 235 240
 Val Ala Ser Leu Leu Ser Leu Val Ile Phe Val Ser Leu Val Gly Phe
 245 250 255
 Glu Pro Ser Val Leu Arg Ala Ser Val Thr Gly Ile Val Gly Leu Leu
 260 265 270
 Ala Ile Ile Asn Ser Ser Arg Met Glu Pro Met His Gly Leu Ser Leu
 275 280 285
 Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr
 290 295 300
 Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln
 305 310 315 320
 Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val
 325 330 335
 Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu
 340 345 350
 Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val
 355 360 365
 Ala Val Leu Ala Asn Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr
 370 375 380
 Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val
 385 390 395 400
 Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His
 405 410 415
 His Val Ala Lys Trp Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile
 420 425 430

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Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp
435 440 445

Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys
450 455 460

Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala
465 470 475 480

Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser
485 490 495

Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp
500 505 510

Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile
515 520 525

Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp
530 535 540

Gly Thr Gln His Ala Ala Asp Gly Arg Phe
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<210> 113

<211> 871

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101) .. (871)

<223> FRXA02385

<400> 113

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Met Ile Glu Val Arg
1 5

ttg gtt ccc gtg gcg gct gtg atg tgg atg gct gtc gct gcg ttg att 163
Leu Val Pro Val Ala Ala Val Met Trp Met Ala Val Ala Ala Leu Ile
10 15 20

atc aat ggt tgc tgg gtg ttg tgc gtg ggg att gtt ggc atc gcg atc 211
Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile Val Gly Ile Ala Ile
25 30 35

att gct gct tgt gtg ttt aaa cac tgg ggt caa gct gtg gtg ata gct 259
Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln Ala Val Val Ile Ala
40 45 50

gca ctg ggc gtt ggt gcc gta gtg atg gct gcg ttg aga atc agc agc 307
Ala Leu Gly Val Gly Ala Val Val Met Ala Ala Leu Arg Ile Ser Ser
55 60 65

gcg aag gca ttt gaa gca ccg caa acc tgg gtg ggt acc gca gaa acc 355
Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val Gly Thr Ala Glu Thr

Parameter	Unit	Value
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β	$^{\circ}$	10
γ	$^{\circ}$	10
δ	$^{\circ}$	10
ϵ	$^{\circ}$	10
ζ	$^{\circ}$	10
η	$^{\circ}$	10
θ	$^{\circ}$	10
ϕ	$^{\circ}$	10
χ	$^{\circ}$	10
ψ	$^{\circ}$	10
ω	$^{\circ}$	10
ν	$^{\circ}$	10
μ	$^{\circ}$	10
λ	$^{\circ}$	10
κ	$^{\circ}$	10
ι	$^{\circ}$	10
\hbar	$^{\circ}$	10
g	$^{\circ}$	10
f	$^{\circ}$	10
e	$^{\circ}$	10
d	$^{\circ}$	10
c	$^{\circ}$	10
b	$^{\circ}$	10
a	$^{\circ}$	10

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Ile Lys Phe Leu Asp	Ser Gly Asp Gln	Leu Ile Gly Leu Arg	Val Glu	
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ggc tat cca gcg ccg att cca gtg ttt tac tct ggt agc gac acc att				451
Gly Tyr Pro Ala	Pro Ile Pro Val Phe Tyr	Ser Gly Ser Asp Thr Ile		
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Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg Ile Lys Pro Asp Ser				
	120	125	130	
ttc cct ggg gtg ggt gat ctg acc att tcc act gaa gac att gat cag				547
Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr Glu Asp Ile Asp Gln				
	135	140	145	
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Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val Asn Gln Val Arg Asp				
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Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly Glu Ser Ser Arg Gly				
	170	175	180	
ctg att cca gcc atg gtg ttg ggg gat acg cgg ttg cag ggg tca att				691
Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg Leu Gln Gly Ser Ile				
	185	190	195	
gaa gcc caa acc tat att gat acg ggg ttg tct cac ctg tca gct gtt				739
Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser His Leu Ser Ala Val				
	200	205	210	
agt gga agc aat gta gcc att gtg gtg tcc tct gtg gtg gtg ttg tcg				787
Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser Val Val Val Leu Ser				
	215	220	225	
tat ttt ctc acc gct ggg cca cgc atc agg gtg gtg gcg tca ttg ctg				835
Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val Val Ala Ser Leu Leu				
	230	235	240	245
tcc tta ggt att ttt gtc tcc ctc gtg ggg ttt gaa				871
Ser Leu Gly Ile Phe Val Ser Leu Val Gly Phe Glu				
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<210> 114

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 114

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Val Gly Ile Ala Ile Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln
35 40 45

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Ala Val Val Ile Ala Ala Leu Gly Val Gly Ala Val Val Met Ala Ala
 50 55 60

Leu Arg Ile Ser Ser Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val
 65 70 75 80

Gly Thr Ala Glu Thr Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile
 85 90 95

Gly Leu Arg Val Glu Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser
 100 105 110

Gly Ser Asp Thr Ile Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg
 115 120 125

Ile Lys Pro Asp Ser Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr
 130 135 140

Glu Asp Ile Asp Gln Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val
 145 150 155 160

Asn Gln Val Arg Asp Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly
 165 170 175

Glu Ser Ser Arg Gly Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg
 180 185 190

Leu Gln Gly Ser Ile Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser
 195 200 205

His Leu Ser Ala Val Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser
 210 215 220

Val Val Val Leu Ser Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val
 225 230 235 240

Val Ala Ser Leu Leu Ser Leu Gly Ile Phe Val Ser Leu Val Gly Phe
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Glu

<210> 115
 <211> 869
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (1)..(846)
 <223> FRXA02388

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tcg gtg att tgc tta ctg ttt tat gat tcc aac ctg gcg gtg cat tac 96
 Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr

002290.062300

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Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Met Leu Gln																															
35																															
cca ctg ctg tac cgt gcc atc ggt cca cca ctg gcg gtg tgg aaa gta																															192
Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val																															
50																															
cca gac atc gtg gtg cgc gct ttc gcg gtg tcc att gcc gct gat ctg																															240
Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu																															
65																															
gtg acc atc ccg att atc gct ctg atg gct cgc caa ata tcc ctc gtg																															288
Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val																															
85																															
gca gtg ctg gcc aac gtg ttg gtt gaa tta gct gtt cca ccc atc acg																															336
Ala Val Leu Asn Val Leu Val Glu Leu Ala Val Pro Ile Thr																															
100																															
ttg ctt ggg ttg att gcc gtg ctg gca agc ctt ctt ccc tgg cca gtg																															384
Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val																															
115																															
gaa tac cca ctc ttg aaa atc att gag ccc ttc acc tgg tgg att cat																															432
Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His																															
130																															
cac gtg gcc aag tgg tgc caa caa tta ccc aat tcg acg ctg gaa ata																															480
His Val Ala Lys Trp Cys Gln Leu Pro Asn Ser Thr Leu Glu Ile																															
145																															
agt gct ggt tgg gca ggg att gcc tgg gcg tgt atg gca gcg gtg tgg																															528
Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp																															
165																															
gtg gtg gtg att atc tac aaa gga tat gtg cgc acc ctt gca gtg tgt																															576
Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys																															
180																															
tgt gtc tgc ttc ttt ctt ttc gcc gcg tgg aat aac aga ctg cca gcc																															624
Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala																															
195																															
caa ata gat ccg aca gag ctg cgg ttt gtc atc atc gcc gat gat tct																															672
Gln Ile Asp Ala Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser																															
210																															
gag ctc act gat gtg ccc gaa cat gca gaa ttg atc atc gtg gaa gac																															720
Val Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp																															
225																															
ccc cac gcc agc atg tcc gat cgc ccc atc gtc acc aga gaa gga atc																															768
Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile																															
245																															
cct gtg ctg tat cca tac cgc gat ggg gag gtc agc ctt cat att gat																															816
Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp																															
260																															

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 Gly Thr Gln His Ala Ala Asp Gly Arg Phe
 275 280

tgg 869

<210> 116

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

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 20 25 30

Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln
 35 40 45

Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val
 50 55 60

Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu
 65 70 75 80

Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val
 85 90 95

Ala Val Leu Ala Asn Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr
 100 105 110

Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val
 115 120 125

Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His
 130 135 140

His Val Ala Lys Trp Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile
 145 150 155 160

Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp
 165 170 175

Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys
 180 185 190

Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala
 195 200 205

Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser
 210 215 220

Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp
 225 230 235 240

Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile
 245 250 255

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Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp
260 265 270

Gly Thr Gln His Ala Ala Asp Gly Arg Phe
275 280

<210> 117

<211> 2019

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1996)

<223> RXA01975

<400> 117

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Leu Ser His His Thr
1 5

cac ctc aat aac tac atc acg agc ttg agt gat aac gct gat ctc cgt 163
His Leu Asn Asn Tyr Ile Thr Ser Leu Ser Asp Asn Ala Asp Leu Arg
10 15 20

gaa aaa gtc acc gca acc gta gac gct ttc cgc cat acc gtc atg gat 211
Glu Lys Val Thr Ala Thr Val Asp Ala Phe Arg His Thr Val Met Asp
25 30 35

gac ttc gac tac atc agt gat caa caa gtc ctg ctt tat ggc gat gtc 259
Asp Phe Asp Tyr Ile Ser Asp Gln Gln Val Leu Leu Tyr Gly Asp Val
40 45 50

caa agc ggt aaa acc tca cac atg ctg gga att atc gca gat tgc ctc 307
Gln Ser Gly Lys Thr Ser His Met Leu Gly Ile Ile Ala Asp Cys Leu
55 60 65

gac agt acg ttt cac acc att gtt att ctg acc tgg cct aac aca cgg 355
Asp Ser Thr Phe His Thr Ile Val Ile Leu Thr Ser Pro Asn Thr Arg
70 75 80 85

ctc gtg caa caa aca tac gac cgt gtt gcc caa gca ttt cca gat act 403
Leu Val Gln Gln Thr Tyr Asp Arg Val Ala Gln Ala Phe Pro Asp Thr
90 95 100

ttg gtg tgc gac cgt gac gga tac aat gat ttc cgt gcg aat caa aag 451
Leu Val Cys Asp Arg Asp Gly Tyr Asn Asp Phe Arg Ala Asn Gln Lys
105 110 115

agc ctc acc cgg cga aaa tct atc gta gtc gtc gga aaa ata cct gca 499
Ser Leu Thr Pro Arg Lys Ser Ile Val Val Val Gly Lys Ile Pro Ala
120 125 130

gtt ctt ggt aat tgg tta cgc gtc ttt aac gac agt ggc gca ctt tct 547
Val Leu Gly Asn Trp Leu Arg Val Phe Asn Asp Ser Gly Ala Leu Ser
135 140 145

006020039.062300

gga cac cct gta ctc att att gat gac gaa gca gat gcg aca agt ctc 595
 Gly His Pro Val Leu Ile Ile Asp Asp Glu Ala Asp Ala Thr Ser Leu 155 160 165
 aac acc aaa gta aat cag tct gat gtt tcg acc att aac cac cag ctc 643
 Asn Thr Lys Val Asn Gln Ser Asp Val Ser Thr Ile Asn His Gln Leu 170 175 180
 act agc ata aga gac ctt gcc aca gga tgc atc tac ctt cag gtc aca 691
 Thr Ser Ile Arg Asp Leu Ala Thr Gly Cys Ile Tyr Leu Gln Val Thr 185 190 195
 ggt aca cct caa gcg gtg ctt ctt caa agc gac gat agc aac tgg gca 739
 Gly Thr Pro Gln Ala Val Leu Leu Gln Ser Asp Asp Ser Asn Trp Ala 200 205 210
 gcg gaa cat gtg ctt cac ttc gca cct ggt gag agc tac atc ggt ggt 787
 Ala Glu His Val Leu His Phe Ala Pro Gly Glu Ser Tyr Ile Gly Gly 215 220 225
 caa ctt ttc ttt tct gag ctc aac aac cct tat cta cga ctt ttc gct 835
 Gln Leu Phe Phe Ser Glu Leu Asn Asn Pro Tyr Leu Arg Leu Phe Ala 230 235 240 245
 aat acc caa ttt gac gag gat tct cgc ttc agc gac gcc att tac acc 883
 Asn Thr Gln Phe Asp Glu Asp Ser Arg Phe Ser Asp Ala Ile Tyr Thr 250 255 260
 tat ctc tta acc gca gca ctg ttc aaa ctt cgc ggt gaa agc ttg tgt 931
 Tyr Leu Leu Thr Ala Ala Leu Phe Lys Leu Arg Gly Glu Ser Leu Cys 265 270 275
 acc atg ctc att cac ccc agc cac act gca tcc agt cat aga gac ttc 979
 Thr Met Leu Ile His Pro Ser His Thr Ala Ser Ser His Arg Asp Phe 280 285 290
 gcg caa gaa gcc cgc ctc caa ctc act ttc gcc ttc gag cga ttc tat 1027
 Ala Gln Glu Ala Arg Leu Gln Leu Thr Phe Ala Phe Glu Arg Phe Tyr 295 300 305
 gaa cca atg att cag cac aat ttc caa cgt gct tat gaa cag ctc gca 1075
 Glu Pro Met Ile Gln His Asn Phe Gln Arg Ala Tyr Glu Gln Leu Ala 310 315 320 325
 caa act gac agc aac ctg cca ccc ttg aga aaa att ctt aac att ctt 1123
 Gln Thr Asp Ser Asn Leu Pro Pro Leu Arg Lys Ile Leu Asn Ile Leu 330 335 340
 ggt ggc atg gaa gat gac ttc tcc atc cac atc gtc aat agc gac aac 1171
 Gly Gly Met Glu Asp Asp Phe Ser Ile His Ile Val Asn Ser Asp Asn 345 350 355
 ccg act gtt gag gaa gat tgg gct gat ggt tat aac att att gtc ggt 1219
 Pro Thr Val Glu Glu Asp Trp Ala Asp Gly Tyr Asn Ile Ile Val Gly 360 365 370
 ggc aac tcg ctt ggg cgc ggt tta aca ttc aac aac ttg caa acc gtt 1267
 Gly Asn Ser Leu Gly Arg Gly Leu Thr Phe Asn Asn Leu Gln Thr Val 375 380 385
 ttc tac gtg cgc gaa tcc aag cga cca caa gca gac acc ctg tgg cag 1315

00602030 006290 006290

Phe Tyr Val Arg Glu Ser Lys Arg Pro Gln Ala Asp Thr Leu Trp Gln
 390 395 400 405
 cac gcc cgc atg ttt ggc tac aaa cgc cac aaa gac acc atg cgt gtg 1363
 His Ala Arg Met Phe Gly Tyr Lys Arg His Lys Asp Thr Met Arg Val
 410 415 420
 ttc atg ccg gcc act att gct caa acc ttc caa gag gtc tat ctc ggc 1411
 Phe Met Pro Ala Thr Ile Ala Gln Thr Phe Gln Glu Val Tyr Leu Gly
 425 430 435
 aac gaa gct att aaa aat cag ctc gat cat ggc acg cat atc aac gac 1459
 Asn Glu Ala Ile Lys Asn Gln Leu Asp His Gly Thr His Ile Asn Asp
 440 445 450
 att cgg gtc att tta ggt gat ggc gtc gca cct act cgt gcc aat gtt 1507
 Ile Arg Val Ile Leu Gly Asp Gly Val Ala Pro Thr Arg Ala Asn Val
 455 460 465
 ctc gac aaa cgc aaa gtt gga aac ctc agc ggt ggc gtc aac tac ttt 1555
 Leu Asp Lys Arg Lys Val Gly Asn Leu Ser Gly Gly Val Asn Tyr Phe
 470 475 480 485
 gcc gct gat cct aga atc aag aat gtc gaa gca ctc gac aaa aaa ctc 1603
 Ala Ala Asp Pro Arg Ile Lys Asn Val Glu Ala Leu Asp Lys Lys Leu
 490 495 500
 ttg gcc tac tta gac aag cac ggt gag gac tcc acc atc ggt atg cgc 1651
 Leu Ala Tyr Leu Asp Lys His Gly Glu Asp Ser Thr Ile Gly Met Arg
 505 510 515
 gcg ata atc acc att ctc aac gcc ttt act gta gac ccc aac gat ctc 1699
 Ala Ile Ile Thr Ile Leu Asn Ala Phe Thr Val Asp Pro Asn Asp Leu
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 gac ctc gcg acc ttc aag gct gcg ctc ctt gac ttt gaa cgc aac caa 1747
 Asp Leu Ala Thr Phe Lys Ala Ala Leu Leu Asp Phe Glu Arg Asn Gln
 535 540 545
 cct cat ctc aca gca cgt atg gtg ctg cga aca aac cgc aaa gtc aat 1795
 Pro His Leu Thr Ala Arg Met Val Leu Arg Thr Asn Arg Lys Val Asn
 550 555 560 565
 cag ggt aca ggc gcc ctg ctc tcc cct act gat caa gct ctc agc cgt 1843
 Gln Gly Thr Gly Ala Leu Leu Ser Pro Thr Asp Gln Ala Leu Ser Arg
 570 575 580
 gca gaa gtc gca cac cca tta ttg atc cta tac cgc att gaa ggt gtt 1891
 Ala Glu Val Ala His Pro Leu Leu Ile Leu Tyr Arg Ile Glu Gly Val
 585 590 595
 aac gat gct gct gcg caa cga ggt gaa cct acg tgg tca agc gac cct 1939
 Asn Asp Ala Ala Ala Gln Arg Gly Glu Pro Thr Trp Ser Ser Asp Pro
 600 605 610
 atc tgg gtg cct aat att aaa ctc cct ggt caa cgt caa ttc tgg tgc 1987
 Ile Trp Val Pro Asn Ile Lys Leu Pro Gly Gln Arg Gln Phe Trp Cys
 615 620 625
 gta gac ggc taaacctgc caccacaaaa aaa 2019
 Val Asp Gly

00602639.066300

06897-9

<213> *Corynebacterium glutamicum*

Gly Glu Ser Leu Cys Thr Met Leu Ile His Pro Ser His Thr Ala Ser

275 280 285
 Ser His Arg Asp Phe Ala Gln Glu Ala Arg Leu Gln Leu Thr Phe Ala
 290 295 300
 Phe Glu Arg Phe Tyr Glu Pro Met Ile Gln His Asn Phe Gln Arg Ala
 305 310 315 320
 Tyr Glu Gln Leu Ala Gln Thr Asp Ser Asn Leu Pro Pro Leu Arg Lys
 325 330 335
 Ile Leu Asn Ile Leu Gly Gly Met Glu Asp Asp Phe Ser Ile His Ile
 340 345 350
 Val Asn Ser Asp Asn Pro Thr Val Glu Glu Asp Trp Ala Asp Gly Tyr
 355 360 365
 Asn Ile Ile Val Gly Gly Asn Ser Leu Gly Arg Gly Leu Thr Phe Asn
 370 375 380
 Asn Leu Gln Thr Val Phe Tyr Val Arg Glu Ser Lys Arg Pro Gln Ala
 385 390 395
 Asp Thr Leu Trp Gln His Ala Arg Met Phe Gly Tyr Lys Arg His Lys
 405 410 415
 Asp Thr Met Arg Val Phe Met Pro Ala Thr Ile Ala Gln Thr Phe Gln
 420 425
 Glu Val Tyr Leu Gly Asn Glu Ala Ile Lys Asn Gln Leu Asp His Gly
 435 440 445
 Thr His Ile Asn Asp Ile Arg Val Ile Leu Gly Asp Gly Val Ala Pro
 450 455 460
 Thr Arg Ala Asn Val Leu Asp Lys Arg Lys Val Gly Asn Leu Ser Gly
 465 470 475 480
 Gly Val Asn Tyr Phe Ala Ala Asp Pro Arg Ile Lys Asn Val Glu Ala
 485 490 495
 Leu Asp Lys Lys Leu Leu Ala Tyr Leu Asp Lys His Gly Glu Asp Ser
 500 505 510
 Thr Ile Gly Met Arg Ala Ile Ile Thr Ile Leu Asn Ala Phe Thr Val
 515 520 525
 Asp Pro Asn Asp Leu Asp Leu Ala Thr Phe Lys Ala Ala Leu Leu Asp
 530 535 540
 Phe Glu Arg Asn Gln Pro His Leu Thr Ala Arg Met Val Leu Arg Thr
 545 550 555 560
 Asn Arg Lys Val Asn Gln Gly Thr Gly Ala Leu Leu Ser Pro Thr Asp
 565 570 575
 Gln Ala Leu Ser Arg Ala Glu Val Ala His Pro Leu Leu Ile Leu Tyr
 580 585 590
 Arg Ile Glu Gly Val Asn Asp Ala Ala Ala Gln Arg Gly Glu Pro Thr
 595 600 605

00602030.062300

Trp Ser Ser Asp Pro Ile Trp Val Pro Asn Ile Lys Leu Pro Gly Gln
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Arg Gln Phe Trp Cys Val Asp Gly
625 630

<210> 119

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..{940}

<223> RXA01954

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atctcgcgga gctcgacgtc gaagaacccg agactcggca gtg ctt gcc gac gac 115
Val Leu Ala Asp Asp
1 5

gtg gtg gtc gtc gcg gag ttc cgg gat cgc atc tac ccc ggc ctg gtg 163
Val Val Val Val Ala Glu Phe Arg Asp Arg Ile Tyr Pro Gly Leu Val
10 15 20

gag aca ggc agg gtt gag cgg ggc ggc gac aag cgg ttc cac acg gtc 211
Glu Thr Gly Arg Val Glu Arg Gly Asp Lys Pro Phe His Thr Val
25 30 35

gtc aac gct gag aac tac cac gcg ctg gag atg ctg acc tat acg cac 259
Val Asn Ala Glu Asn Tyr His Ala Leu Glu Met Leu Thr Tyr Thr His
40 45 50

cgg cat tcc atc gac gcc atc tac atc gac ccg ccg tac aac acc ggg 307
Arg His Ser Ile Asp Ala Ile Tyr Ile Asp Pro Pro Tyr Asn Thr Gly
55 60 65

gcg agg gac tgg aag tac gac aac gat tac gtc gcg agt gat gac gac 355
Ala Arg Asp Trp Lys Tyr Asp Asn Asp Tyr Val Ala Ser Asp Asp Asp
70 75 80 85

tat cga cac tcg aaa tgg ctg gcg ttc atg gag cga cgg ttg aag atc 403
Tyr Arg His Ser Lys Trp Leu Ala Phe Met Glu Arg Arg Leu Lys Ile
90 95 100

tgt cgg gag ctc atg cgt agc gat gct act ctt gtg gca cct atc gat 451
Cys Arg Glu Leu Met Arg Ser Asp Ala Thr Leu Val Ala Pro Ile Asp
105 110 115

gag cat gaa gta aac cgt ttg ggc gtg ttg cta gat cag ctc ttc ccg 499
Glu His Glu Val Asn Arg Leu Gly Val Leu Leu Asp Gln Leu Phe Pro
120 125 130

gaa tct acg cgg caa ctc gtc aca att gtc aac aac cct aaa ggc gtt 547
Glu Ser Thr Arg Gln Leu Val Thr Ile Val Asn Asn Pro Lys Gly Val
135 140 145

00602039 062300

ttt	cag	gga	tat	ctt	tcg	agg	gtc	gaa	gag	tat	gcg	ttc	ttt	gta	ttt	595
Thr	Gln	Gly	Tyr	Leu	Ser	Arg	Val	Glu	Glu	Tyr	Ala	Phe	Phe	Val	Phe	
150					155					160				165		
ggc	cct	gac	gcg	cga	atc	ggc	tcg	gtc	gat	gac	gac	ctt	ctg	acg	cat	643
Gly	Pro	Asp	Ala	Arg	Ile	Gly	Ser	Val	Asp	Asp	Asp	Leu	Leu	Thr	His	
				170					175					180		
cga	gac	atg	gcc	gat	gct	gaa	ggg	gaa	ctg	cag	agg	cct	cga	tgg	aag	691
Arg	Asp	Met	Ala	Asp	Ala	Glu	Gly	Glu	Leu	Gln	Arg	Pro	Arg	Trp	Lys	
			185					190					195			
ggg	ctc	ttg	cgg	tcg	ggc	gac	gac	tcg	ctt	cga	gct	gac	cgt	aaa	gat	739
Gly	Leu	Leu	Arg	Ser	Gly	Asp	Asp	Ser	Leu	Arg	Ala	Asp	Arg	Lys	Asp	
		200				205						210				
atg	ttc	tat	ccg	gtg	tgg	ttc	gat	gag	tcg	act	ggg	cga	ctc	agc	cac	787
Met	Phe	Tyr	Pro	Val	Trp	Phe	Asp	Glu	Ser	Thr	Gly	Arg	Leu	Ser	His	
	215					220					225					
gcg	ggc	gaa	gca	ttg	cca	ctt	gac	gaa	act	cct	gac	ttc	agt	ccg	cag	835
Ala	Gly	Glu	Ala	Leu	Pro	Leu	Asp	Glu	Thr	Pro	Asp	Phe	Ser	Pro	Gln	
230				235						240				245		
gat	ggc	ctg	acg	ccg	atc	tgg	cct	att	agg	cgg	gac	atg	aag	gag	ggg	883
Asp	Gly	Leu	Thr	Pro	Ile	Trp	Pro	Ile	Arg	Arg	Asp	Met	Lys	Glu	Gly	
				250				255						260		
cct	acc	cgg	gca	gcg	cca	cgc	cgt	tcg	atc	ctt	gac	tac	gcg	cta	cac	931
Pro	Thr	Arg	Ala	Ala	Pro	Arg	Arg	Ser	Ile	Leu	Asp	Tyr	Ala	Leu	His	
			265					270					275			
cct	cat	ctg	tgaagagcca	ccaaac	ctg	gac										963
Pro	His	Leu														
		280														
<210> 120																
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<212> PRT																
<213> Corynebacterium glutamicum																
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Val	Leu	Ala	Asp	Asp	Val	Val	Val	Val	Ala	Glu	Phe	Arg	Asp	Arg	Ile	
1					5				10					15		
Tyr	Pro	Gly	Leu	Val	Glu	Thr	Gly	Arg	Val	Glu	Arg	Gly	Gly	Asp	Lys	
			20					25					30			
Pro	Phe	His	Thr	Val	Val	Asn	Ala	Glu	Asn	Tyr	His	Ala	Leu	G		

Arg Arg Leu Lys Ile Cys Arg Glu Leu Met Arg Ser Asp Ala Thr Leu
 100 105
 Val Ala Pro Ile Asp Glu His Glu Val Asn Arg Leu Gly Val Leu Leu
 115 120 125
 Asp Gln Leu Phe Pro Glu Ser Thr Arg Gln Leu Val Thr Ile Val Asn
 130 135 140
 Asn Pro Lys Gly Val Thr Gln Gly Tyr Leu Ser Arg Val Glu Glu Tyr
 145 150 155 160
 Ala Phe Phe Val Phe Gly Pro Asp Ala Arg Ile Gly Ser Val Asp Asp
 165 170 175
 Asp Leu Leu Thr His Arg Asp Met Ala Asp Ala Glu Gly Glu Leu Gln
 180 185 190
 Arg Pro Arg Trp Lys Gly Leu Leu Arg Ser Gly Asp Asp Ser Leu Arg
 195 200 205
 Ala Asp Arg Lys Asp Met Phe Tyr Pro Val Trp Phe Asp Glu Ser Thr
 210 215 220
 Gly Arg Leu Ser His Ala Gly Glu Ala Leu Pro Leu Asp Glu Thr Pro
 225 230 235 240
 Asp Phe Ser Pro Gln Asp Gly Leu Thr Pro Ile Trp Pro Ile Arg Arg
 245 250 255
 Asp Met Lys Glu Gly Pro Thr Arg Ala Ala Pro Arg Arg Ser Ile Leu
 260 265 270
 Asp Tyr Ala Leu His Pro His Leu
 275 280

<210> 121
 <211> 441
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(418)
 <223> RXA02236

<400> 121
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 ccttttgtca ctaaaaacca cagcataacg gaggaacccc gtg gcc ctt cca cag 115
 Val Ala Leu Pro Gln
 1 5
 ttg act gat gag cag cgc aag gca gcg ctt gct aag gca gca gag gca 163
 Leu Thr Asp Glu Gln Arg Lys Ala Ala Leu Ala Lys Ala Ala Glu Ala
 10 15 20
 cgc aag gca cgc gca gag ctc aaa gag aac ctg aag cgc gcc aac act 211
 Arg Lys Ala Arg Ala Glu Leu Lys Glu Asn Leu Lys Arg Gly Asn Thr
 25 30 35

002290.662300

aac ctc agg gaa gtt ctg gac aag gct gag tct gac gag atc atc ggc 259
 Asn Leu Arg Glu Val Leu Asp Lys Ala Glu Ser Asp Glu Ile Ile Gly
 40 45 50
 aag acc aag gtc tcc gct ctc ctc gag gct ctc cct aag gtt ggc aag 307
 Lys Thr Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly Lys
 55 60 65
 gtc aag gca aag gag att atg gac gag ctg ggc att gct cag acc cgt 355
 Val Lys Ala Lys Glu Ile Met Asp Glu Leu Gly Ile Ala Gln Thr Arg
 70 75 80 85
 cgt ctt cgt gga ctg ggt gac cgt cag cgt cgc gca ctt ctc gag cgt 403
 Arg Leu Arg Gly Leu Gly Asp Arg Gln Arg Arg Ala Leu Leu Glu Arg
 90 95 100
 ttc ggc ttc gag gat taattcttca gtgtcgggagc ata 441
 Phe Gly Phe Glu Asp
 105

<210> 122
 <211> 106
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 122
 Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Lys Ala Ala Leu Ala
 1 5 10 15
 Lys Ala Ala Glu Ala Arg Lys Ala Arg Ala Glu Leu Lys Glu Asn Leu
 20 25 30
 Lys Arg Gly Asn Thr Asn Leu Arg Glu Val Leu Asp Lys Ala Glu Ser
 35 40 45
 Asp Glu Ile Ile Gly Lys Thr Lys Val Ser Ala Leu Leu Glu Ala Leu
 50 55 60
 Pro Lys Val Gly Lys Val Lys Ala Lys Glu Ile Met Asp Glu Leu Gly
 65 70 75 80
 Ile Ala Gln Thr Arg Arg Leu Arg Gly Leu Gly Asp Arg Gln Arg Arg
 85 90 95
 Ala Leu Leu Glu Arg Phe Gly Phe Glu Asp
 100 105

<210> 123
 <211> 720
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> {101}..(697)
 <223> RXN01795

<400> 123

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caacttcgct	gaatacggtg	tccacaaatt	cgcggaacgt	gtg Val 1	ctc Leu Ile ggt Val ggt Lys 5	115
att Ile	cgc Arg	cgt Arg	gac Asp	acc Thr 10	ggc Gly Phe Asp Phe Lys 15	163
ggc Gly	cct Pro	cgc Arg	ggt Gly	gac Asp 25	atg Met Pro Tyr Lys 30	211
ggc Gly	gtg Val	aag Lys 40	gat Asp Val	gtc Pro	ccc Pro Thr Asn Asn 45	259
cgc Arg	acc Thr 55	ggt Val	gaa Glu	gtg Val	ctt Leu Lys 60	307
gcg Ala 70	atc Ile	ccc Pro	aaa Lys	gat Asp	gac Asp 75	355
gtt Val	tac Tyr	cgt Arg	cgc Arg	ttg Leu 90	cac His Arg Asp Glu Pro 95	403
ggt Gly	ggc Gly	ggg Gly	ggg Gly	ggt Gly	aca Thr 105	451
ttg Leu	acc Thr	aac Asn	cgc Arg	gag Glu	cgg Ala 120	499
gag Glu	ttt Phe	ttg Leu	gga Gly	tca Ser	aac Asn 140	547
gtt Val	cct Pro	cct Pro	gta Val	ggt Gly	atg Met 155	595
tac Tyr	acc Thr	ggg Gly	aat Asn	tac Tyr	act Thr	643
ctg Leu	cag Gln	acg Thr	ctc Ser	tcc Ser	ile Lys	691
gct Ala	gat Asp	taagtagata	tatgaagccc	acc		720

<210> 124

<211> 199

06 SEP 04

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 124

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His
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Pro Ala Pro Thr His Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala
 20 25 30

Gly Glu Ala Leu Lys Gly Val Lys Asp Val Pro Thr Asn Asn Asn His
 35 40 45

Met Lys Ile Met Pro Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu
 50 55 60

Gly Glu Asn Phe Thr Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys
 65 70 75 80

Gly Met Ile Ser His Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser
 85 90 95

Lys Thr Leu Ile Ala Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr
 100 105 110

Glu Lys Asn Arg Ala Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser
 115 120 125

Phe Pro Asp Asp Phe Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg
 130 135 140

Gln Ile Gly Asn Ala Val Pro Pro Val Gly Met His Ala Val Gly Glu
 145 150 155 160

Arg Leu Met Asn Leu Tyr Thr Gly Asn Tyr Thr Pro Val Asp Leu Glu
 165 170 175

Glu Gln His Ala Tyr Leu Gln Thr Leu Ser Ile Lys Glu Arg Leu Ala
 180 185 190

Leu Ala Asp Gln Glu Ala Asp
 195

<210> 125

<211> 996

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(973)

<223> RXN02267

<400> 125

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accaacgatt caagccttat cagttttgta caggaaaata gtg caa aaa tgg ggt 115
 Val Gln Lys Trp Gly
 1 5

00602639.066260

tta agc ttc gtg gag agg att gtc atc gtg aac aac gtg caa cag ttt 163
 Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn Asn Val Gln Gln Phe
 10 15 20

cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg 211
 His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro
 25 30 35

ctt gac cga gcc atc ggc gaa cac ttt gat cgt cag aac aaa ccg atg 259
 Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg Gln Asn Lys Pro Met
 40 45 50

tcc aga ttc atc gga acg ctc att ctg ccg tta gcc aaa ctg gaa gaa 307
 Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu Ala Lys Leu Glu Glu
 55 60 65

gcc gcc caa tac acc ggc gat gaa gtc ctt cgc gtg tgc gca gta atc 355
 Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg Val Ser Ala Val Ile
 70 75 80 85

agt act gat ggg ctc gct gat ctg cga agg gat ttt tac gaa ctc ccc 403
 Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp Phe Tyr Glu Leu Pro
 90 95 100

aac atc gac atc gcc tcg gtg gaa atc aag ctg gtc ggc gca gcc ctc 451
 Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu Val Gly Ala Ala Leu
 105 110 115

acc aac acc gct tgg ttg gga gat gtg gaa aaa ctc atc caa caa cat 499
 Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys Leu Ile Gln Gln His
 120 125 130

cgc aac act ttc gta tgg gtt gag att ccg aca gcc ctg gtc acc gca 547
 Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr Ala Leu Val Thr Ala
 135 140 145

gat att gtc cga aaa ctc cgc cac atg gga gct ggc ctg aaa tac aga 595
 Asp Ile Val Arg Lys Leu Arg His Met Gly Ala Glu Lys Tyr Arg
 150 155 160 165

act gga ggt gat agg gaa gag ctc ttc ccc tca ccg cag gac ttg gtc 643
 Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser Pro Gln Asp Leu Val
 170 175 180

act gtg ctg cgc acc gcc atc gat gct gca ttg ccg ttt aaa ctc act 691
 Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu Pro Phe Lys Leu Thr
 185 190 195

gca gcc ctg cat cgt gct ctc agg tat cgt gac gag aaa acc gcc cga 739
 Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp Glu Lys Thr Gly Arg
 200 205 210

ctt cac ttc gga ttc ctc aac att gca gcc gcc gtg gcg aca ctt cgt 787
 Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala Val Ala Thr Leu Arg
 215 220 225

gct gga aaa ggc gag gca gag gca ctg aag atc ctt gaa ggc gat gat 835
 Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile Leu Glu Gly Asp Asp
 230 235 240 245

gcc gct ccg ctt att cac gca cta caa agc ggc gaa aac tgg ccg gat 883

00602339.0662300

Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly Glu Asn Trp Arg Asp
 250 255 260

tcc ttc cgc agc ttc agt acc tgc aat gtt gtt gaa cca ctc aac act 931
 Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val Glu Pro Leu Asn Thr
 265 270 275

ctg att gat ctt gat gtg ttg gcg gaa gga gac gta cat ccc 973
 Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp Val His Pro
 280 285 290

taaggatcga cgctagtttag atc 996

<210> 126
 <211> 291
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
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Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr
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Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg
 35 40 45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu
 50 55 60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg
 65 70 75 80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp
 85 90 95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu
 100 105 110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys
 115 120 125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr
 130 135 140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala
 145 150 155 160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser
 165 170 175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu
 180 185 190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp
 195 200 205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala
 210 215 220

00602639.062300

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile
 225 230 235 240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly
 245 250 255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val
 260 265 270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp
 275 280 285

Val His Pro
 290

<210> 127
 <211> 729
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <223> RXN02988

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 Met Ser Thr Lys Pro
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act att gtg tcc aca ttt tct ggt tgc ggt ggc etc gat ctt ggc etc 163
 Thr Ile Val Ser Thr Phe Ser Gly Cys Gly Gly Leu Asp Leu Gly Leu
 10 15 20

caa gag gtc gga ttc gac ccc att tgg gcc aac gac ttc tca gaa gaa 211
 Gln Glu Val Gly Phe Asp Pro Ile Trp Ala Asn Asp Phe Ser Glu Glu
 25 30 35

gca gtc caa acc tat aag cac aac atc ggt gac cac att gtt cac ggc 259
 Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp His Ile Val His Gly
 40 45 50

gac atc act gaa att gat ccg ttt act gat gac acc atc cct gac ggc 307
 Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp Thr Ile Pro Asp Gly
 55 60 65

gat ctc gtc acc ggc ggc ttc ccg tgc cag gac ttc tcc atg atc tgg 355
 Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp Phe Ser Met Ile Trp
 70 75 80 85

aag cgt cct gga ctc gac ggc aag cgt ggc acc ctg tac caa aac ttc 403
 Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr Leu Tyr Gln Asn Phe
 90 95 100

cgt gac ttt gtt gca gca aag aag cct aaa gcc ttt atc gca gaa aac 451
 Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala Phe Ile Ala Glu Asn
 105 110 115

002230 062300

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Val Lys Gly Leu Leu Thr Ala Asn Gln His Lys Ala Ile Lys Thr Ile	
120 125 130	
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Leu Lys Thr Ser Lys Leu Leu Ser Leu Ala Thr Ser Ser Ser Leu Ala	
135 140 145	
tgt aca act tcg ctg aat acg gtg tcc cac aat tcc gcg aac gtg tgc	595
Cys Thr Thr Ser Leu Asn Thr Val Ser His Asn Ser Ala Asn Val Cys	
150 155 160 165	
tca ttg ttg gca ttc gcc gtg aca ccg gct ttg att tca agc acc cag	643
Ser Leu Leu Ala Phe Ala Val Thr Pro Ala Leu Ile Ser Ser Thr Gln	
170 175 180	
ctc cta ccc atg gcc ctc gcg gtg aca tgc cgt ata aga ctg ccg gcg	691
Leu Leu Pro Met Ala Leu Ala Val Thr Cys Arg Ile Arg Leu Pro Ala	
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Asp Phe Ser Glu Glu Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp	
35 40 45	
His Ile Val His Gly Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp	
50 55 60	
Thr Ile Pro Asp Gly Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp	
65 70 75 80	
Phe Ser Met Ile Trp Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr	
85 90 95	
Leu Tyr Gln Asn Phe Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala	
100 105 110	
Phe Ile Ala Glu Asn Val Lys Gly Leu Leu Thr Ala Asn Gln His Lys	
115 120 125	
Ala Ile Lys Thr Ile Leu Lys Thr Ser Lys Leu Leu Ser Leu Ala Thr	
130 135 140	
Ser Ser Ser Leu Ala Cys Thr Thr Ser Leu Asn Thr Val Ser His Asn	
145 150 155 160	

Ser Ala Asn Val Cys Ser Leu Leu Ala Phe Ala Val Thr Pro Ala Leu
165 170 175

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101) . . (565)

<223> RXN00127

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gaagcgcgcca acattggcgc ggcttgattt agattttaccg gtg tgg acg ttg tgc 115
Val Trp Thr Leu Ser
1 5

ccg tat gac ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac 163
Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His
10 15 20

ggc cgt gca gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tgc 211
Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser
25 30 35

ata agc tat ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg 259
Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu
40 45 50

gtt cgg gcg ccc acc cgc gcc acc tcg cga cgc cgg cgg ggc ggc gat 307
Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly Gly Asp
55 60 65

ccg gtt gag cgg gtg tgc aat gca tca cgc tta tgc acg ttt ccc tgc 355
Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys
70 75 80 85

ctt caa atc tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa 403
Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln
90 95 100

cag cga aga ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt 451
Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly
105 110 115

tct gtc ttg atc atc gac gat gtg gta aca acg ggg gca act att tcc 499
Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser
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<400> 131
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                                     Met Arg Asn Tyr Pro
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aag	gca	ccc	gtg	tgg	atg	cac	cga	ctc	tta	gac	cgc	atc	cac	acc	ggc	211
Lys	Ala	Pro	Val	Trp	Met	His	Arg	Leu	30	Leu	Asp	Arg	Ile	His	Thr	Gly
cgc	atg	gcc	aac	cag	ctg	gac	ggt	cgc	gaa	acg	ctc	ggc	gac	aca	gac	259
Arg	Met	Ala	Asn	Pro	Leu	Asp	45	Gly	Ala	Glu	Thr	Leu	Gly	Asp	Thr	Asp
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Ser	Glu	Lys	Arg	Ala	Ala	Val	60	Leu	Met	Leu	Phe	Ser	Gly	Ser	Glu	Thr
tcc	ttt	gac	ctg	ccc	aat	gac	gcc	tcc	gtg	ctg	ctg	acg	cac	cgc	acc	355
Ser	Phe	Asp	Leu	Pro	Asn	Asp	75	Ala	Ser	Val	Leu	Leu	Thr	His	Arg	Thr
cag	acg	atg	cgt	tcc	cat	gca	ggt	cag	att	gcc	ttt	ccc	ggt	ggc	cga	403
Pro	Thr	Met	Arg	Ser	His	Ala	Gly	Gln	95	Ile	Ala	Phe	Pro	Gly	Gly	Arg
atc	gac	ccc	acc	gat	act	aac	gcc	gtg	gac	tgc	gcc	ttc	cgc	gag	gcc	451
Ile	Asp	Pro	Thr	Asp	Thr	Asn	Ala	Val	110	Asp	Cys	Ala	Phe	Arg	Glu	Ala
tgg	gaa	gaa	acc	ggg	ctg	gat	cgc	cgc	acc	gca	acc	cca	tta	gcc	cag	499
Trp	Glu	Glu	Thr	Gly	Leu	Asp	125	Arg	Arg	Thr	Ala	Thr	Pro	Leu	Ala	Gln
ctc	aac	gag	gtg	cac	atc	cgt	gcc	acc	gga	tac	ccc	gtc	tac	cca	atc	547
Leu	Asn	Glu	Val	His	Ile	Arg	140	Ala	Thr	Gly	Tyr	Pro	Val	Tyr	Pro	Ile
ctt	gga	cac	tgg	cac	acc	cca	tca	ccc	gtc	gcc	gtg	gcc	agc	cca	cac	595
Leu	Gly	His	Trp	His	Thr	Pro	Ser	Pro	Val	Ala	Val	Ala	Ser	Pro	His	
gaa	acc	gac	gaa	gtt	ttg	gac	gcc	cca	ctc	tac	gac	ctc	atc	gac	ccc	643
Glu	Thr	Asp	Glu	Val	Leu	Asp	Ala	Pro	Leu	Tyr	Asp	Leu	Ile	Asp	Pro	
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Lys	Asn	Arg	Leu	Met	Val	Gly	Trp	Arg	Glu	Trp	His	Gly	Pro	Ala	Phe	
cga	atc	aac	gac	tac	atc	atc	tgg	gga	ttc	acc	ggc	gga	cta	ctc	tcc	739
Arg	Ile	Asn	Asp	Tyr	Ile	Ile	205	Gly	Phe	Thr	Gly	Gly	Leu	Leu	Ser	
gcg	atc	ctc	gac	acc	gcc	ggc	tgg	gcc	acc	gaa	tgg	gac	acc	gac	cgc	787
Ala	Ile	Leu	Asp	Thr	Ala	Gly	Trp	Ala	Thr	Glu	Trp	Asp	Thr	Asp	Arg	
atc	ttc	gac	ctg	gaa	aat	aca	ttg	tca	aca	tct	cgc	aac	aat	gag	cgt	835
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864

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 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (83)..(574)
 <223> RXN03102

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                Val Val Glu Leu Leu Lys Ser Arg Gly Glu
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acg ctg gcg ttt tgt gaa tcc ctc acc gcc ggc ctt gcc agt gcg acg 160
Thr Leu Ala Phe Cys Glu Ser Leu Thr Ala Gly Leu Ala Ser Ala Thr
                15                    20                25

atc gca gag atc ccc gcc gcc tca gtg gta ctt aaa ggc ggg ctg gtc 208
Ile Ala Glu Ile Pro Gly Ala Ser Val Val Leu Lys Gly Gly Leu Val
                30                    35                40

acc tat gcc acc gag ctt aag gtt gcg ctt gcc ggt gtg ccg cag gag 256
Thr Tyr Ala Thr Glu Leu Lys Val Ala Leu Ala Gly Val Pro Gln Glu
                45                    50                55

ctt atc gac gcg cac gcc gtt gtt tcc ccg cag tgc gcc cgt gcg atg 304
Leu Ile Asp Ala His Gly Val Val Ser Pro Gln Cys Ala Arg Ala Met
                60                    65                70

gca acg ggg gcc gca cac aga tgc cag gca gat tgg gcg gtt tcg ctc 352
Ala Thr Gly Ala Ala His Arg Cys Gln Ala Asp Trp Ala Val Ser Leu
                75                    80                85                90

acg gcc gtt gct gcc ccc agc aaa caa gat ggt cat ccg gtg ggg gaa 400
Thr Gly Val Ala Gly Pro Ser Lys Gln Asp Gly His Pro Val Gly Glu
                95                    100                105

gtg tgg atc gga gtg gct ggt cct gcg cat ttt ggg gcg tcg gga aca 448
Val Trp Ile Gly Val Ala Gly Pro Ala His Phe Gly Ala Ser Gly Thr
                110                    115                120

att gac gcg tat cgt gcg ttt gaa agt gaa caa cag gta ata ttg gct 496
Ile Asp Ala Tyr Arg Ala Phe Glu Ser Glu Gln Val Ile Leu Ala
                125                    130                135

gaa ttg gga cgg cat cat att aga gag tct gct gtg cag caa agc ttt 544
Glu Leu Gly Arg His His Ile Arg Glu Ser Ala Val Gln Gln Ser Phe
                140                    145                150

cgc ctg ctg att gac cat att gag tcg cag tgactcaagt ttccaggtaa 594
Arg Leu Leu Ile Asp His Ile Glu Ser Gln
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act                                                                    597

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<210> 134
 <211> 164

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<212> PRT

<213> *Corynebacterium glutamicum*

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Ala Ser Val Val Leu Lys Gly Gly Leu Val Thr Tyr Ala Thr Glu Leu
 35 40 45

Lys Val Ala Leu Ala Gly Val Pro Gln Glu Leu Ile Asp Ala His Gly
 50 55 60

Val Val Ser Pro Gln Cys Ala Arg Ala Met Ala Thr Gly Ala Ala His
 65 70 75 80

Arg Cys Gln Ala Asp Trp Ala Val Ser Leu Thr Gly Val Ala Gly Pro
 85 90 95

Ser Lys Gln Asp Gly His Pro Val Gly Glu Val Trp Ile Gly Val Ala
 100 105 110

Gly Pro Ala His Phe Gly Ala Ser Gly Thr Ile Asp Ala Tyr Arg Ala
 115 120 125

Phe Glu Ser Glu Gln Gln Val Ile Leu Ala Glu Leu Gly Arg His His
 130 135 140

Ile Arg Glu Ser Ala Val Gln Gln Ser Phe Arg Leu Leu Ile Asp His
 145 150 155 160

Ile Glu Ser Gln

<210> 135

<211> 933

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(910)

<223> RXN03118

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 Met Lys Pro Thr Val
 1 5

aat gtt gtg ttc aat gcg cat cac ccc aaa gat acg cag ccg ttg gat 163
 Asn Val Val Phe Asn Ala His His Pro Lys Asp Thr Gln Pro Leu Asp
 10 15 20

aag ttc ttc gat aaa gaa ctt aaa gac aca cat cat ctc gat ata acg 211
 Lys Phe Phe Asp Lys Glu Leu Lys Asp Thr His His Leu Asp Ile Thr

00602630.062300

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gtg	ggt	tat	atc	agt	gag	aaa	tca	cta	caa	tat	ttg	ctt	ctt	att	gca	259														
Val	Gly	Tyr	Ile	Ser	Glu	Lys	Ser	Leu	Gln	Tyr	Leu	Leu	Leu	Ile	Ala															
		40					45					50																		
ggc	act	tac	ccc	gac	ctc	acc	att	aca	ctt	acc	tgt	gga	atg	cac	gct	307														
Gly	Thr	Tyr	Pro	Asp	Leu	Thr	Ile	Thr	Leu	Thr	Cys	Gly	Met	His	Ala															
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cgt	gaa	ggc	atg	act	gct	gcc	caa	ctg	cat	cat	gcg	cga	gtg	ctc	cat	355														
Arg	Glu	Gly	Met	Thr	Ala	Ala	Gln	Leu	His	His	Ala	Arg	Val	Leu	His															
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gac	tac	tta	agc	gac	cat	gat	cga	ggc	ggg	gtg	ttc	gtt	att	ccc	cga	403														
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ggg	tac	acc	tct	aca	ttc	gag	ccc	ggc	gtc	atc	tta	gac	ccc	gca	cct	547														
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gaa	gat	ctc	gtg	ctt	cat	ctc	aac	cgt	gat	gtc	gta	ccc	cta	tgt	gtc	595														
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ccc	att	gac	acc	gcg	cat	gtc	ccc	atc	att	aaa	gat	caa	gaa	tcc	ccg	643														
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Met	Lys	His	Val	Ala	Glu	Ala	Thr	Ala	Val	Ser	Thr	Ser	Asp	Val	Val															
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gcc	atc	atg	tcc	agc	cca	ttt	act	tat	agt	ttt	gac	ctt	aaa	ctc	aaa	739														
Ala	Ile	Met	Ser	Ser	Pro	Phe	Thr	Tyr	Ser	Phe	Asp	Leu	Lys	Leu	Lys															
			200			205						210																		
gcc	act	gcc	agc	agc	aac	ctc	aat	gct	cat	aac	tca	ggc	ggt	ggc	gcg	787														
Ala	Thr	Ala	Ser	Ser	Asn	Leu	Asn	Ala	His	Asn	Ser	Gly	Gly	Gly	Ala															
			215			220				225																				
cgc	aaa	cag	aaa	aac	ggt	agc	ttc	ctt	gca	cgc	aat	tgg	tat	gag	ggc	835														
Arg	Lys	Gln	Lys	Asn	Gly	Ser	Phe	Leu	Ala	Arg	Asn	Trp	Tyr	Glu	Gly															
				235						240				245																
gaa	atc	att	gtc	ggc	gtc	gag	aca	aca	aga	ctc	cca	ggc	tac	cca	caa	883														
Glu	Ile	Ile	Val	Gly	Val	Glu	Thr	Thr	Arg	Leu	Pro	Gly	Tyr	Pro	Gln															
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aac	aaa	tcc	gaa	ttc	act	gcg	ggc	cac	tgatgacggc	tggtcatttg						930														
Asn	Lys	Ser	Glu	Phe	Thr	Ala	Gly	His																						
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ttt

933

<210> 136

<211> 270

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 136

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His	Leu	Asp	Ile	Thr	Val	Gly	Tyr	Ile	Ser	Glu	Lys	Ser	Leu	Gln	Tyr
	35						40					45			

Leu	Leu	Leu	Ile	Ala	Gly	Thr	Tyr	Pro	Asp	Leu	Thr	Ile	Thr	Leu	Thr
	50					55					60				

Cys	Gly	Met	His	Ala	Arg	Glu	Gly	Met	Thr	Ala	Ala	Gln	Leu	His	His
65					70					75				80	

Ala	Arg	Val	Leu	His	Asp	Tyr	Leu	Ser	Asp	His	Asp	Arg	Gly	Gly	Val
				85					90					95	

Phe	Val	Ile	Pro	Arg	Leu	Arg	Tyr	His	Gly	Lys	Ile	Tyr	Leu	Phe	His
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Lys	Asn	Gln	His	Thr	Asp	Pro	Ile	Ala	Tyr	Ile	Gly	Ser	Ala	Asn	Leu
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Ser	Ala	Ile	Val	Pro	Gly	Tyr	Thr	Ser	Thr	Phe	Glu	Pro	Gly	Val	Ile
	130					135					140				

Leu	Asp	Pro	Ala	Pro	Glu	Asp	Leu	Val	Leu	His	Leu	Asn	Arg	Asp	Val
145					150					155				160	

Val	Pro	Leu	Cys	Val	Pro	Ile	Asp	Thr	Ala	His	Val	Pro	Ile	Ile	Lys
			165						170					175	

Asp	Gln	Glu	Ser	Pro	Met	Lys	His	Val	Ala	Glu	Ala	Thr	Ala	Val	Ser
		180						185					190		

Thr	Ser	Asp	Val	Val	Ala	Ile	Met	Ser	Ser	Pro	Phe	Thr	Tyr	Ser	Phe
		195				200						205			

Asp	Leu	Lys	Leu	Lys	Ala	Thr	Ala	Ser	Ser	Asn	Leu	Asn	Ala	His	Asn
	210					215					220				

Ser	Gly	Gly	Gly	Ala	Arg	Lys	Gln	Lys	Asn	Gly	Ser	Phe	Leu	Ala	Arg
225					230					235				240	

Asn	Trp	Tyr	Glu	Gly	Glu	Ile	Ile	Val	Gly	Val	Glu	Thr	Thr	Arg	Leu
			245						250					255	

Pro	Gly	Tyr	Pro	Gln	Asn	Lys	Ser	Glu	Phe	Thr	Ala	Gly	His		
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 <211> 1263
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1240)
 <223> RXN02989

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 Met Ala Pro Lys Lys
 1 5
 aca gca aca aag gca act gcc gcc aag ggg aat gat cgt cag aag gca 163
 Thr Ala Thr Lys Ala Thr Ala Ala Lys Gly Asn Asp Arg Gln Lys Ala
 10 15 20
 ctt gat gcc gca cta gcc ctg att gag aag gat ttc ggt aaa ggc gct 211
 Leu Asp Ala Ala Leu Ala Leu Ile Glu Lys Asp Phe Gly Lys Gly Ala
 25 30 35
 gtc atg cgt ctg ggt gat gag aat cgt ccg cca atc cag acc atc tca 259
 Val Met Arg Leu Gly Asp Glu Asn Arg Pro Pro Ile Thr Ile Ser
 40 45 50
 tct ggt aac acc gcg att gat att gcc ttg ggt atc ggt gga ttc cca 307
 Ser Gly Asn Thr Ala Ile Asp Ile Ala Leu Gly Ile Gly Gly Phe Pro
 55 60 65
 cgt ggt cga atc gtt gag gtg tat ggc cca gaa tca tca ggt aaa acc 355
 Arg Gly Arg Ile Val Glu Val Tyr Gly Pro Glu Ser Ser Gly Lys Thr
 70 75 80 85
 acc gtt gca ctg cac gca att gcg cag gca caa aag gcc gcc gcc atc 403
 Thr Val Ala Leu His Ala Ile Ala Gln Ala Gln Lys Ala Gly Gly Ile
 90 95 100
 gct gca ttc att gac gcc gag cac gcg ttg gat cca gat tat gct cgc 451
 Ala Ala Phe Ile Asp Ala Glu His Ala Leu Asp Pro Asp Tyr Ala Arg
 105 110 115
 aag ctt ggt gta gat act gat gcg ctt ctg gtt tcg cag cca gac act 499
 Lys Leu Gly Val Asp Thr Asp Ala Leu Leu Val Ser Gln Pro Asp Thr
 120 125 130
 ggt gag caa gca cta gaa atc gcc gac atg ctg gtt cgt tcc gcc gca 547
 Gly Glu Gln Ala Leu Glu Ile Ala Asp Met Leu Val Arg Ser Gly Ala
 135 140 145
 atc gac atc atc gtg att gac tcg gtg gct gcg ctg aca cca aag gct 595
 Ile Asp Ile Ile Val Ile Asp Ser Val Ala Ala Leu Thr Pro Lys Ala
 150 155 160 165
 gaa att gaa gcc gaa atg gcc gat agc cac gtt ggt ctt cag gcc cgc 643
 Glu Ile Glu Gly Glu Met Gly Asp Ser His Val Gly Leu Gln Ala Arg
 170 175 180

002290.4620960
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ctc atg agc cag gcg ctt cgt aag atg aca ggt gcg ctg tac aac tcg 691
 Leu Met Ser Gln Ala Leu Arg Lys Met Thr Gly Ala Leu Tyr Asn Ser
 185 190 195

ggt acc acc gcg atc ttc att aac cag ctg cgt gaa aag atc ggt gtg 739
 Gly Thr Thr Ala Ile Phe Ile Asn Gln Leu Arg Glu Lys Ile Gly Val
 200 205 210

atg ttc ggt tcc cca gaa acc acc ggt ggt aag gcc ctg aag ttc 787
 Met Phe Gly Ser Pro Glu Thr Thr Thr Gly Lys Ala Leu Lys Phe
 215 220 225

tac gca tct gtt cgt tgt gac att cga cga atc cag act ctg aag gac 835
 Tyr Ala Ser Val Arg Cys Asp Ile Arg Arg Ile Gln Thr Leu Lys Asp
 230 235 240 245

gga cag gat gcc att ggt aac cgc acc cgc ttg aag gtc gtt aag aac 883
 Gly Gln Asp Ala Ile Gly Asn Arg Thr Arg Leu Lys Val Val Lys Asn
 250 255 260

aag gtc tcc cca ccg ttc aag atc gct gaa ttc gac atc atg tac gcc 931
 Lys Val Ser Pro Phe Lys Ile Ala Glu Phe Asp Ile Met Tyr Gly
 265 270 275

gaa gcc atc tcc cgt gaa tcc tcc gtc att gac ttg gca gtg gac aac 979
 Glu Gly Ile Ser Arg Glu Ser Ser Val Ile Asp Leu Ala Val Asp Asn
 280 285 290

ggc att gtg aag aag tca ggt tcc tgg ttc acc tac gag gcc gaa cag 1027
 Gly Ile Val Lys Lys Ser Gly Ser Trp Phe Thr Tyr Glu Gly Glu Gln
 295 300 305

ctt ggt caa ggt aag gaa aag gtg cgt ctt tcc ctg aag gag aac cct 1075
 Leu Gly Gln Gly Lys Glu Lys Val Arg Leu Ser Leu Lys Glu Asn Pro
 310 315 320 325

gaa ctg acc gat gag ctg gaa gat aag atc ttc aag aag ctg gga gta 1123
 Glu Leu Thr Asp Glu Leu Glu Asp Lys Ile Phe Lys Lys Leu Gly Val
 330 335 340

ggc aag tac gct gca gcc tca gat gaa ctg acc gac gat cca gta gag 1171
 Gly Lys Tyr Ala Ala Ala Ser Asp Glu Leu Thr Asp Asp Pro Val Glu
 345 350 355

ctc gtg cct aac gtt gac ttc gat gat gaa gcc gac acc gaa gcc gac 1219
 Leu Val Pro Asn Val Asp Phe Asp Asp Glu Ala Asp Thr Glu Ala Asp
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<210> 138

<211> 380

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 138

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006028330.062300

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Phe Gly Lys Gly	Ala Val Met Arg	Leu Gly Asp Glu	Asn Arg Pro Pro
	35	40	45
Ile Gln Thr Ile	Ser Ser Gly Asn	Thr Ala Ile Asp	Ile Ala Leu Gly
	50	55	60
Ile Gly Gly Phe	Pro Arg Gly Arg	Ile Val Glu Val	Tyr Gly Pro Glu
	65	70	75
Ser Ser Gly Lys	Thr Thr Val Ala	Leu His Ala Ile	Ala Gln Ala Gln
	85	90	95
Lys Ala Gly Gly	Ile Ala Ala Phe	Ile Asp Ala Glu	His Ala Leu Asp
	100	105	110
Pro Asp Tyr Ala	Arg Lys Leu Gly	Val Asp Thr Asp	Ala Leu Leu Val
	115	120	125
Ser Gln Pro Asp	Thr Gly Glu Gln	Ala Leu Glu Ile	Ala Asp Met Leu
	130	135	140
Val Arg Ser Gly	Ala Ile Asp Ile	Ile Val Ile Asp	Ser Val Ala Ala
	145	150	155
Leu Thr Pro Lys	Ala Glu Ile Glu	Gly Glu Met Gly	Asp Ser His Val
	165	170	175
Gly Leu Gln Ala	Arg Leu Met Ser	Gln Ala Leu Arg	Lys Met Thr Gly
	180	185	190
Ala Leu Tyr Asn	Ser Gly Thr Thr	Ala Ile Phe Ile	Asn Gln Leu Arg
	195	200	205
Glu Lys Ile Gly	Val Met Phe Gly	Ser Pro Glu Thr	Thr Thr Gly Gly
	210	215	220
Lys Ala Leu Lys	Phe Tyr Ala Ser	Val Arg Cys Asp	Ile Arg Arg Ile
	225	230	235
Gln Thr Leu Lys	Asp Gly Gln Asp	Ala Ile Gly Asn	Arg Thr Arg Leu
	245	250	255
Lys Val Val Lys	Asn Lys Val Ser	Pro Pro Phe Lys	Ile Ala Glu Phe
	260	265	270
Asp Ile Met Tyr	Gly Glu Gly Ile	Ser Arg Glu Ser	Ser Val Ile Asp
	275	280	285
Leu Ala Val Asp	Asn Gly Ile Val	Lys Lys Ser Gly	Ser Trp Phe Thr
	290	295	300
Tyr Glu Gly Glu	Gln Leu Gly Gln	Gly Lys Glu Lys	Val Arg Leu Ser
	305	310	315
Leu Lys Glu Asn	Pro Glu Leu Thr	Asp Glu Leu Glu	Asp Lys Ile Phe
	325	330	335

00602639 062300

Lys Lys Leu Gly Val Gly Lys Tyr Ala Ala Ala Ser Asp Glu Leu Thr
340 345 350

Asp Asp Pro Val Glu Leu Val Pro Asn Val Asp Phe Asp Asp Glu Ala
355 360 365

Asp Thr Glu Ala Asp Thr Glu Ala Asp Ala Glu Asp
370 375 380

<210> 139

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101) .. (1183)

<223> RXN03168

<400> 139

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Met Ser Thr Arg Thr
1 5

acg cca caa gac cgt tat acc gac gaa tac ggc atc gaa cgc gtc aac 163
Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly Ile Glu Arg Val Asn
10 15 20

aag gat gaa ccc ggc ctg gtg gac aaa ctc cgg gac aag cac gac tgg 211
Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg Asp Lys His Asp Trp
25 30 35

ttt gat cat ctc atg cgc atg aat gaa cgt ttc ggc gca aaa ggt ggc 259
Phe Asp His Leu Met Arg Met Asn Glu Arg Phe Gly Ala Lys Gly Gly
40 45 50

aac caa ttg tgc gcg ggt att acg tat ttc tcc gtg ctg tgc atc ttc 307
Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser Val Leu Ser Ile Phe
55 60 65

cgc att gcc atg ctt gtc ttc ggt att gca ggt gtc atc ctt gcc gga 355
Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly Val Ile Leu Ala Gly
70 75 80 85

aac cct gaa gtt ctc aca gat att caa aat cga atc aac gat gct tta 403
Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg Ile Asn Asp Ala Leu
90 95 100

gaa ggc gag atc ggt aac acc gtc aac ggc atc att gat tcc gcg att 451
Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile Ile Asp Ser Ala Ile
105 110 115

gcg cag cgt ggt gct gtg ttg ggc att ggt ggt gta act gcc ctg tgg 499
Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly Val Thr Ala Leu Trp
120 125 130

tct gga ctg ggg tgg atg gcg aac ctg cgc ttt gga gtt tcc cgc atg 547

0602630

Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met
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 Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile Gln Lys Lys Leu Thr
 150 155 160 165
 gac ttg gtc gcg ctg atc gtc ttg ctg ctg gcc atg gcc gta gcc ttc 643
 Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala Met Gly Val Ala Phe
 170 175 180
 ggt atc acg gcg ctc ggt gct tcc gga cta acc aaa aac ctg ctg gac 691
 Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr Lys Asn Leu Leu Asp
 185 190 195
 ttt gtg ggc ctg ggg gag att ccg ggc att agc tac atc acc tgg gtg 739
 Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser Tyr Ile Thr Trp Val
 200 205 210
 gtc gca gca ctt gtt ggt gtc ttg gct aac ttc ctg gtg ttc atg tgg 787
 Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe Leu Val Phe Met Trp
 215 220 225
 ctg att ttc tcc ctg cca cgt acc aaa gtt ccc atg aaa ccg ggt ctt 835
 Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro Met Lys Pro Gly Leu
 230 235 240 245
 cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt 883
 Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val
 250 255 260
 gga tcg ctg ttg gct tca aat gca ttg agt aac ccc gcg ggt gca gca 931
 Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn Pro Ala Gly Ala Ala
 265 270 275
 ttc ggt ccg atc atc ggc atc atg gtt gtg ctg tat ttg atc tgg cgc 979
 Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu Tyr Leu Ile Trp Arg
 280 285 290
 atc ctc atg tat tgc tct gcg tgg gct gcc acc agt gaa gaa gcg ttg 1027
 Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr Ser Glu Glu Ala Leu
 295 300 305
 cgt ctt gcg act gtt cca gca cca gag cct gcg atc att ccg gtt cgc 1075
 Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg
 310 315 320 325
 cat gaa att gat cca ggt gaa gaa gtc tcc caa tct gct cga aaa gtg 1123
 His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val
 330 335 340
 ggc att gga gtg gcc gtg ggt gcc gcg act gcg ggt gct ttt gcg ctg 1171
 Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala Gly Ala Phe Ala Leu
 345 350 355
 ttg cgt aaa aaa tagtttttat taagggcatt ccc 1206
 Leu Arg Lys Lys
 360

<210> 140

09602830, 067304

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Ile	Glu	Arg	Val	Asn	Lys	Asp	Glu	Pro	Gly	Leu	Val	Asp	Lys	Leu	Arg
			20					25					30		
Asp	Lys	His	Asp	Trp	Phe	Asp	His	Leu	Met	Arg	Met	Asn	Glu	Arg	Phe
		35					40					45			
Gly	Ala	Lys	Gly	Gly	Asn	Gln	Leu	Ser	Ala	Gly	Ile	Thr	Tyr	Phe	Ser
	50					55					60				
Val	Leu	Ser	Ile	Phe	Pro	Ile	Ala	Met	Leu	Val	Phe	Gly	Ile	Ala	Gly
	65				70					75					80
Val	Ile	Leu	Ala	Gly	Asn	Pro	Glu	Val	Leu	Thr	Asp	Ile	Gln	Asn	Arg
				85					90					95	
Ile	Asn	Asp	Ala	Leu	Glu	Gly	Glu	Ile	Gly	Asn	Thr	Val	Asn	Gly	Ile
		100						105					110		
Ile	Asp	Ser	Ala	Ile	Ala	Gln	Arg	Gly	Ala	Val	Leu	Gly	Ile	Gly	Gly
		115					120					125			
Val	Thr	Ala	Leu	Trp	Ser	Gly	Leu	Gly	Trp	Met	Ala	Asn	Leu	Arg	Phe
	130					135					140				
Gly	Val	Ser	Arg	Met	Trp	Ala	Ile	Asp	Pro	Thr	Glu	Gly	Asn	Phe	Ile
	145				150					155					160
Gln	Lys	Lys	Leu	Thr	Asp	Leu	Val	Ala	Leu	Ile	Val	Leu	Leu	Leu	Ala
				165					170					175	
Met	Gly	Val	Ala	Phe	Gly	Ile	Thr	Ala	Leu	Gly	Ala	Ser	Gly	Leu	Thr
		180						185					190		
Lys	Asn	Leu	Leu	Asp	Phe	Val	Gly	Leu	Gly	Glu	Ile	Pro	Gly	Ile	Ser
		195					200					205			
Tyr	Ile	Thr	Trp	Val	Val	Ala	Ala	Leu	Val	Gly	Val	Leu	Ala	Asn	Phe
	210					215					220				
Leu	Val	Phe	Met	Trp	Leu	Ile	Phe	Ser	Leu	Pro	Arg	Thr	Lys	Val	Pro
	225				230					235					240
Met	Lys	Pro	Gly	Leu	Gln	Ala	Ala	Leu	Leu	Gly	Ala	Ile	Gly	Phe	Glu
				245					250					255	
Val	Val	Lys	Gln	Val	Gly	Ser	Leu	Leu	Ala	Ser	Asn	Ala	Leu	Ser	Asn
			260					265					270		
Pro	Ala	Gly	Ala	Ala	Phe	Gly	Pro	Ile	Ile	Gly	Ile	Met	Val	Val	Leu
			275				280					285			
Tyr	Leu	Ile	Trp	Arg	Ile	Leu	Met	Tyr	Cys	Ser	Ala	Trp	Ala	Ala	Thr
	290					295					300				

Ser Glu Glu Ala Leu Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala
305 310 315 320

Ile Ile Arg Val Arg His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln
325 330 335

Ser Ala Arg Lys Val Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala
340 345 350

Gly Ala Phe Ala Leu Leu Arg Lys Lys
355 360

<210> 141

<211> 899

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(876)

<223> RXN02431

<400> 141

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tcc aag ctt gcc tca atg ggg gtg gaa aca att ggt gat cta gca gcg 96
Ser Lys Leu Ala Ser Met Gly Val Glu Thr Ile Gly Asp Leu Ala Ala
20 25 30

cta acc caa aaa gaa gta gaa atc agc ctc ggt gca acc atc gga ata 144
Leu Thr Gln Lys Glu Val Glu Ile Ser Leu Gly Ala Thr Ile Gly Ile
35 40 45

tca ctg tgg aac ctt gcc cga gga atc gac gac cgc cct gtg gaa ccc 192
Ser Leu Trp Asn Leu Ala Arg Gly Ile Asp Asp Arg Pro Val Glu Pro
50 55 60

cgc gcc gaa gca aaa cag atc tcc caa gag cac acc tat gaa aaa gac 240
Arg Ala Glu Ala Lys Gln Ile Ser Gln Glu His Thr Tyr Glu Lys Asp
65 70 75 80

ctc ctc acc agg caa caa gta gat gct gcc atc att cga tca gcc gaa 288
Leu Leu Thr Arg Gln Gln Val Asp Ala Ala Ile Ile Arg Ser Ala Glu
85 90 95

ggc gca cac cga cgg ctc ctc aaa gac gga cgc ggt gcc aga act gtc 336
Gly Ala His Arg Arg Leu Leu Lys Asp Gly Arg Gly Ala Arg Thr Val
100 105 110

agc gtg aaa ctg cgg atg gcc gac ttt cgt att gag tct cgt tcc tac 384
Ser Val Lys Leu Arg Met Ala Asp Phe Arg Ile Glu Ser Arg Ser Tyr
115 120 125

acc ttg tcc tat gcc acc gat gat tac gca act ctt gag gca aca gca 432
Thr Leu Ser Tyr Ala Thr Asp Asp Tyr Ala Thr Leu Glu Ala Thr Ala
130 135 140

005290-0220960

ttc cga ctt gcc cgc tac ccc gga gaa gta ggc ccc atc cgc ctt gtc 480
Phe Arg Leu Ala Arg Tyr Pro Gly Glu Val Gly Pro Ile Arg Leu Val
145 150 155 160

gga gta agt ttt tct ggt ttg gaa gaa tcc cgc caa gac atc ctc ttc 528
Gly Val Ser Phe Ser Gly Leu Glu Glu Ser Arg Gln Asp Ile Leu Phe
165 170 175

ccg gaa ctt gac caa caa atc atc gta cca cca gca ccc gac acc gat 576
Pro Glu Leu Asp Gln Gln Ile Ile Val Pro Pro Ala Pro Asp Thr Asp
180 185 190

tat	gag	gta	ggc	gtg	caa	tcc	tct	tct	agt	tcc	gaa	agt	act	caa	gtt	624
Tyr	Glu	Val	Gly	Val	Gln	Ser	Ser	Ser	Ser	Ser	Glu	Ser	Thr	Gln	Val	
		195					200					205				

gaa gcg ccg caa gat gtc gcg ttg agt atg tgg tgc gca acg caa gat 672
Glu Ala Pro Gln Asp Val Ala Leu Ser Met Trp Cys Ala Thr Gln Asp
210 215 220

gtc tac cac cca gaa tat ggc cac ggt tgg gta caa ggt gcc ggt cac 720
Val Tyr His Pro Glu Tyr Gly His Gly Trp Val Gln Gly Ala Gly His
225 230 235 240

ggt gtt gta tca gta cgt ttt gaa acc cgc agc acc aca aaa ggg cga 768
Gly Val Val Ser Val Arg Phe Glu Thr Arg Ser Thr Thr Lys Gly Arg
245 250 255

act aaa agt ttt tcc atg gat gac ccg gac ctc acc ccg gca gac cct 816
Thr Lys Ser Phe Ser Met Asp Asp Pro Asp Leu Thr Pro Ala Asp Pro
260 265 270

cta gat agt ttg gat tgg gct gac tgg ttt gct gaa aat ggt gaa acg 864
Leu Asp Ser Leu Asp Trp Ala Asp Trp Phe Ala Glu Asn Gly Glu Thr
275 280 285

ggg gat gac gaa tagggtttca tcgggtttcg ggg 899
Gly Asp Asp Glu
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<210> 142

<211> 292

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 142

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Ser Lys Leu Ala Ser Met Gly Val Glu Thr Ile Gly Asp Leu Ala Ala
20 25 30

Leu Thr Gln Lys Glu Val Glu Ile Ser Leu Gly Ala Thr Ile Gly Ile
35 40 45

Ser Leu Trp Asn Leu Ala Arg Gly Ile Asp Asp Arg Pro Val Glu Pro
50 55 60

Arg Ala Glu Ala Lys Gln Ile Ser Gln Glu His Thr Tyr Glu Lys Asp
65 70 75 80

[illegible]

Leu Leu Thr Arg Gln Gln Val Asp Ala Ala Ile Ile Arg Ser Ala Glu
85 90 95

Gly Ala His Arg Arg Leu Leu Lys Asp Gly Arg Gly Ala Arg Thr Val
100 105 110

Ser Val Lys Leu Arg Met Ala Asp Phe Arg Ile Glu Ser Arg Ser Tyr
115 120 125

Thr Leu Ser Tyr Ala Thr Asp Asp Tyr Ala Thr Leu Glu Ala Thr Ala
130 135 140

Phe Arg Leu Ala Arg Tyr Pro Gly Glu Val Gly Pro Ile Arg Leu Val
145 150 155 160

Gly Val Ser Phe Ser Gly Leu Glu Glu Ser Arg Gln Asp Ile Leu Phe
165 170 175

Pro Glu Leu Asp Gln Gln Ile Ile Val Pro Pro Ala Pro Asp Thr Asp
180 185 190

Tyr Glu Val Gly Val Gln Ser Ser Ser Ser Glu Ser Thr Gln Val
195 200 205

Glu Ala Pro Gln Asp Val Ala Leu Ser Met Trp Cys Ala Thr Gln Asp
210 215 220

Val Tyr His Pro Glu Tyr Gly His Gly Trp Val Gln Gly Ala Gly His
225 230 235 240

Gly Val Val Ser Val Arg Phe Glu Thr Arg Ser Thr Thr Lys Gly Arg
245 250 255

Thr Lys Ser Phe Ser Met Asp Asp Pro Asp Leu Thr Pro Ala Asp Pro
260 265 270

Leu Asp Ser Leu Asp Trp Ala Asp Trp Phe Ala Glu Asn Gly Glu Thr
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Gly Asp Asp Glu
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<210> 143

<211> 456

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(433)

<223> RXN02985

<400> 143

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aaaggaaacc gccttcacaca ttgtggggagg cggttttctc atg cga tta gaa tct 115
Met Arg Leu Glu Ser
1 5

00602039.062300

tat gcc atg gct aag aaa gta gac acc tgc aac gct acc ccc gct cta 163
 Tyr Ala Met Ala Lys Lys Val Asp Thr Ser Asn Ala Thr Pro Ala Leu
 10 15 20

gcc ctt ctt acg gag agg cag att cct ttt gag ctg gat gtt cat gat 211
 Ala Leu Leu Thr Glu Arg Gln Ile Pro Phe Glu Leu Asp Val His Asp
 25 30 35

gta gat cca aaa tca tca aag ggc ttt gca ttg gat gcc tct gaa gta 259
 Val Asp Pro Lys Ser Ser Lys Gly Phe Ala Leu Asp Ala Ser Glu Val
 40 45 50

atg ggt gtg gag cgc gaa gtg gtg ttt aaa acg ctc atg gca gat att 307
 Met Gly Val Glu Pro Glu Val Val Phe Lys Thr Leu Met Ala Asp Ile
 55 60 65

gat ggt gaa cac gtg gtc gcg att gtt cca gcc agc aga acg ttg aat 355
 Asp Gly Glu His Val Val Ala Ile Val Pro Ala Ser Arg Thr Leu Asn
 70 75 80 85

ctc aag cag ttg gct aag gct gga aaa ggt aag cat gca aac atg atg 403
 Leu Lys Gln Leu Ala Lys Ala Gly Lys Gly Lys His Ala Asn Met Met
 90 95 100

gat cgc agc cgt gca cag gta gtt acg ggg taagtcacctg gtggaatctc 453
 Asp Arg Ser Arg Ala Gln Val Val Thr Gly
 105 110

acc 456

<210> 144
 <211> 111
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 144
 Met Arg Leu Glu Ser Tyr Ala Met Ala Lys Lys Val Asp Thr Ser Asn
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 20 25 30

Leu Asp Val His Asp Val Asp Pro Lys Ser Ser Lys Gly Phe Ala Leu
 35 40 45

Asp Ala Ser Glu Val Met Gly Val Glu Pro Glu Val Val Phe Lys Thr
 50 55 60

Leu Met Ala Asp Ile Asp Gly Glu His Val Val Ala Ile Val Pro Ala
 65 70 75 80

Ser Arg Thr Leu Asn Leu Lys Gln Leu Ala Lys Ala Gly Lys Gly Lys
 85 90 95

His Ala Asn Met Met Asp Arg Ser Arg Ala Gln Val Val Thr Gly
 100 105 110

<210> 145
 <211> 261

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(238)

<223> RXN02986

<400> 145

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				Val	Phe	Leu	Asp	Glu	
				1				5	

tct	gca	att	ctc	cag	gag	cga	atc	tac	gtc	agc	gca	ggg	cga	cgc	ggg	163
Ser	Ala	Ile	Leu	Gln	Glu	Arg	Ile	Tyr	Val	Ser	Ala	Gly	Arg	Arg	Gly	
			10						15				20			

tgg	tcc	ctg	att	atc	gcc	ccg	gat	gat	gtt	ctt	ctg	gct	acc	gat	ggg	211
Trp	Ser	Leu	Ile	Ile	Ala	Pro	Asp	Asp	Val	Leu	Leu	Ala	Thr	Asp	Gly	
			25					30					35			

ggt	tac	gcg	gat	att	gct	gat	cat	tca	taaaaggtaa	aaccaccccc	258
Val	Tyr	Ala	Asp	Ile	Ala	Asp	His	Ser			
		40				45					

cgc 261

<210> 146

<211> 46

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 146

Val	Phe	Leu	Asp	Glu	Ser	Ala	Ile	Leu	Gln	Glu	Arg	Ile	Tyr	Val	Ser
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Ala	Gly	Arg	Arg	Gly	Trp	Ser	Leu	Ile	Ile	Ala	Pro	Asp	Asp	Val	Leu
			20					25					30		

Leu	Ala	Thr	Asp	Gly	Val	Tyr	Ala	Asp	Ile	Ala	Asp	His	Ser
		35					40					45	

<210> 147

<211> 2790

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2767)

<223> RXS00061

<400> 147

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				Val	Thr	Glu	Lys	Thr	

00602379.062300

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gac cag acc tta atg ett atc gac ggc cac tgg atg gct ttc cgc gca			163
Asp Gln Thr Leu Met	10	15	20
ttc ttt gct ttg ccg gct gag aat ttc tcc acg tgg ggc ggg cag gcc			211
Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala	25	30	35
acc aat gct gtc tat ggc ttt ctc tgg atg ctg tcc acg ttg ttg aag			259
Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys	40	45	50
gat gag cag cct act cat gtg gcg gtg gct ttc gat gtg ggg cgt aag			307
Asp Glu Gln Pro Thr His Val Ala Val Ala Phe Asp Val Gly Arg Lys	55	60	65
acg ttc cgt acc gat atg ttc ccg gcg tat aag gcg cag cgt gaa gca			355
Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys Ala Gln Arg Glu Ala	70	75	80
acg cca cct gag ttt aag ggc cag gtg gaa atc ctc aag gag gtg ttg			403
Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile Leu Lys Glu Val Leu	90	95	100
tcc act ttg gga att acg act att gag aaa atc gat ttt gag gct gat			451
Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile Asp Phe Glu Ala Asp	105	110	115
gat gtg atc gcc acg ttg tct gtg gcg gcg aaa cct tta ggc ttt aag			499
Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys Pro Leu Gly Phe Lys	120	125	130
acg ctg att gtt acg ggt gac cgt gat tcc ttc cag ttg gtc aat gac			547
Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe Gln Leu Val Asn Asp	135	140	145
acc acc acg gtg ttg tat ccg atg aag ggc gtg tct gtg ctg cac cgt			595
Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val Ser Val Leu His Arg	150	155	160
ttc acg ccg gaa gca gtg gag gag aag tat gga ctg aca ccg agg cag			643
Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly Leu Thr Pro Arg Gln	170	175	180
tat ccg gag ttt gca gcg ctg cgt ggt gat cct tcc gat aac ttg cct			691
Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro Ser Asp Asn Leu Pro	185	190	195
aat att cct ggc gtg ggc gag aag act gct acc aag tgg att gcc cag			739
Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr Lys Trp Ile Ala Gln	200	205	210
tat gaa act ttg gat aat ttg ctt gat cac gct gat gag atc aag ggc			787
Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala Asp Glu Ile Lys Gly	215	220	225
aag gtt ggc gcc agc ctg cgt gag gcg att gag cag gtc cgg atg aac			835
Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu Gln Val Arg Met Asn	230	235	240
			245

00602339-062300

cgc aag ctc acg gag atg gtg aag gat ctg gag ctg ccg ctt ggt ccg 883
 Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu Leu Pro Leu Gly Pro
 250 255 260

gac gat ttt gag atg aag cct gtg cag gtt gcg gag gtt gcg gcg aag 931
 Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala Glu Val Ala Ala Lys
 265 270 275

ttt gac gat ctg gag ttt ggt acc aat ttg cgt gag ccg gtg ctg gcg 979
 Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg Glu Arg Val Leu Ala
 280 285 290

gtg gtg aag gcc gag ggt tcc gct gcc ccc gtg gag gaa gtg gaa gcg 1027
 Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val Glu Glu Val Glu Ala
 295 300 305

gaa cag gtt gtc gtc gat acg caa tct ttg gcg caa tgg ctg cct gct 1075
 Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala Gln Trp Leu Pro Ala
 310 315 320 325

agg gct ggc cag gcg ctt gct tta gcg ctg gct gga gtg gct aaa cct 1123
 Arg Ala Gly Gln Ala Leu Ala Leu Ala Gly Val Ala Lys Pro
 330 335 340

gct gct ggc gac acg tat gcg cta gcg att gcg gat acc aag cgc cat 1171
 Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala Asp Thr Lys Arg His
 345 350 355

gcg gtg ttg gtt gat gtg gct gat att tca gcg gag gat gaa aag gcg 1219
 Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala Glu Asp Glu Lys Ala
 360 365 370

ctg gcc acg tgg ttg gcg tcg gaa gat cca aag atg ctg cac gcc gct 1267
 Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys Met Leu His Gly Ala
 375 380 385

aag gcc gcc tat cat atg ctc gct ggg cgc ggt ttt gag ctg cac gcc 1315
 Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly Phe Glu Leu His Gly
 390 395 400 405

gtg gtg cat gac acg gcg atc gcg gca tac ttg ctg cgt ccg gcc caa 1363
 Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu Leu Arg Pro Gly Gln
 410 415 420

cgc acc tat gag ctt gcc gac gtc tac cag ccg cat ctt caa cga cag 1411
 Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg His Leu Gln Arg Gln
 425 430 435

ttg tct aca aac gac aat ggc ggc cag ctc acg ctg ctc gac gca gct 1459
 Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr Leu Leu Asp Ala Ala
 440 445 450

gat gac caa tcg ctt gtt gat gat gtc att gca atc ctt gag ctg tct 1507
 Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala Ile Leu Glu Leu Ser
 455 460 465

gaa gaa ttg acc aaa cag ctt cag gag att caa gct ttt gag ctt tac 1555
 Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln Ala Phe Glu Leu Tyr
 470 475 480 485

00602300 00602300 00602300

cat gac ctg gaa att ccg ctg tcg gga att ctg gcg cgc atg gag gcc 1603
 His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu Ala Arg Met Glu Ala 500
 490 495

atc ggt atc gct gtt gat gtt gcc act ttg gaa gag cag ttg aag act 1651
 Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu Glu Gln Leu Lys Thr 515
 505 510

ttc att ggt cag gtt gct cag gaa gag gaa gca gct cgc gag ctc gct 1699
 Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala Ala Arg Glu Leu Ala 530
 520 525

gag gat cca acc ctg aat ctc tcg agc ccg aag cag ctg caa gtg gtg 1747
 Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys Gln Leu Gln Val Val 545
 535 540

ctt ttt gag acg ttc gga atg ccg aaa acc aag aaa acc aag acc ggc 1795
 Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys Lys Thr Lys Thr Gly 565
 550 555 560 565

tac tct acg gct gcc gcg gaa att gaa gcc cta gcg atc aag aat ccg 1843
 Tyr Ser Thr Ala Ala Glu Ile Glu Ala Leu Ala Ile Lys Asn Pro 580
 570 575

cac cca ttc cta gat cac ctg ttg gca cac cgt cag tac caa aag atg 1891
 His Pro Phe Leu Asp His Leu Leu Ala His Arg Gln Tyr Lys Met 595
 585 590

aag acc act ctg gaa ggt ctc atc cgt gag gtg gct cct gat ggc cgt 1939
 Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg 610
 600 605

att cac acc acc ttc aac cag acg gtg gcg tct acg gga cgt ttg tca 1987
 Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser Thr Gly Arg Leu Ser 625
 615 620

tcc act gat ccc aac ctg caa aac att cct gtg cgc act gag gct ggc 2035
 Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly 645
 630 635 640 645

cga aag att cgt tcg gga ttc gtc gta ggc gag ggg tat gaa acc ttg 2083
 Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu 660
 650 655

ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt 2131
 Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu 675
 665 670

tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg 2179
 Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu 690
 680 685

cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg 2227
 His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val 705
 695 700

acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg 2275
 Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val 725
 710 715 720 725

tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct 2323

00602030 062300

Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala
 730 735 740
 ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga 2371
 Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly
 745 750 755
 gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc 2419
 Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly
 760 765 770
 tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc 2467
 Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr
 775 780 785
 tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac 2515
 Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn
 790 795 800 805
 gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc 2563
 Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile
 810 815 820
 cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg 2611
 Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu
 825 830 835
 ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg 2659
 Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu
 840 845 850
 gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag 2707
 Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys
 855 860 865
 ctg tcc gtt cct ttg gaa gtt tca gct ggt gat gcc gtt aac tgg gat 2755
 Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp
 870 875 880 885
 gct gca gcg cac taagaggtaa ctgccttttc gtc 2790
 Ala Ala Ala His

<210> 148

<211> 889

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 148

Val Thr Glu Lys Thr Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser
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Met Ala Phe Arg Ala Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr
 20 25 30

Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu
 35 40 45

Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe
 50 55 60

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Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys
 65 70 75 80
 Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile
 85 90 95
 Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile
 100 105 110
 Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys
 115 120 125
 Pro Leu Gly Phe Lys Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe
 130 135 140
 Gln Leu Val Asn Asp Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val
 145 150 155 160
 Ser Val Leu His Arg Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly
 165 170 175
 Leu Thr Pro Arg Gln Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro
 180 185 190
 Ser Asp Asn Leu Pro Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr
 195 200 205
 Lys Trp Ile Ala Gln Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala
 210 215 220
 Asp Glu Ile Lys Gly Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu
 225 230 235 240
 Gln Val Arg Met Asn Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu
 245 250 255
 Leu Pro Leu Gly Pro Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala
 260 265 270
 Glu Val Ala Ala Lys Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg
 275 280 285
 Glu Arg Val Leu Ala Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val
 290 295 300
 Glu Glu Val Glu Ala Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala
 305 310 315 320
 Gln Trp Leu Pro Ala Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala
 325 330 335
 Gly Val Ala Lys Pro Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala
 340 345 350
 Asp Thr Lys Arg His Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala
 355 360 365
 Glu Asp Glu Lys Ala Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys
 370 375 380

00602039.062300

Met Leu His Gly Ala Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly
 385 390 395 400
 Phe Glu Leu His Gly Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu
 405 410 415
 Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg
 420 425 430
 His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr
 435 440 445
 Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala
 450 455 460
 Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln
 465 470 475 480
 Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu
 485 490 495
 Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu
 500 505 510
 Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala
 515 520 525
 Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys
 530 535 540
 Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys
 545 550 555 560
 Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Glu Ile Glu Ala Leu
 565 570 575
 Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg
 580 585 590
 Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val
 595 600 605
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser
 610 615 620
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val
 625 630 635 640
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu
 645 650 655
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg
 660 665 670
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg
 675 680 685
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val
 690 695 700
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met

00602030 0620300

705 710 715 720
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln
 725 730 735
 Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe
 740 745 750
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu
 755 760 765
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr
 770 775 780
 Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu
 785 790 795 800
 Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile
 805 810 815
 Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val
 820 825 830
 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val
 835 840 845
 Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met
 850 855 860
 Asp Asn Ala Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp
 865 870 875 880
 Gly Val Asn Trp Asp Ala Ala Ala His
 885

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 <211> 1683
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(1660)
 <223> RXS00212

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 cgcgtgatcg aagatatccc gcaccagctt cagggcactg atg aat atc ctg tgc 115
 Met Asn Ile Leu Cys
 1 5

 ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163
 Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile
 10 15 20

 tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211
 Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe
 25 30 35

005290" 6520960

gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259
Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile
40 45 50

gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307
Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly
55 60 65

ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355
Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala
70 75 80 85

ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403
Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr
90 95 100

gat cca gaa gat gtg gtg aaa aag gtc agc tac tgg gct gat cac cgc 451
Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr Trp Ala Asp His Arg
105 110 115

cac gac gca ctc cat gag atg gat ggc ctg gtg att aag gtc gat gac 499
His Asp Ala Leu His Glu Met Asp Gly Leu Val Ile Lys Val Asp Asp
120 125 130

atc gca tct cag cgt gct ttg ggt tcc acc agc cgc gcg cct cgc tgg 547
Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser Arg Ala Pro Arg Trp
135 140 145

gcc att gcg tac aag tac cct ccg gag gag gtc acc acc aag ctg ctt 595
Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val Thr Thr Lys Leu Leu
150 155 160 165

gat att cag gtt ggc gtt ggt cgc acc ggc cgt gtc acc cca ttc gcg 643
Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg Val Thr Pro Phe Ala
170 175 180

gtc atg gag ccg gtt ctt gtt gca gga tca acg gtg tct atg gcg acg 691
Val Met Glu Pro Val Leu Val Ala Gly Ser Thr Val Ser Met Ala Thr
185 190 195

ctg cat aac cag agc gaa gtc aag cgt aaa ggc gtg ctc atc ggt gac 739
Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly Val Leu Ile Gly Asp
200 205 210

acc gtg gtt atc cgc aag gcg ggc gag gtt atc cca gag gtg ctt ggc 787
Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile Pro Glu Val Leu Gly
215 220 225

cct gtc gta gag ctt cgt gac ggc aca gag cgc gag tac atc ttc cca 835
Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg Glu Tyr Ile Phe Pro
230 235 240 245

acg ctg tgc cct gaa tgc ggt acc cgt ctg gcg ccc gcg aag gcc gat 883
Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala Pro Ala Lys Ala Asp
250 255 260

gac gtg gat tgg cgt tgc ccc aac atg caa agc tgt cca ggt cag ctg 931
Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser Cys Pro Gly Gln Leu
265 270 275

tcc acg cgt ttg acc tac ctt gct ggt cgt ggc gct ttt gat att gaa 979

00602039 062300

Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly Ala Phe Asp Ile Glu
 280 285 290
 gca ttg ggc gaa aag ggc gct gaa gac ctc att cgc acc ggc att ttg 1027
 Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile Arg Thr Gly Ile Leu
 295 300 305
 ctt gac gag tct ggc ctg ttc gac ctc aca gag gac gat ctg ctg agc 1075
 Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu Asp Asp Leu Leu Ser
 310 315 320 325
 tcc aat gtc tac acc acc aac gcc ggc aaa gta aat gcc agc ggc aag 1123
 Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val Asn Ala Ser Gly Lys
 330 335 340
 aaa ctg ctg gac aac ctg caa aaa tcc aag cag acc gac ctc tgg cga 1171
 Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln Thr Asp Leu Trp Arg
 345 350 355
 gtc ctc gtg gca tta tct atc agg cac gta ggc ccc acc gca gcg cgc 1219
 Val Leu Val Ala Leu Ser Ile Arg His Val Gly Pro Thr Ala Ala Arg
 360 365 370
 gcc ctt gca ggt cgc tac cac tcc atc cag gcg ctt atc gac gcc ccc 1267
 Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala Leu Ile Asp Ala Pro
 375 380 385
 ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa 1315
 Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln
 390 395 400 405
 tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac 1363
 Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp
 410 415 420
 aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc 1411
 Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val
 425 430 435
 gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg 1459
 Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu
 440 445 450
 gaa ggc ttc acc aga gat tgg gtg aag gaa gcc atc atc tcc cgt ggc 1507
 Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly
 455 460 465
 gga aaa gcc tct gga tct gtc tgg aag aaa act gac tac gtg gtg att 1555
 Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile
 470 475 480 485
 ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg 1603
 Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu
 490 495 500
 cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca 1651
 Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser
 505 510 515
 gct gac gaa tagtcgcaca tgaaaatgcc cca 1683
 Ala Asp Glu

00602639.062300

520

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<212> PRT
<213> Corynebacterium glutamicum

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Ser Leu Trp Arg Ile Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp
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Gly Gly Lys Pro Phe Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
 35             40             45

Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile
 50             55             60

Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His
 65             70             75             80

Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr
 85             90             95

Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr
100             105             110

Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val
115             120             125

Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser
130             135             140

Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val
145             150             155             160

Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg
165             170             175

Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr
180             185             190

Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly
195             200             205

Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile
210             215             220

Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg
225             230             235

Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala
245             250             255

Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser
260             265             270

Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly

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00602839.062700

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                275                280                285
Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile
  290                295                300
Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu
  305                310                315                320
Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val
                325                330                335
Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln
                340                345                350
Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly
                355                360                365
Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala
                370                375                380
Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly
  385                390                395                400
Thr Ile Ile Ala Gln Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His
                405                410                415
Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu
                420                425                430
Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val
                435                440                445
Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala
                450                455                460
Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr
  465                470                475                480
Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala
                485                490                495
Glu Glu Leu Gly Leu Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu
                500                505                510
Leu Asn Thr Gly Ser Ala Asp Glu
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<212> DNA
<213> Corynebacterium glutamicum

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<222> {101}..(673)
<223> RXS00213

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<210> 152
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<400> 152
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 Glu Lys Val Arg Tyr His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu
 20 25 30
 Ile Pro Asp Ala Asp Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu
 35 40 45
 Glu Glu Asp His Pro Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val
 50 55 60
 Val Gly Ala Pro Val Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His
 65 70 75 80
 Leu Glu Arg Met Leu Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu
 85 90 95
 Arg Asp Trp Leu Gly Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu
 100 105 110
 Lys Ile Asp Gly Leu Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu
 115 120 125
 Glu Arg Ala Ala Thr Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr
 130 135 140
 Ala Asn Ala Arg Val Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr
 145 150 155 160
 Asp Glu Tyr Pro Val Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe
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 Ile Thr Val Glu Asp Phe Pro Gly Gly Gln Arg Ala Ala His Cys
 180 185 190

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 <223> RXS00724

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 tccgccacca tgtgcgcaaa tactccacca cggctctggc gtg gga att ggt gat 115
 Val Gly Ile Gly Asp 5
 gcc act gag gcc gat ctt gtt acc atc gtg ggt cag gtc gcc ttt gcc 163
 Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly Gln Val Ala Phe Ala 20
 10 15
 aag cag tcc tat acc cag tcc gcc aag atg ctg tac aag gtt aca gtc 211
 Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu Tyr Lys Val Thr Val 35
 25 30

002290-002300

ttg act gag acg gaa cgc atc ggc att tcc ttc ttc gga gcc aag cac 259
 Leu Thr 40 Glu Thr Glu Arg Ile Gly Ile Ser Phe Phe Gly Ala Lys His 50

att ccg cgt ctt ctc cca gaa ggc act cgt cgc ctt ttt acc ggc aag 307
 Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala Leu Phe Thr Gly Lys 55 60 65

gtg aag ttt ttt cgc aac gaa cct cag cta tct cat cca gag ttc att 355
 Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser His Pro Glu Phe Ile 70 75 80 85

gtg atc cca gat cct gga tca ggc cgc cga ctc acc gcc act ggc ggt 403
 Val Ile Pro Asp 90 Gly Ser Gly Arg Arg Leu Thr Ala Thr Gly Gly 95 100

atg aaa tct ctg gct gcc tac ggc gat gtg gaa gaa gtg gca ctt cgt 451
 Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu Glu Val Ala Leu Arg 105 110 115

ttg gtg gat cgc gaa tac atc ccg atc tat gcc ggc acc gcc acc atg 499
 Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala Gly Thr Ala Thr Met 120 125 130

act acc tgg cgc atc atg gct gca gtg caa cgc gta ctg gaa acc atg 547
 Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg Val Leu Glu Thr Met 135 140 145

ccg gtg atc aaa gaa cca ctg agc gtg gtg ccc gaa ggc atg ccc agt 595
 Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro Glu Gly Met Pro Ser 150 155 160 165

ttc gac gag gcc atc cgc ggc att cac gat cca ggc cat gaa tct ccc 643
 Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro Gly His Glu Ser Pro 170 175 180

agc acg ttt atc aac cgt ctg aaa tac aac gaa gca cta tcg ctg gcc 691
 Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu Ala Leu Ser Leu Ala 185 190 195

acg gtg atg gcg atc ccg cgt gcc gat acc aag aac cgc aaa gca cca 739
 Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys Asn Arg Lys Ala Pro 200 205 210

ccc atg ccg cgc gca ctc aaa ggc cat cag cac atg ctc atc gat gca 787
 Pro Met Pro Arg Ala Leu Lys Gly His Gln His Met Leu Ile Asp Ala 215 220 225

ctc aac ttt cag ctc aca gtg gga cag aag caa gtg atc cgt gag atc 835
 Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln Val Ile Arg Glu Ile 230 235 240 245

agc gcg gac att gaa caa cgc gtt ccc atg tct cgt ctg ctc caa ggt 883
 Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser Arg Leu Leu Gln Gly 250 255 260

gag gtt ggt tcg ggt aaa acc atc gtg tcg ttg atc gcg atg ctg cag 931
 Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu Ile Ala Met Leu Gln 265 270 275

005290.6220960

gca att gat tcc ggt agg cag tgc gcc atg ctc gcc ccg acg gaa gtg 979
 Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu Ala Pro Thr Glu Val
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ttg gcc acc cag cat gcc cgc agc ctg agc aaa act ctc gac gac gca 1027
 Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys Thr Leu Asp Asp Ala
 295 300 305

ggc ctt gat atc aat gtt gtg ctc ttg act ggc tcg atg ccc acg gga 1075
 Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly Ser Met Pro Thr Gly
 310 315 320 325

gcc aag aag gag gct ctg ctg gaa atc atc tcc ggt gac gca gac att 1123
 Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser Gly Asp Ala Asp Ile
 330 335 340

gtg gtc gcc acg cat cgc ctg atc cag gac acc gtg gag ttc ttc gac 1171
 Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp
 345 350 355

ctt gcc ctc gtg gtg gtg gat gag cag cac cgt ttc gcc gtg gag caa 1219
 Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Val Glu Gln
 360 365 370

cgc gat caa ctg cgg acc aag gcc agg gaa gcc ctg acc ccg cac cta 1267
 Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu
 375 380 385

ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg 1315
 Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val
 390 395 400 405

ttc gcc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca gcc ggg cgc 1363
 Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg
 410 415 420

cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct gcc tgg gtt 1411
 Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val
 425 430 435

aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa 1459
 Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln
 440 445 450

gcc tat gtg gtg tgt ccg cgc att gaa gcc gaa gcc gcc gtg ctg gaa 1507
 Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Gly Val Leu Glu
 455 460 465

atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga 1555
 Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly
 470 475 480 485

atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag 1603
 Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln
 490 495 500

gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att 1651
 Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile
 505 510 515

gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag 1699

00602639 062300

Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu
 520 525 530
 gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt 1747
 Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val
 535 540 545
 ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac 1795
 Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp
 550 555 560 565
 gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc 1843
 Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr
 570 575 580
 gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc 1891
 Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly
 585 590 595
 gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939
 Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His
 600 605 610
 ctc tcg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987
 Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp
 615 620 625
 gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035
 Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val
 630 635 640 645
 agc gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077
 Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu Glu Lys Ser
 650 655
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe
 35 40 45
 Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala
 50 55 60
 Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser
 65 70 75 80
 His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu
 85 90 95

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Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu
 100 105 110
 Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala
 115 120
 Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg
 130 135 140
 Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro
 145 150 155 160
 Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro
 165 170 175
 Gly His Glu Ser Pro Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu
 180 185 190
 Ala Leu Ser Leu Ala Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys
 195 200 205
 Asn Arg Lys Ala Pro Pro Met Pro Arg Ala Leu Lys Gly His Gln His
 210 215 220
 Met Leu Ile Asp Ala Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln
 225 230 235 240
 Val Ile Arg Glu Ile Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser
 245 250 255
 Arg Glu Leu Gln Gly Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu
 260 265 270
 Ile Ala Met Leu Gln Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu
 275 280 285
 Ala Pro Thr Glu Val Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys
 290 295 300
 Thr Leu Asp Asp Ala Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly
 305 310 315 320
 Ser Met Pro Thr Gly Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser
 325 330 335
 Gly Asp Ala Asp Ile Val Val Gly Thr His Ala Leu Ile Gln Asp Thr
 340 345 350
 Val Glu Phe Phe Asp Leu Gly Leu Val Val Val Asp Glu Gln His Arg
 355 360 365
 Phe Gly Val Glu Gln Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly
 370 375 380
 Leu Thr Pro His Leu Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr
 385 390 395 400
 Ile Ala Met Thr Val Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu
 405 410 415

00602839 062300

Leu Pro Gly Gly Arg Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His
 420 425 430
 Lys Pro Gly Trp Val Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val
 435 440 445
 Leu Ala Gly Arg Gln Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu
 450 455 460
 Gly Gly Val Leu Glu Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro
 465 470 475 480
 Gly Leu Asn Val Gly Met Leu His Gly Arg Met Asp Thr Asp Leu Lys
 485 490 495
 Asp Ser Val Met Gln Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val
 500 505 510
 Ala Thr Thr Val Ile Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val
 515 520 525
 Met Leu Ile Arg Glu Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln
 530 535 540
 Leu Arg Gly Arg Val Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu
 545 550 555 560
 His Thr Thr Phe Asp Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala
 565 570 575
 Ile Ser Thr Thr Thr Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln
 580 585 590
 Val Arg Gln Glu Gly Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp
 595 600 605
 Thr Lys Leu Arg His Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu
 610 615 620
 Arg Ala Leu Ile Asp Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg
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 Glu Lys Ser

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 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(880)
 <223> RXS00823

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tcatttcta gatgaatcaa atccgcgccta acttaagggt atg ggt tcc att act 115
Met Gly Ser Ile Thr
1 5

ccg cag aag cgg cct cgc gtg ggg tct cac atc gcg aac aag ggt caa 163
Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile Ala Asn Lys Gly Gln
10 15 20

gag act gat atc ggg cga aaa cgc cga gct cga cgc atc aat cgc aca 211
Glu Thr Asp Ile Gly Arg Lys Arg Ala Arg Arg Ile Asn Arg Thr
25 30 35

ctc acc gtg gca tat ccg gat gcg cac tgc gaa tta gat ttc acc aat 259
Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu Leu Asp Phe Thr Asn
40 45 50

ccg cta gaa ctc acg gtc gcc acc att ttg tcc gcc cag tgc acg gac 307
Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser Ala Gln Cys Thr Asp
55 60 65

gtt cgc gtg aac cag gtg acg ccc gcg ttg ttc aag cgc tat ccg acg 355
Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe Lys Arg Tyr Pro Thr
70 75 80 85

gcc aca gat tac gcc aac gcc gat cgc acg gaa ttg gag gag ttc atc 403
Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu Leu Glu Glu Phe Ile
90 95 100

cgt ccg aca ggc ttt tac cgc aac aag gcc act tct tta atc ggc ctg 451
Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr Ser Leu Ile Gly Leu
105 110 115

ggt gag gca cta att tcg ctt cac gac ggc cag gtc ccc ggt acc ctt 499
Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln Val Pro Gly Thr Leu
120 125 130

gag cag cta gtt gag ctg ccg ggg gtc ggg cgg aaa acc gcc aac gtg 547
Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val
135 140 145

gtg ctg gga aat gct ttc ggt gtt ccg gga atc acg gtg gat aca cac 595
Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile Thr Val Asp Thr His
150 155 160 165

ttt ggc agg ttg gtg cgt cgc ctg aag ctc act gat gaa gaa gat ccc 643
Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr Asp Glu Glu Asp Pro
170 175 180

gtc aag gtg gaa aaa gtg atg aac gaa ctc atc gaa aag cct gag tgg 691
Val Lys Val Glu Lys Val Met Asn Glu Leu Ile Glu Lys Pro Glu Trp
185 190 195

acc atg ttt tca cat agg ctg atc ttc cac gga cgt agg ata tgt cat 739
Thr Met Phe Ser His Arg Leu Ile Phe His Gly Arg Arg Ile Cys His
200 205 210

agt cga cgc gcc gcc tgt gga gcc tgc atg ctg gca gct gat tgc cca 787
Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu Ala Ala Asp Cys Pro
215 220 225

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tcc ttt ggt ttg gag ggg ccg tca gat cca ttt gag gcg caa aaa ctc 835
 Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe Glu Ala Gln Lys Leu
 230 235 240 245

att aaa agt gat gat agg gag cac ctg ctg aaa atg gca gga atg 880
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tagaaaaaaa atgacaagca gtg 903

<210> 156

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Gly Ser Ile Thr Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile
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 20 25 30

Arg Ile Asn Arg Thr Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu
 35 40 45

Leu Asp Phe Thr Asn Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser
 50 55 60

Ala Gln Cys Thr Asp Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe
 65 70 75 80

Lys Arg Tyr Pro Thr Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu
 85 90 95

Leu Glu Glu Phe Ile Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr
 100 105 110

Ser Leu Ile Gly Leu Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln
 115 120 125

Val Pro Gly Thr Leu Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg
 130 135 140

Lys Thr Ala Asn Val Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile
 145 150 155 160

Thr Val Asp Thr His Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr
 165 170 175

Asp Glu Glu Asp Pro Val Lys Val Glu Lys Val Met Asn Glu Leu Ile
 180 185 190

Glu Lys Pro Glu Trp Thr Met Phe Ser His Arg Leu Ile Phe His Gly
 195 200 205

Arg Arg Ile Cys His Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu
 210 215 220

Ala Ala Asp Cys Pro Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe
 225 230 235 240

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Glu Ala Gln Lys Leu Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys
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Met Ala Gly Met
 260

<210> 157
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(889)
 <223> RXS00898

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 Met Arg Ile Val Asn
 1 5
 tgg aac gtc aac tct gct cgc act cgt gtg gac cgg atg gtc gat ttt 163
 Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp Arg Met Val Asp Phe
 10 15 20
 ttg ctt cgc cat gat gtt gat gta tta tta gcg gtg cag gaa acc aag tgt 211
 Leu Leu Arg His Asp Val Asp Val Leu Ala Val Gln Glu Thr Lys Cys
 25 30 35
 aaa gat gag caa ttt ccc acc gag cgt ttc acc gaa atc ggc tat gag 259
 Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr Glu Ile Gly Tyr Glu
 40 45 50
 gta gcc cat ttc ggc ctt aac cag tgg aat ggt gtc gcc att att tcc 307
 Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly Val Ala Ile Ile Ser
 55 60 65
 cgc gtt ggc att gaa aat gtg gaa acc cac ttc cct gcc caa cgg gga 355
 Arg Val Gly Ile Glu Asn Val Glu Thr His Phe Pro Ala Gln Pro Gly
 70 75 80 85
 ttc aac aaa gac atc acc aag gaa caa tcc atc gaa gcc cgc gcc atc 403
 Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile Glu Ala Arg Ala Ile
 90 95 100
 ggc gcc cgc tgc ggt ggt gtc cag gtg tgg agc ctc tat gtt ccc aac 451
 Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser Leu Tyr Val Pro Asn
 105 110 115
 ggc cgc gaa atc gca gat cct cac tac gac tac aaa ctg cgc tgg cta 499
 Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr Lys Leu Arg Trp Leu
 120 125 130
 ttc tcc ctg cgc aac tac gtg atc gac acc ttg gaa tac cgc ccc gag 547
 Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu Glu Tyr Arg Pro Glu
 135 140 145

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gaa aaa ctg gtg ttg ctc ggc gac ttc aac atc gcg ccc aca gac atc 595
 Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile Ala Pro Thr Asp Ile 165
 150 155 160

gac gtc tgg gac atc gca gcc ttc gaa gga aaa acc cac gtc acc gaa 643
 Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys Thr His Val Thr Glu 180
 170 175

cca gaa cgt gca gct ttc gac ggc ctc atc gaa gcc gga ctc aaa gaa 691
 Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu Ala Gly Leu Lys Glu 195
 185 190

acc acc ccc gga cct ggt acc tac acc tac tgg gat tac aaa ggc gca 739
 Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp Asp Tyr Lys Gly Ala 210
 200 205

cgc ttc ctc aaa ggc gaa ggc atg cgc atc gat ttc cag ctc gca tcc 787
 Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp Phe Gln Leu Ala Ser 225
 215 220

ccg gcc ctt gct gca acc gcg ggt gaa acc ttt gtg gac gtt gaa gaa 835
 Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe Val Asp Val Glu Glu 245
 230 235 240

cgc agc gga acc ggc gcc tct gac cac gca cca gtc atc gtt gat tac 883
 Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro Val Ile Val Asp Tyr 260
 250 255

aag gtg taactgcgta tgatctttca gat 912
 Lys Val

<210> 158
 <211> 263
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 158
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Arg Met Val Asp Phe Leu Leu Arg His Asp Val Asp Val Leu Ala Val 30
 20 25

Gln Glu Thr Lys Cys Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr 45
 35 40

Glu Ile Gly Tyr Glu Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly 60
 50 55

Val Ala Ile Ile Ser Arg Val Gly Ile Glu Asn Val Glu Thr His Phe 80
 65 70 75

Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile 95
 85 90

Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser 110
 100 105

Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr

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115	120	125	
Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu 130 135 140			
Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile 145 150 155			
Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys 165 170 175			
Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu 180 185 190			
Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp 195 200 205			
Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp 210 215 220			
Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe 225 230 235 240			
Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro 245 250 255			
Val Ile Val Asp Tyr Lys Val 260			
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<223> RXS01066			
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Met Arg Arg Asp Ser 5			
1			
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Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala			
10 15 20			
gac cgc att att gtg ctg ctc acc cga gac cac gcc atc gtg cgc gga 211			
Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly			
25 30 35			
gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259			
Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu			
40 45 50			
cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307			
Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu			

55 60 65

tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355
 Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70 75 80 85

atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc 403
 Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile
 90 95 100

gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa 451
 Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu
 105 110 115

acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc 499
 Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu
 120 125 130

aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc gcc tgg gca 547
 Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala
 135 140 145

cca agc ctt ttc gac tgc gca gcc tgc gcc cga cca gga cct cac aac 595
 Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn
 150 155 160 165

gca ttc cac cca ggc gtc gcc ggg gca gtg tgc ctg tac tgc cga ccg 643
 Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro
 170 175 180

ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg 691
 Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu
 185 190 195

gtc gcc aac gcc caa gca gcc cgc att ccc cgg gaa cac cca gag cag 739
 Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln
 200 205 210

caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att 787
 Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile
 215 220 225

gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag 836
 Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala
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gcttaggcgt ccg 849

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 <213> *Corynebacterium glutamicum*

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[illegible]

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<213> Corynebacterium glutamicum

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<222> (101)..(1717)
<223> RXS02145

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tcattgagcc actcggccct gcattctggg agcgtaaagc atg agt cta gct acc      115
                                     Met Ser Leu Ala Thr
                                     1           5

gtg gga aac aat ctt gat tcc cgt tac acc atg gcg tcg ggt atc cgt      163

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Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met Ala Ser Gly Ile Arg	
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cgc cag atc aac aag gtc ttc cca act cac tgg tcc ttc atg ctc ggc	211
Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp Ser Phe Met Leu Gly	
25 30 35	
gag att gcg ctt tac agc ttc atc gtc ttg ctg ctg act ggt gtc tac	259
Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu Leu Thr Gly Val Tyr	
40 45 50	
ctg acc ctg ttc ttc gac cca tca atc acc aag gtc att tat gac ggc	307
Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys Val Ile Tyr Asp Gly	
55 60 65	
ggc tac ctc cca ctg aac ggt gtg gag atg tcc cgt gca tac gca act	355
Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser Arg Ala Tyr Ala Thr	
70 75 80 85	
gcg ttg gat att tcc ttc gag gtt cgc ggt ggt ctg ttc atc cgc cag	403
Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly Leu Phe Ile Arg Gln	
90 95 100	
atg cac cac tgg gca gcc ctg ctg ttc gtt gta tcc atg ctg gtt cac	451
Met His His Trp Ala Ala Leu Leu Phe Val Val Ser Met Leu Val His	
105 110 115	
atg ctc cgt att ttc ttc acc ggt gcg ttc cgt cgc cca cgt gaa gca	499
Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg Arg Pro Arg Glu Ala	
120 125 130	
aac tgg atc atc ggt gtt gtt ctg atc atc ctg ggt atg gct gaa ggc	547
Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu Gly Met Ala Glu Gly	
135 140 145	
ttc atg ggt tac tcc ctg cct gat gac ctg ctc tct ggt gtt ggt ctt	595
Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu Ser Gly Val Gly Leu	
150 155 160 165	
cga atc atg tcc gcc atc atc gtt ggt ctt ccg atc ata ggt acc tgg	643
Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro Ile Ile Gly Thr Trp	
170 175 180	
atg cac tgg ctg atc ttc ggt gga gac ttc cca tcc gat ctg atg ctg	691
Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro Ser Asp Leu Met Leu	
185 190 195	
gac cgc ttc tac atc gca cac gtt cta atc atc cca gct atc ctg ctt	739
Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile Pro Ala Ile Leu Leu	
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ggc ttg atc gca gct cac ctg gca ctt gtt tgg tac cag aag cac acc	787
Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp Tyr Gln Lys His Thr	
215 220 225	
cag ttc cca ggc gct ggc cgc act gag aac aac gtg atc ggt atc cga	835
Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn Val Ile Gly Ile Arg	
230 235 240 245	
atc atg cct ctg ttc gca gtt aag gct gtt gct ttc ggc ctc atc gtc	883
Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala Phe Gly Leu Ile Val	

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250										255										260									
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Phe	Gly	Phe	Leu	Ala	Leu	Leu	Ala	Gly	Val	Thr	Thr	Ile	Asn	Ala	Ile														931
			265					270					275																
tgg	aat	ctt	gga	cgc	tac	aac	cct	tca	cag	gtg	tct	gct	ggt	tcc	cag														979
Trp	Asn	Leu	Gly	Pro	Tyr	Asn	Pro	Ser	Gln	Val	Ser	Ala	Gly	Ser	Gln														
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cct	gac	gtt	tac	atg	ctg	tgg	aca	gat	ggt	gct	gct	cgt	gtc	atg	cgc														1027
Pro	Asp	Val	Tyr	Met	Leu	Trp	Thr	Asp	Gly	Ala	Ala	Arg	Val	Met	Pro														
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gca	tgg	gag	ctc	tac	ctc	ggt	aac	tac	act	att	cca	gca	gtc	ttc	tgg														1075
Ala	Trp	Glu	Leu	Tyr	Leu	Gly	Asn	Tyr	Thr	Ile	Pro	Ala	Val	Phe	Trp														
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Val	Ala	Val	Met	Leu	Gly	Ile	Leu	Val	Val	Leu	Leu	Val	Thr	Tyr	Pro														
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Phe	Ile	Glu	Arg	Lys	Phe	Thr	Gly	Asp	Asp	Ala	His	His	Asn	Leu	Leu														
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cag	cgt	cct	cgc	gat	gtt	cca	gtc	cgc	acc	tca	ctc	ggt	gtc	atg	gcg														1219
Gln	Arg	Pro	Arg	Asp	Val	Pro	Val	Arg	Thr	Ser	Leu	Gly	Val	Met	Ala														
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ctt	gtc	ttc	tac	atc	ctg	ctt	acc	gtt	tct	ggt	ggt	aac	gat	gtt	tac														1267
Leu	Val	Phe	Tyr	Ile	Leu	Leu	Thr	Val	Ser	Gly	Gly	Asn	Asp	Val	Tyr														
			375				380					385																	
gca	atg	cag	ttc	cat	gtt	tca	ctg	aac	gcg	atg	acc	tgg	atc	ggt	cgt														1315
Ala	Met	Gln	Phe	His	Val	Ser	Leu	Asn	Ala	Met	Thr	Trp	Ile	Gly	Arg														
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atc	ggc	ctc	atc	gtt	gga	cca	gct	att	gca	tac	ttc	atc	act	tac	cga														1363
Ile	Gly	Leu	Ile	Val	Gly	Pro	Ala	Ile	Ala	Tyr	Phe	Ile	Thr	Tyr	Arg														
					410				415					420															
ctg	tgc	atc	ggc	ttg	cag	cgc	tct	gac	cgc	gag	gtc	ctg	gag	cac	ggc														1411
Leu	Cys	Ile	Gly	Leu	Gln	Arg	Ser	Asp	Arg	Glu	Val	Leu	Glu	His	Gly														
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atc	gag	acc	ggt	atc	atc	aag	cag	atg	cca	aat	ggt	gcc	ttc	att	gaa														1459
Ile	Glu	Thr	Gly	Ile	Ile	Lys	Gln	Met	Pro	Asn	Gly	Ala	Phe	Ile	Glu														
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gtt	cac	cag	cca	ctt	ggc	cca	gtt	gat	gac	cat	ggt	cac	cca	atc	cca														1507
Val	His	Gln	Pro	Leu	Gly	Pro	Val	Asp	Asp	His	Gly	His	Pro	Ile	Pro														
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ctg	cca	tac	gct	ggc	gct	gcg	gtt	cca	aag	cag	atg	aac	cag	ctt	ggt														1555
Leu	Pro	Tyr	Ala	Gly	Ala	Ala	Val	Pro	Lys	Gln	Met	Asn	Gln	Leu	Gly														
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tac	gct	gag	gtt	gaa	acc	cgc	ggt	gga	ttc	ttc	gga	cct	gat	cca	gaa														1603
Tyr	Ala	Glu	Val	Glu	Thr	Arg	Gly	Gly	Phe	Phe	Gly	Pro	Asp	Pro	Glu														
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 Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His Ala Asn His Ile Glu
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gaa gcg aac act ctt cgt gca ctc aac gag gca aac att gag cgt gac 1699
 Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala Asn Ile Glu Arg Asp
 520 525 530

aag aat gag ggc aag aac tagtttctag gacttcattct ctg 1740
 Lys Asn Glu Gly Lys Asn
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<212> PRT

<213> *Corynebacterium glutamicum*

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 20 25 30

Ser Phe Met Leu Gly Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu
 35 40 45

Leu Thr Gly Val Tyr Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys
 50 55 60

Val Ile Tyr Asp Gly Gly Tyr Leu Pro Leu Asn Gly Val Glu Met Ser
 65 70 75 80

Arg Ala Tyr Ala Thr Ala Leu Asp Ile Ser Phe Glu Val Arg Gly Gly
 85 90 95

Leu Phe Ile Arg Gln Met His His Trp Ala Ala Leu Leu Phe Val Val
 100 105 110

Ser Met Leu Val His Met Leu Arg Ile Phe Phe Thr Gly Ala Phe Arg
 115 120 125

Arg Pro Arg Glu Ala Asn Trp Ile Ile Gly Val Val Leu Ile Ile Leu
 130 135 140

Gly Met Ala Glu Gly Phe Met Gly Tyr Ser Leu Pro Asp Asp Leu Leu
 145 150 155 160

Ser Gly Val Gly Leu Arg Ile Met Ser Ala Ile Ile Val Gly Leu Pro
 165 170 175

Ile Ile Gly Thr Trp Met His Trp Leu Ile Phe Gly Gly Asp Phe Pro
 180 185 190

Ser Asp Leu Met Leu Asp Arg Phe Tyr Ile Ala His Val Leu Ile Ile
 195 200 205

Pro Ala Ile Leu Leu Gly Leu Ile Ala Ala His Leu Ala Leu Val Trp
 210 215 220

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Tyr Gln Lys His Thr Gln Phe Pro Gly Ala Gly Arg Thr Glu Asn Asn
 225 230 235 240
 Val Ile Gly Ile Arg Ile Met Pro Leu Phe Ala Val Lys Ala Val Ala
 245 250 255
 Phe Gly Leu Ile Val Phe Gly Phe Leu Ala Leu Leu Ala Gly Val Thr
 260 265 270
 Thr Ile Asn Ala Ile Trp Asn Leu Gly Pro Tyr Asn Pro Ser Gln Val
 275 280 285
 Ser Ala Gly Ser Gln Pro Asp Val Tyr Met Leu Trp Thr Asp Gly Ala
 290 295 300
 Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile
 305 310 315 320
 Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu
 325 330 335
 Leu Val Thr Tyr Pro Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala
 340 345 350
 His His Asn Leu Leu Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser
 355 360 365
 Leu Gly Val Met Ala Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly
 370 375 380
 Gly Asn Asp Val Tyr Ala Met Gln Phe His Val Ser Leu Asn Ala Met
 385 390 395 400
 Thr Trp Ile Gly Arg Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr
 405 410 415
 Phe Ile Thr Tyr Arg Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu
 420 425 430
 Val Leu Glu His Gly Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn
 435 440 445
 Gly Ala Phe Ile Glu Val His Gln Pro Leu Gly Pro Val Asp Asp His
 450 455 460
 Gly His Pro Ile Pro Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln
 465 470 475 480
 Met Asn Gln Leu Gly Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe
 485 490 495
 Gly Pro Asp Pro Glu Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His
 500 505 510
 Ala Asn His Ile Glu Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala
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 Asn Ile Glu Arg Asp Lys Asn Glu Gly Lys Asn
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<223> RXS02476
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				Met	Ser	Phe	Thr	Ala								
				1				5								
ttt	caa	aca	gcc	ctg	ctc	gtg	tgg	ttt	aga	gca	aat	gcc	cgc	gat	ctt	163
Phe	Gln	Thr	Ala	Leu	Leu	Val	Trp	Phe	Arg	Ala	Asn	Ala	Arg	Asp	Leu	
				10				15						20		
gcg	tgg	cgt	gat	ccc	aat	act	tca	gca	tgg	gga	att	ctc	ctt	tca	gag	211
Ala	Trp	Arg	Asp	Pro	Asn	Thr	Ser	Ala	Trp	Gly	Ile	Leu	Leu	Ser	Glu	
				25				30					35			
gtg	atg	agc	caa	caa	act	ccc	gtc	gcg	cga	gtc	gag	ccg	att	tgg	cgt	259
Val	Met	Ser	Gln	Gln	Thr	Pro	Val	Ala	Arg	Val	Glu	Pro	Ile	Trp	Arg	
				40			45					50				
gag	tgg	atg	gaa	aaa	tgg	ccc	act	ccg	gaa	gat	ttc	gcg	aat	gcg	agc	307
Glu	Trp	Met	Glu	Lys	Trp	Pro	Thr	Pro	Glu	Asp	Phe	Ala	Asn	Ala	Ser	
						60					65					
acc	gat	gag	att	ttg	cgg	tcg	tgg	ggc	aag	ttg	ggc	tat	cca	cgt	agg	355
70	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	Gly	Tyr	Pro	Arg	Arg	
					75					80					85	
gcg	ctg	agg	ttg	aag	gaa	tgt	gcg	gag	gtg	atc	gtc	gaa	aag	cat	gcc	403
Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	Val	Glu	Lys	His	Ala	
				90					95					100		
ggc	gag	gtg	ccg	gat	acg	gtg	gag	gcg	ctg	ctc	gcg	ttg	ccg	ggg	atc	451
Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Gly	Ile	
			105				110					115				
ggt	gat	tac	acg	gcg	cgc	gcg	gtc	gcg	gcg	ttt	cat	ttt	ggg	cag	cgc	499
Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	His	Phe	Gly	Gln	Arg	
			120				125					130				
gtg	ccg	gtg	gtc	gat	acg	aac	gtg	cgt	cgc	gtg	tac	cag	cgc	gcg	gta	547
Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	Tyr	Gln	Arg	Ala	Val	
	135					140					145					
gcc	gga	cgt	tac	ctt	gcg	ggg	cct	gcg	aaa	aag	caa	gag	ctt	atc	gac	595
Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	Gln	Glu	Leu	Ile	Asp	
150					155				160						165	
gtc	tcc	ctt	ctc	ctt	ccc	aac	act	cac	gcc	cca	gaa	ttc	tct	gcc	gca	643
Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	Glu	Phe	Ser	Ala	Ala	
					170				175					180		

cta atg gag ttg ggt gct ctt atc tgc acg gcc act tcc cca aag tgt	691
Ile Met Glu Leu Gly Ala Leu Ile Cys Thr Ala Thr Ser Pro Lys Cys	
185	190
gac acc tgc cca ctg ctt gac cag tgt caa tgg caa aaa ctt ggc tgt	739
Asp Thr Cys Pro Leu Leu Asp Gln Cys Gln Trp Gln Lys Leu Gly Cys	
200	205
ccc tcc ccg agt gaa gag gag ctg gct tca gcg aaa aag cgt gtg cag	787
Pro Ser Pro Ser Glu Glu Glu Leu Ala Ser Ala Lys Lys Arg Val Gln	
215	220
aaa ttt gtg gga acc gac cga caa gtc cgt gcc cta atc atg gac gta	835
Lys Phe Val Gly Thr Asp Arg Gln Val Arg Gly Leu Ile Met Asp Val	
230	235
ctg cgc aat gcc acc gca cct gtg cca cta tcc gcg att gat gtc gtg	883
Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser Ala Ile Asp Val Val	
250	255
tgg cct gac gat gcc caa cgc tcc cgg gcg ctg ttt tcg ctc att gag	931
Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu Phe Ser Leu Ile Glu	
265	270
gac gga ctc gcg gaa caa aat gag gcg ggt tat ttc cac ctg cca cgg	979
Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr Phe His Leu Pro Arg	
280	285
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Ile Leu Leu Ser Glu Val Met Ser Gln Gln Thr Pro Val Ala Arg Val	
35	40
Glu Pro Ile Trp Arg Glu Trp Met Glu Lys Trp Pro Thr Pro Glu Asp	
50	55
Phe Ala Asn Ala Ser Thr Asp Glu Ile Leu Arg Ser Trp Gly Lys Leu	
65	70
Gly Tyr Pro Arg Arg Ala Leu Arg Leu Lys Glu Cys Ala Glu Val Ile	
85	90
Val Glu Lys His Ala Gly Glu Val Pro Asp Thr Val Glu Ala Leu Leu	
100	105
Ala Leu Pro Gly Ile Gly Asp Tyr Thr Ala Arg Ala Val Ala Ala Phe	
115	120
	125

His Phe Gly Gln Arg Val Pro Val Val Asp Thr Asn Val Arg Arg Val
130 135 140

Tyr Gln Arg Ala Val Ala Gly Arg Tyr Leu Ala Gly Pro Ala Lys Lys
145 150 155 160

Gln Glu Leu Ile Asp Val Ser Leu Leu Leu Pro Asn Thr His Ala Pro
165 170 175

Glu Phe Ser Ala Ala Ile Met Glu Leu Gly Ala Leu Ile Cys Thr Ala
180 185 190

Thr Ser Pro Lys Cys Asp Thr Cys Pro Leu Leu Asp Gln Cys Gln Trp
195 200 205

Gln Lys Leu Gly Cys Pro Ser Pro Ser Glu Glu Glu Leu Ala Ser Ala
210 215 220

Lys Lys Arg Val Gln Lys Phe Val Gly Thr Asp Arg Gln Val Arg Gly
225 230 235 240

Leu Ile Met Asp Val Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser
245 250 255

Ala Ile Asp Val Val Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu
260 265 270

Phe Ser Leu Ile Glu Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr
275 280 285

Phe His Leu Pro Arg
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<210> 165

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(697)

<223> RXS02990

<400> 165

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Met Asp Ile Gln Ala
1 5

gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct 163
Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala
10 15 20

cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag 211
His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys
25 30 35

aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca 259

09602839 062200

Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Asn Gln Arg Ala
 40 45 50
 cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag 307
 Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu
 55 60 65
 gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg 355
 Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu
 70 75 80 85
 ctt gat gat gaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc 403
 Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val Arg Gln Arg Ala Ala
 90 95 100
 agg cga gga aaa tct tcg cgt gcg ctg gac cgc gaa ctg cag gaa aaa 451
 Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg Glu Leu Gln Glu Lys
 105 110 115
 ggc gtc gac aag caa acg cgt gct gcg gcg ctt gag caa atc gac cag 499
 Gly Val Asp Lys Gln Thr Arg Ala Ala Leu Glu Gln Ile Asp Gln
 120 125 130
 gcc gat gag cgg gac acg gcg cgg gcg gtg gcc gtg aaa aag gcg gcg 547
 Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala Val Lys Lys Ala Arg
 135 140 145
 tca gag acc aag att ccg cag gac cgc gcc gac tac gac aaa gcg ctt 595
 Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp Tyr Asp Lys Ala Leu
 150 155 160 165
 cgg cgc gtg gtt ggt gcg ctg gca cgg cgg gga ttt ccg gct gga atg 643
 Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly Phe Pro Ala Gly Met
 170 175 180
 tcc atg gac ctt gcg cgg gaa gcg cta gac gcg cga atc gag gat ttg 691
 Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala Arg Ile Glu Asp Leu
 185 190 195
 aaa aac taaaccocgg atgggaatca tcc 720
 Lys Asn

<210> 166

<211> 199

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 166

Met Asp Ile Gln Ala Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp
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 20 25 30

Glu Lys Glu Glu Lys Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu
 35 40 45

Leu Asn Gln Arg Ala Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys
 50 55 60

00602379.66230960

Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu
65 70 75 80

Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val
85 90 95

Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg
100 105 110

Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Leu
115 120 125

Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala
130 135 140

Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp
145 150 155 160

Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly
165 170 175

Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala
180 185 190

Arg Ile Glu Asp Leu Lys Asn
195

<210> 167

<211> 747

<212> DNA

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<222> {101}..(724)

<223> RXS03098

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ttccgtcacc accctcttcg agggcgaggc ctaaacaccc atg ccc acc acg gac 115
Met Pro Thr Thr Asp
1 5

gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163
Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala
10 15 20

cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211
Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu
25 30 35

ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259
Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser
40 45 50

ggc cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307
Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala
55 60 65

00602830 00602830

gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355
 Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val 85
 70 75 80

ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403
 Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser 100
 90 95

tgg tgg gac acc gtc gat tcc cta gca aaa cgg atc ggc gcc aaa cac 451
 Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His 115
 105 110

gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499
 Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp Glu Asp Phe Trp Val 130
 120 125

cgc cgc atc gcg atc atc cac caa ctg ggc cgc aag aaa aac acc gac 547
 Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp 145
 135 140

gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc ggc tcc agc gag 595
 Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu 165
 150 155 160

ttc ttc atc aac aaa gcg atc gcc tgg gca ctg cgg gat ttc gcc cgc 643
 Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg 180
 170 175

cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ett tcc 691
 His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser 195
 185 190

cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcatcatctg 744
 Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile 205
 200

agc 747

<210> 168
 <211> 208
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 168
 Met Pro Thr Thr Asp Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro 15
 1 5 10

Leu Ala Asp Pro Ala Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp 30
 20 25

Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys 45
 35 40

Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser 60
 50 55

Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp 80
 65 70 75

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His	Ile	Asn	Arg	Val	Gly	Ile	Thr	Asp	Leu	Gly	Phe	Ala	Lys	Ala	Leu
				85					90					95	
Val	Gln	Thr	Lys	Ser	Trp	Trp	Asp	Thr	Val	Asp	Ser	Leu	Ala	Lys	Pro
			100					105					110		
Ile	Gly	Ala	Lys	His	Asp	Asp	Asp	Leu	Met	Lys	Thr	Trp	Ala	Leu	Asp
		115					120					125			
Glu	Asp	Phe	Trp	Val	Arg	Arg	Ile	Ala	Ile	Ile	His	Gln	Leu	Gly	Arg
		130				135					140				
Lys	Lys	Asn	Thr	Asp	Ala	Ala	Leu	Leu	Ala	Trp	Ile	Ile	Glu	Gln	Asn
				150						155					160
Leu	Gly	Ser	Ser	Glu	Phe	Phe	Ile	Asn	Lys	Ala	Ile	Gly	Trp	Ala	Leu
				165					170					175	
Arg	Asp	Phe	Ala	Arg	His	Asp	Pro	Ser	Trp	Val	Arg	Ala	Phe	Val	Asp
			180					185					190		
Ala	Thr	Asp	Leu	Ser	Pro	Leu	Ser	Arg	Arg	Glu	Ala	Leu	Lys	Asn	Ile
		195					200				205				

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<210> 169
<211> 806
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(783)
<223> RXS03175
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Val	Arg	Ala	Ser	Glu	Lys	Asp	Thr	Ala	Thr	Ala	Leu	Gln	Pro	Ala	Leu			
1				5					10					15				
gat	aac	gga	tgg	cac	tac	att	ggt	gcc	cca	gca	gct	gcc	aag	gga	cgt		96	
Asp	Asn	Gly	Trp	His	Tyr	Ile	Gly	Ala	Pro	Ala	Ala	Ala	Lys	Gly	Arg			
			20					25					30					
gcc	ggt	gtc	ggc	att	tgt	tct	agg	cat	gaa	ctt	gaa	gat	gtg	aac	atc		144	
Ala	Gly	Val	Gly	Ile	Leu	Ser	Arg	His	Glu	Leu	Glu	Asp	Val	Asn	Ile			
			35				40					45						
ggt	ttt	gga	tct	ttc	ctt	gac	tcc	ggc	cgc	tac	att	gaa	gca	acc	atc		192	
Gly	Phe	Gly	Ser	Phe	Leu	Asp	Ser	Gly	Arg	Tyr	Ile	Glu	Ala	Thr	Ile			
						55					60							
aaa	gac	acc	acc	ctg	gat	gtg	cca	gta	acc	gtg	gca	tct	ctt	tac	ctc		240	
Lys	Asp	Thr	Thr	Leu	Asp	Val	Pro	Val	Thr	Val	Ala	Ser	Leu	Tyr	Leu			
65					70					75				80				
ccc	tca	ggt	tca	gcg	ggc	acc	gac	aag	cag	gat	gaa	aag	tac	cgc	ttc		288	
Pro	Ser	Gly	Ser	Ala	Gly	Thr	Asp	Lys	Gln	Asp	Glu	Lys	Tyr	Arg	Phe			

	85	90	95	
ctc gat gaa ttc gaa ggg ttc ctg gac cag cgc gct aaa gaa cgc tcc				336
Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser				
	100	105	110	
cac atg gtc atc ggt ggc gac tgg aac atc tgc cac cgc cgc gaa gac				384
His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp				
	115	120	125	
ctg aaa aac tgg aaa acc aac caa aag aaa tcc ggt ttc ctt ccc gac				432
Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp				
	130	135	140	
gaa cgc gca ttc atg gat tca gtc ttt ggc acc ttc cca gat gag gca				480
Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala				
	145	150	155	160
acc cag gtt gca ggg gcc ggc gac ttc ttc ggt gcc gtg gac tat gaa				528
Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu				
	165	170	175	
gga acg agg cgt cga gaa gca act acg gac cct cgc tgg ttc gac gtt				576
Gly Thr Arg Arg Glu Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val				
	180	185	190	
gca cgt cgc ctg caa cct gaa ggc gac ggc ccc tac act tgg tgg acc				624
Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr				
	195	200	205	
tac cgc gga aaa gcc ttc gac acc ggc gcc gga tgg cgc atc gac tac				672
Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr				
	210	215	220	
caa gca gca acc gca gcg atg ctc gaa cgc gca gaa cgc tcc tgg gta				720
Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val				
	225	230	235	240
gac aaa gcc gct gca tac gat ttg cgc tgg tca gat cac tca cca ctg				768
Asp Lys Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu				
	245	250	255	
aac gtg atc tac tcc taaaatgctg ctgacaattc tat				806
Asn Val Ile Tyr Ser				
	260			

<210> 170

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Val	Arg	Ala	Ser	Glu	Lys	Asp	Thr	Ala	Thr	Ala	Leu	Gln	Pro	Ala	Leu
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Asp	Asn	Gly	Trp	His	Tyr	Ile	Gly	Ala	Pro	Ala	Ala	Ala	Lys	Gly	Arg
	20							25					30		

Ala	Gly	Val	Gly	Ile	Leu	Ser	Arg	His	Glu	Leu	Glu	Asp	Val	Asn	Ile
		35						40				45			

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Gly	Phe	Gly	Ser	Phe	Leu	Asp	Ser	Gly	Arg	Tyr	Ile	Glu	Ala	Thr	Ile		
						55										60	
Lys	Asp	Thr	Thr	Leu	Asp	Val	Pro	Val	Thr	Val	Ala	Ser	Leu	Tyr	Leu		
						70										80	
Pro	Ser	Gly	Ser	Ala	Gly	Thr	Asp	Lys	Gln	Asp	Glu	Lys	Tyr	Arg	Phe		
						85										95	
Leu	Asp	Glu	Phe	Glu	Gly	Phe	Leu	Asp	Gln	Arg	Ala	Lys	Glu	Arg	Ser		
						100										110	
His	Met	Val	Ile	Gly	Gly	Asp	Trp	Asn	Ile	Cys	His	Arg	Arg	Glu	Asp		
						115										125	
Leu	Lys	Asn	Trp	Lys	Thr	Asn	Gln	Lys	Lys	Ser	Gly	Phe	Leu	Pro	Asp		
						130										140	
Glu	Arg	Ala	Phe	Met	Asp	Ser	Val	Phe	Gly	Thr	Phe	Pro	Asp	Glu	Ala		
						145										155	160
Thr	Gln	Val	Ala	Gly	Ala	Gly	Asp	Phe	Phe	Gly	Ala	Val	Asp	Tyr	Glu		
						165										175	
Gly	Thr	Arg	Arg	Arg	Glu	Ala	Thr	Thr	Asp	Pro	Ala	Trp	Phe	Asp	Val		
						180										190	
Ala	Arg	Arg	Leu	Gln	Pro	Glu	Gly	Asp	Gly	Pro	Tyr	Thr	Trp	Trp	Thr		
						195										205	
Tyr	Arg	Gly	Lys	Ala	Phe	Asp	Thr	Gly	Ala	Gly	Trp	Arg	Ile	Asp	Tyr		
						210										220	
Gln	Ala	Ala	Thr	Ala	Ala	Met	Leu	Glu	Arg	Ala	Glu	Arg	Ser	Trp	Val		
						225										235	240
Asp	Lys	Ala	Ala	Ala	Tyr	Asp	Leu	Arg	Trp	Ser	Asp	His	Ser	Pro	Leu		
						245										250	255
Asn	Val	Ile	Tyr	Ser													
						260											

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<210> 171
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum
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<220>
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<222> (101)..(1183)
<223> RXN03069
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<400> 171
actatgcgga aaagtggaag aggggtttgtg atatatgtca cgatcgagga attggggaga 60
gatcgagaag ttgcgctcgg ggaggtacag ggcacgcttc atg cac gag ggt agg 115
                               Met His Glu Gly Arg
                               1           5

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cga tac tct gcc ccg tat acc ttc ggt acc aag ggt gag gcg cag gag 163
 Arg Tyr Ser Ala Pro Tyr Thr Phe Gly Thr Lys Gly Glu Ala Gln Glu
 10 15 20

ttc ttg gcc tct gaa cgc acg gcc atc atc aat ggc aca tgg gat 211
 Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn Gly Thr Trp Met Asp
 25 30 35

ttt gag atg cgg gag agg ttc gag cag gca cag cgc gaa gcc gaa gaa 259
 Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln Arg Glu Ala Glu Glu
 40 45 50

cgc atg atg gag acc ttc ttc agt tat gca tgc agg tgg ata gaa acc 307
 Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser Arg Trp Ile Glu Thr
 55 60 65

cgg aca aat gcc Caa gga aag aaa ctc agc Caa ggg gtg aaa gat gat 355
 Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln Gly Val Lys Asp Asp
 70 75 80 85

tac ttt cgt tat ata aaa tca gat cga cta agt tat tgg gct gat tat 403
 Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser Tyr Trp Ala Asp Tyr
 90 95 100

gcg ctc tgt gaa atc act gtc gct gat gtc cgt gag tgg tat agc gat 451
 Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg Glu Trp Tyr Ser Asp
 105 110 115

act att cag gac ggt aaa ttg acc tca atg gcg cgg agt tac agc atg 499
 Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala Arg Ser Tyr Ser Met
 120 125 130

atg aag tct gtc atg gag act gca gtg gag gat ggc att atc ccg atg 547
 Met Lys Ser Val Met Glu Thr Ala Val Glu Asp Gly Ile Ile Pro Met
 135 140 145

aat ccg tgc aaa gtc cgt ggc ggg ggt aat acg aaa aca ggc aaa aag 595
 Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr Lys Thr Gly Lys Lys
 150 155 160 165

gtt gat gtc cca acc gat gcc gag ctt gag gcg atc att ggt gca ctg 643
 Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala Ile Ile Gly Ala Leu
 170 175 180

ccg agt aag tac ttt tgt ttg gct att gtt gct gcc gct ggt gca ctt 691
 Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala Ala Ala Gly Ala Leu
 185 190 195

cga ttc ggt gaa atc gtt gcg ctg cgt acc act gat gtg gat gtt tat 739
 Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr Asp Val Asp Val Tyr
 200 205 210

ttt gat cgc agc gga ttt gta gat tgt gtt cga ata agg att tct ccg 787
 Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg Ile Arg Ile Ser Arg
 215 220 225

agc att agg cac acg aga tac cat ggc cga gtt gaa ggt ccg cct aaa 835
 Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys
 230 235 240 245

act gaa gct ggt gtt cgt agc ctc tat atc tat ggc aaa gat gca gca 883

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Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr Gly Lys Asp Ala Ala
 250 255 260
 gaa att gcc aag cat gtg gac acg att gat gtg ggt ttg cga cta tgg 931
 Glu Ile Ala Lys His Val Asp Thr Ile Asp Val Gly Leu Arg Leu Trp
 265 270 275
 agc tcg atg aga gat cct gat gaa ccc atg ccg tat cac acc ttt aag 979
 Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro Tyr His Thr Phe Lys
 280 285 290
 cac aac tgg gat agg gcg cgg gaa agt gtc cac agt aaa gcg acc gtt 1027
 His Asn Trp Asp Arg Ala Arg Glu Ser Val His Ser Lys Ala Thr Val
 295 300 305
 cac tcg atg agg cat tat tcg ggt acg aag tat gca cag gtt ggg gcg 1075
 His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr Ala Gln Val Gly Ala
 310 315 320 325
 aca ctc aag gag gtg atg gcg cgg ctg ggg cac tca aca cct agt gca 1123
 Thr Leu Lys Glu Val Met Ala Arg Leu Gly His Ser Thr Pro Ser Ala
 330 335 340
 gca ctg cgt tat cag cac tca gcc gag cgt gat gaa gag cta gca aag 1171
 Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp Glu Glu Leu Ala Lys
 345 350 355
 cgc atg gcg cgc taaacactcg gcagtgagtt tca 1206
 Arg Met Ala Arg
 360
 <210> 172
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 172
 Met His Glu Gly Arg Arg Tyr Ser Ala Pro Tyr Thr Phe Gly Thr Lys
 1 5 10 15
 Gly Glu Ala Gln Glu Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn
 20 25 30
 Gly Thr Trp Met Asp Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln
 35 40 45
 Arg Glu Ala Glu Glu Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser
 50 55 60
 Arg Trp Ile Glu Thr Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln
 65 70 75 80
 Gly Val Lys Asp Asp Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser
 85 90 95
 Tyr Trp Ala Asp Tyr Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg
 100 105 110
 Glu Trp Tyr Ser Asp Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala
 115 120 125

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Arg Ser Tyr Ser Met Met Lys Ser Val Met Glu Thr Ala Val Glu Asp
 130 135 140
 Gly Ile Ile Pro Met Asn Pro Cys Lys Val Arg Gly Gly Asn Thr
 145 150 155 160
 Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala
 165 170 175
 Ile Ile Gly Ala Leu Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala
 180 185 190
 Ala Ala Gly Ala Leu Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr
 195 200 205
 Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg
 210 215 220
 Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val
 225 230 235 240
 Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr
 245 250 255
 Gly Lys Asp Ala Ala Glu Ile Ala Lys His Val Asp Thr Ile Asp Val
 260 265 270
 Gly Leu Arg Leu Trp Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro
 275 280 285
 Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His
 290 295 300
 Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr
 305 310 315 320
 Ala Gln Val Gly Ala Thr Leu Lys Glu Val Met Ala Arg Leu Gly His
 325 330 335
 Ser Thr Pro Ser Ala Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp
 340 345 350
 Glu Glu Leu Ala Lys Arg Met Ala Arg
 355 360

<210> 173
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1183)
 <223> FRXA02890

<400> 173
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 gatcgaaaag ttgcgcctcgc ggaggtacag ggcacgcttc atg cac gag ggt agg 115

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	Met	His	Glu	Gly	Arg	
	1				5	
cga tac tct gcc cgc cat acc ttc ggt acc aag ggt gag gcg cag gag						163
Arg Tyr Ser Ala Pro His Thr Phe Gly Thr Lys Gly Glu Ala Gln Glu						
	10				20	
ttc ttg gcc tct gaa cgc acg gcc atc atc aat gcc aca tgg atg gat						211
Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn Gly Thr Trp Met Asp						
	25				35	
ttt gag atg cgc gag agg ttc gag cag gca cag cgc gaa gcc gaa gaa						259
Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln Arg Glu Ala Glu Glu						
	40				50	
cgc atg atg gag acc ttc ttc agt tat gca tcg agg tgg ata gaa acc						307
Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser Arg Trp Ile Glu Thr						
	55				65	
cgc aca aat gcc caa gga aag aaa ctc agc caa ggg gtg aaa gat gat						355
Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln Gly Val Lys Asp Asp						
	70				80	
tac ttt cgt tat ata aaa tca gat cga cta agt tat tgg gct gat tat						403
Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser Tyr Trp Ala Asp Tyr						
	90				95	
gcg ctc tgt gaa atc act gtc gct gat gtc cgt gag tgg tat agc gat						451
Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg Glu Trp Tyr Ser Asp						
	105				115	
act att cag gac ggt aaa ttg acc tca atg gcg cgc agt tac agc atg						499
Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala Arg Ser Tyr Ser Met						
	120				130	
atg aag tct gtc atg gag act gca gtg gag gat gcc att atc ccg atg						547
Met Lys Ser Val Met Glu Thr Ala Val Glu Asp Gly Ile Ile Pro Met						
	135				145	
aat cgc tgc aaa gtc cgt ggc ggg ggt aat acg aaa aca gcc aaa aag						595
Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr Lys Thr Gly Lys Lys						
	150				160	
gtt gat gtc cca acc gat gcc gag ctt gag gcg atc att ggt gca ctg						643
Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala Ile Ile Gly Ala Leu						
	170				175	
ccg agt aag tac ttt tgt ttg gct att gtt gct gcc gct ggt gca ctt						691
Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala Ala Ala Gly Ala Leu						
	185				195	
cga ttc ggt gaa atc gtt gcg ctg cgt acc act gat gtg gat gtt tat						739
Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr Asp Val Asp Val Tyr						
	200				210	
ttt gat cgc agc gga ttt gta gat tgt gtt cga ata agg att tct cgc						787
Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg Ile Arg Ile Ser Arg						
	215				225	
agc att agg cac acg aga tac cat ggc cga gtt gaa ggt ccg cct aaa						835
Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys						

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230	235	240	245	
act gaa gct ggt gtt cgt agc ctc tat atc tat ggc aaa gat gca gca				883
Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr Gly Lys Asp Ala Ala	250	255	260	
gaa att gcc aag cat gtg gac acg att gat gtg ggt ttg cga cta tgg				931
Glu Ile Ala Lys His Val Asp Thr Ile Asp Val Gly Leu Arg Leu Trp	265	270	275	
agc tcg atg aga gat cct gat gaa ccc atg ccg tat cac acc ttt aag				979
Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro Tyr His Thr Phe Lys	280	285	290	
cac aac tgg gat agg gcg cgg gaa agt gtc cac agt aaa gcg acc gtt				1027
His Asn Trp Asp Arg Ala Arg Glu Ser Val His Ser Lys Ala Thr Val	295	300	305	
cac tcg atg agg cat tat tcg ggt acg aag tat gca cag gtt ggg gcg				1075
His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr Ala Gln Val Gly Ala	310	315	320	325
aca ctc aag gag gtg atg gcg cgg ctg ggg cac tca aca cct agt gca				1123
Thr Leu Lys Glu Val Met Ala Arg Leu Gly His Ser Thr Pro Ser Ala	330	335	340	
gca ctg cgt tat cag cac tca gcc gag cgt gat gaa gag cta gca aag				1171
Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp Glu Glu Leu Ala Lys	345	350	355	
cgc atg gcg cgc taaacactcg gcagtgagtt tca				1206
Arg Met Ala Arg	360			
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<400> 174				
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Gly Glu Ala Gln Glu Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn	20	25	30	
Gly Thr Trp Met Asp Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln	35	40	45	
Arg Glu Ala Glu Glu Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser	50	55	60	
Arg Trp Ile Glu Thr Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln	65	70	75	80
Gly Val Lys Asp Asp Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser	85	90	95	
Tyr Trp Ala Asp Tyr Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg	100	105	110	

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Glu Trp Tyr Ser Asp Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala
 115 120
 Arg Ser Tyr Ser Met Met Lys Ser Val Met Glu Thr Ala Val Glu Asp
 130 135 140
 Gly Ile Ile Pro Met Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr
 145 150 155 160
 Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala
 165 170 175
 Ile Ile Gly Ala Leu Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala
 180 185 190
 Ala Ala Gly Ala Leu Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr
 195 200 205
 Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg
 210 215 220
 Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val
 225 230 235 240
 Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr
 245 250 255
 Gly Lys Asp Ala Ala Glu Ile Ala Lys His Val Asp Thr Ile Asp Val
 260 265 270
 Gly Leu Arg Leu Trp Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro
 275 280 285
 Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His
 290 295 300
 Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr
 305 310 315 320
 Ala Gln Val Gly Ala Thr Leu Lys Glu Val Met Ala Arg Leu Gly His
 325 330 335
 Ser Thr Pro Ser Ala Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp
 340 345 350
 Glu Glu Leu Ala Lys Arg Met Ala Arg
 355 360

<210> 175

<211> 1035

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{1012}

<223> RXA01601

<400> 175

09602039.062000

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gtcgaaaagc gcacggcatt gttcctgaca tgaaaaaact atg aag gct cgc gtt 115
Met Lys Ala Arg Val
1 5

tta gcg aaa aca tgg ctg aca cat ttg gcc gtg gag cgt ggc ttg tgc 163
Leu Ala Lys Thr Trp Leu Thr His Leu Ala Val Glu Arg Gly Leu Ser
10 15 20

gca aat acg ctg agt aat tat cgg cgc gat gtg gaa cgc tat tgc gac 211
Ala Asn Thr Leu Ser Asn Tyr Arg Arg Asp Val Glu Arg Tyr Cys Asp
25 30 35

tgg ctc gag gca gct ggg ctg gat gat att cgt gat atc acc acc gcg 259
Trp Leu Glu Ala Ala Gly Leu Asp Ile Arg Asp Ile Thr Thr Ala
40 45 50

cat gtg gaa agt tat gtc aaa gac ctg cgc cgc ggg att gat gga caa 307
His Val Glu Ser Tyr Val Lys Asp Leu Arg Arg Gly Ile Asp Gly Gln
55 60 65

caa gcg ttg tct gcg tcc tgg gca ggt cgc gcg ctc atc gtc gcg cgc 355
Gln Ala Leu Ser Ala Ser Ser Ala Gly Arg Ala Leu Ile Val Ala Arg
70 75 80 85

ggg ttg cac aag ttt gca ttg atg gag ggc gag gtg gct gcg gac gtt 403
Gly Leu His Lys Phe Ala Leu Met Glu Gly Glu Val Ala Ala Asp Val
90 95 100

gcg gct gat gtg tgg cca ccg gcc atg ggc cgg cat tta cct gac acg 451
Ala Ala Asp Val Ser Pro Pro Ala Met Gly Arg His Leu Pro Asp Thr
105 110 115

ctc agc atc aac gag gta gcc ctg ctt atc gac gcg atc cca cat tca 499
Leu Ser Ile Asn Glu Val Ala Leu Leu Ile Asp Ala Ile Pro His Ser
120 125 130

gat atc gcc act ccc gtt gat ctc cgt gac cga gcg ctg gtg gaa tta 547
Asp Ile Ala Thr Pro Val Asp Leu Arg Asp Arg Ala Leu Val Glu Leu
135 140 145

ctt tat gga act ggc gcg cgt atc tct gag gcg att ggg ctg gca gtt 595
Leu Tyr Gly Thr Gly Ala Arg Ile Ser Glu Ala Ile Gly Leu Ala Val
150 155 160 165

gat gat gtg tgg gaa atg cct gaa gtt ctt cgc atc acg ggc aaa ggt 643
Asp Asp Val Ser Glu Met Pro Glu Val Leu Arg Ile Thr Gly Lys Gly
170 175 180

tcc aaa caa cgg atc gtg cct ttt ggt tgg atg gca caa caa gcg gtc 691
Ser Lys Gln Arg Ile Val Pro Phe Gly Ser Met Ala Gln Gln Ala Val
185 190 195

cgg gaa tat ttg gtc aga gcc aga ccc gcg ttg agt aag ggg aaa agc 739
Arg Glu Tyr Leu Val Arg Ala Arg Pro Ala Leu Ser Lys Gly Lys Ser
200 205 210

cat gcg ctt ttt ctc aac caa cgc ggc ggt ccg cta tct cgg caa tct 787
His Ala Leu Phe Leu Asn Gln Arg Gly Gly Pro Leu Ser Arg Gln Ser
215 220 225

00502239, 062300

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gcg tgg gca gtg ctg aag aaa acg gtt gag cgc gca ggt tta gat aaa      835
Ala Trp Ala Val Leu Lys Lys Thr Val Glu Arg Ala Gly Leu Asp Lys
230                235                240                245

gat att tct ccc cac acc ctg cgg cac agc ttt gcc acc cat ctc ctc      883
Asp Ile Ser Pro His Thr Leu Arg His Ser Phe Ala Thr His Leu Leu
                250                255                260

gaa ggt ggc gcc gat gtc cgt gtg gtg cag gaa ctc ctg ggt cat tct      931
Glu Gly Gly Ala Asp Val Arg Val Val Gln Glu Leu Gly His Ser
                265                270                275

tct gtg acg acc act cag att tac acg cac atc aca gcc gat agc ttg      979
Ser Val Thr Thr Thr Gln Ile Tyr Thr His Ile Thr Ala Asp Ser Leu
                280                285                290

cgg gaa gtg tgg cgc ggg gct cat cct cgt gcg tgaagacct tgcgaattct 1032
Arg Glu Val Trp Arg Gly Ala His Pro Arg Ala
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taa                                                    1035

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<212> PRT
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<400> 176
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Glu Arg Tyr Cys Asp Trp Leu Glu Ala Ala Gly Leu Asp Asp Ile Arg
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Asp Ile Thr Thr Ala His Val Glu Ser Tyr Val Lys Asp Leu Arg Arg
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Gly Ile Asp Gly Gln Gln Ala Leu Ser Ala Ser Ser Ala Gly Arg Ala
 65                70                75                80

Leu Ile Val Ala Arg Gly Leu His Lys Phe Ala Leu Met Glu Gly Glu
 85                90                95

Val Ala Ala Asp Val Ala Ala Asp Val Ser Pro Pro Ala Met Gly Arg
100                105                110

His Leu Pro Asp Thr Leu Ser Ile Asn Glu Val Ala Leu Leu Ile Asp
115                120                125

Ala Ile Pro His Ser Asp Ile Ala Thr Pro Val Asp Leu Arg Asp Arg
130                135                140

Ala Leu Val Glu Leu Leu Tyr Gly Thr Gly Ala Arg Ile Ser Glu Ala
145                150                155                160

Ile Gly Leu Ala Val Asp Asp Val Ser Glu Met Pro Glu Val Leu Arg

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165 170 175

Ile Thr Gly Lys Gly Ser Lys Gln Arg Ile Val Pro Phe Gly Ser Met
180 185 190

Ala Gln Gln Ala Val Arg Glu Tyr Leu Val Arg Ala Arg Pro Ala Leu
195 200 205

Ser Lys Gly Lys Ser His Ala Leu Phe Leu Asn Gln Arg Gly Gly Pro
210 215 220

Leu Ser Arg Gln Ser Ala Trp Ala Val Leu Lys Lys Thr Val Glu Arg
225 230 235 240

Ala Gly Leu Asp Lys Asp Ile Ser Pro His Thr Leu Arg His Ser Phe
245 250 255

Ala Thr His Leu Leu Glu Gly Gly Ala Asp Val Arg Val Val Gln Glu
260 265 270

Leu Leu Gly His Ser Ser Val Thr Thr Thr Gln Ile Tyr Thr His Ile
275 280 285

Thr Ala Asp Ser Leu Arg Glu Val Trp Arg Gly Ala His Pro Arg Ala
290 295 300

<210> 177
<211> 339
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(316)
<223> RXA01228

<400> 177
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gcagaagatc attgaccaaa tcaccaccaa ggggtgcgagc gtg cac ttc atc aag 115
Val His Phe Ile Lys
1 5

gaa aac ctg atc ttc tcg gcg gaa tcc aat gct ttg cgg gcc cag ctc 163
Glu Asn Leu Ile Phe Ser Ala Glu Ser Asn Ala Leu Arg Ala Gln Leu
10 15 20

atg ctg agc att ctc ggc tcc ttc gct gag ttc gaa cgc tcc atc atc 211
Met Leu Ser Ile Leu Gly Ser Phe Ala Glu Phe Glu Arg Ser Ile Ile
25 30 35

cgg gag cgc caa gcc gag ggg atc gcc tgg cga aaa agg ccg gca agt 259
Arg Glu Arg Gln Ala Glu Gly Ile Ala Trp Arg Lys Arg Pro Ala Ser
40 45 50

aca agg gcc gca aac gcg ccc tca ccc cgg acg acg tcg aga aag ccc 307
Thr Arg Ala Ala Asn Ala Pro Ser Pro Arg Thr Thr Ser Arg Lys Pro

00002339.062300

55

60

65

gga aac ggg tagaagctgg tgagtccaag gtg
 Gly Asn Gly
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339

<210> 178

<211> 72

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

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Leu Arg Ala Gln Leu Met Leu Ser Ile Leu Gly Ser Phe Ala Glu Phe
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Glu Arg Ser Ile Ile Arg Glu Arg Gln Ala Glu Gly Ile Ala Trp Arg
 35 40 45

Lys Arg Pro Ala Ser Thr Arg Ala Ala Asn Ala Pro Ser Pro Arg Thr
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Thr Ser Arg Lys Pro Gly Asn Gly
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<210> 179

<211> 1431

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1408)

<223> RXN03130

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ggtatctaag ctaaccaaacc accaacaataa ggctctaccc atg aag tct acc ggc 115
 Met Lys Ser Thr Gly
 1 5

aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc 163
 Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr
 10 15 20

atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211
 Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp
 25 30 35

gca ctc gac tac acc tcc acc tgc cca gaa tgc tcc caa cct ggg gtg 259
 Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val
 40 45 50

ttt cgt cat cac acc cac cgg atg ctc att gat tta ccc atc gtc ggg 307
 Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly
 55 60 65

00602639 062300

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Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn	
70 75 80	
ccc aca tgt aag caa aag tat ttc caa gca gaa cta agc tgc gct gac	403
Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp	
90 95 100	
cac ggt aaa aag gtc acc cac cgg gtc acc cgc tgg att tta caa cgc	451
His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg	
105 110 115	
ctt gct att gac cgg atg agt gtt cac gca acc cgc aaa gca ctt ggg	499
Leu Ala Ile Asp Arg Met Ser Val His Ala Thr Ala Lys Ala Leu Gly	
120 125 130	
cta ggg tgg gat tta acc tgc caa cta gcc ctc gat atg tgc cgt gag	547
Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu Asp Met Cys Arg Glu	
135 140 145	
ctg gtc tat aac gat cct cac cat ctt gat gga gtg tat gtc att ggg	595
Leu Val Tyr Asn Asp Pro His His Leu Asp Gly Val Tyr Val Ile Gly	
150 155 160 165	
gtg gat gag cat aag tgg tca cat aat agg gct aag cat ggt gat ggg	643
Val Asp Glu His Lys Trp Ser His Asn Arg Ala Lys His Gly Asp Gly	
170 175 180	
ttt gtc acc gtg att gtc gat atg acc ggg cat cgg tat gac tca cgg	691
Phe Val Thr Val Ile Val Asp Met Thr Gly His Arg Tyr Asp Ser Arg	
185 190 195	
tgt cct gcc cgg tta tta gat gtc gtc cca ggt cgt agt gct gat gct	739
Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly Arg Ser Ala Asp Ala	
200 205 210	
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Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln Phe Arg Asn Gln Ile	
215 220 225	
cgg atc gtg tcc atg gat gga ttc caa ggc tac gcc aca gca agt aaa	835
Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr Ala Thr Ala Ser Lys	
230 235 240 245	
gaa ctc att cct tct gct cgt cgc gtg atg gat cca ttc cat gtt gtg	883
Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp Pro Phe His Val Val	
250 255 260	
cgg ctt gct ggt gac aag ctc acc gcc tgc cgg caa cgc ctc cag cgg	931
Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg Gln Arg Leu Gln Arg	
265 270 275	
gag aaa tac cag cgt cgt ggt tta agc cag gat ccg ttg tat aaa aac	979
Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn	
280 285 290	
cgg aag acc ttg ttg acc acg cac aag tgg ttg agt cct cgt cag caa	1027
Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu Ser Pro Arg Gln Gln	
295 300 305	

00602829 062300

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 Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Asp Tyr Gly Ala Leu
 310 315 320 325

aag ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg 1123
 Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met
 330 335 340

ggt aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag 1171
 Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln
 345 350 355

ctt cgg gtg ttg aag ggg cgg aat aag gaa ctc gcg cag ttg ggt cgt 1219
 Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Tyr Phe Gln Gly Arg
 360 365 370

agt ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt 1267
 Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly
 375 380 385

gtc tcc aac ggt cgg gtc gaa gcg atc aac gga cgg ttg gag cat ttg 1315
 Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu
 390 395 400 405

cgt ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg 1363
 Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg
 410 415 420

tgc ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc 1408
 Cys Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
 425 430 435

taaaacagga agagcccgta aac 1431

<210> 180
 <211> 436
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 180
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 20 25 30

Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys
 35 40 45

Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp
 50 55 60

Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg
 65 70 75 80

Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu
 85 90 95

Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg
 100 105 110

00602039 0603300

Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr
 115 120 125
 Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu
 130 135 140
 Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly
 145 150 155 160
 Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala
 165 170 175
 Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His
 180 185 190
 Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly
 195 200 205
 Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln
 210 215 220
 Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr
 225 230 235 240
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp
 245 250 255
 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg
 260 265 270
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp
 275 280 285
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu
 290 295 300
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys
 305 310 315 320
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile
 325 330 335
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg
 340 345 350
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu
 355 360 365
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala
 370 375 380
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly
 385 390 395 400
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn
 405 410 415
 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys
 420 425 430

002290-062300

Ile Asn Ala Leu
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<210> 181
<211> 489
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(466)
<223> RXN01969

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Leu Trp Ala Tyr Asp
1 5
aaa gcc tac ggg gcg tta aag ctt gcg tgg ctt gcg tat cag gcg att 163
Lys Ala Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile
10 15 20
att gat tgt tat cag atg ggt aat aag cgt gaa gcg aag aag aaa atg 211
Ile Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met
25 30 35
cgg acc att att gat cag ctt cgg gtg ttg aag ggg cgg aat aag gaa 259
Arg Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu
40 45 50
ctc gcg cag ttg ggt cgt agt ttg ttt aaa cga ctt ggt gat gtg ttg 307
Leu Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu
55 60 65
gcg tat ttc gat gtt ggt gtc tcc aac ggt cgg gtc gaa gcg atc aac 355
Ala Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn
70 75 80 85
gga cgg ttg gag cat ttg cgt ggg att gct cta ggt ttc cgt aat ttg 403
Gly Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu
90 95 100
aac cac tac att ctg cgg tgc ctt atc cat tca ggg cag ttg gtc cat 451
Asn His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His
105 110 115
aag atc aat gca ctc taaaacagga agagccactt aag 489
Lys Ile Asn Ala Leu
120

<210> 182
<211> 122
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 182
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Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu Arg Val Leu Lys	35	40	45
Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg	50	55	60
Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val Ser Asn Gly Pro	65	70	75
Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Ala Leu	85	90	95
Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys Leu Ile His Ser	100	105	110
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<210> 183

<211> 1431

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> {101}..(1408)

<223> FRXA00263

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Met Lys Ser Thr Gly
1 5

aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc 163

Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr
10 15 20

atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211

Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp
25 30 35

gca ctc gac tac acc tcc acc tgc cca gaa tgc tcc caa cct ggg gtg 259

Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val
40 45 50

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Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly
55 60 65

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Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn
70 75 80 85

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His	Gly	Lys	Lys 105	Val	Thr	His	Arg	Val	Thr	Arg	Trp	Ile	Leu	Gln	Arg	
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Leu	Ala	Ile	Asp	Arg	Met	Ser	Val	His	Ala	Thr	Ala	Lys 130	Ala	Leu	Gly	
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Leu	Val	Tyr	Asn	Asp	Pro	His	His	Leu	Asp	Gly 160	Val	Tyr	Val	Ile	Gly 165	
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Val	Asp	Glu	His	Lys 170	Trp	Ser	His	Asn	Arg	Ala	Lys	His	Gly	Asp	Gly 180	
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Phe	Val	Thr	Val	Ile	Val	Asp	Met	Thr	Gly 190	His	Arg	Tyr	Asp	Ser	Arg	
tgt	cct	gcc	cgg	tta	tta	gat	gtc	gtc	cca	ggt	cgt	agt	gct	gat	gct	739
Cys	Pro	Ala	Arg	Leu	Leu	Asp	Val	Val	Pro	Gly	Arg	Ser	Ala	Asp	Ala	
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Leu	Arg	Ser	Trp	Leu	Gly	Ser	Arg	Gly	Glu	Gln	Phe	Arg	Asn	Gln	Ile	
cgg	atc	gtg	tcc	atg	gat	gga	ttc	caa	ggc	tac	gcc	aca	gca	agt	aaa	835
Arg	Ile	Val	Ser	Met	Asp	Gly	Phe	Gln	Gly	Tyr	Ala	Thr	Ala	Ser	Lys 245	
gaa	ctc	att	cct	tct	gct	cgt	cgc	gtg	atg	gat	cca	ttc	cat	gtt	gtg	883
Glu	Leu	Ile	Pro	Ser	Ala	Arg	Arg	Val	Met	Asp	Pro	Phe	His	Val	Val 260	
cgg	ctt	gct	ggt	gac	aag	ctc	acc	gcc	tgc	cgg	caa	cgc	ctc	cag	cgg	931
Arg	Leu	Ala	Gly	Asp	Lys	Leu	Thr	Ala	Cys	Arg	Gln	Arg	Leu	Gln	Arg	
gag	aaa	tac	cag	cgt	cgt	ggt	tta	agc	cag	gat	cgg	ttg	tat	aaa	aac	979
Glu	Lys	Tyr	Gln	Arg	Arg	Gly	Leu	Ser	Gln	Asp	Pro	Leu	Tyr	Lys	Asn	
cgg	aag	acc	ttg	ttg	acc	acg	cac	aag	tgg	ttg	agt	cct	cgt	cag	caa	1027
Arg	Lys	Thr	Leu	Leu	Thr	Thr	His	Lys	Trp	Leu	Ser	Pro	Arg	Gln	Gln	
gaa	agc	ttg	gag	cag	ttg	tgg	gcg	tat	gac	aaa	gac	tac	ggg	gcg	tta	1075
Glu	Ser	Leu	Glu	Gln	Leu	Trp	Ala	Tyr	Asp	Lys	Asp	Tyr	Gly	Ala	Leu 325	
aag	ctt	gcg	tgg	ctt	gcg	tat	cag	gcg	att	att	gat	tgt	tat	cag	atg	1123

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 ggt aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag 1171
 Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln
 345 350 355
 ctt cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt 1219
 Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg
 360 365 370
 agt ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt 1267
 Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly
 375 380 385
 gtc tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg 1315
 Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu
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 cgt ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg 1363
 Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg
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 Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp
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 65 70 75 80
 Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu
 85 90 95
 Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg
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 Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr
 115 120 125
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130 135 140
 Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly
 145 150 155
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 165 170 175
 Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His
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 Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly
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 Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln
 210 215 220
 Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr
 225 230 235 240
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp
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 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg
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 275 280 285
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu
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 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys
 305 310 315 320
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile
 325 330 335
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg
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 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu
 355 360 365
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala
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 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly
 385 390 395 400
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn
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 Ile Asn Ala Leu
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 Met Thr Thr Pro His
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 Ser His Arg Ala Pro Arg Leu Ala Ser Thr Val Ile Ile Ala Arg Glu
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 Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln Arg Gln Ser
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 act atg gct tat gca gca aac gct gtt gtt ttc cca gcc gcc ggt gtt 259
 Thr Met Ala Tyr Ala Ala Asn Ala Val Val Phe Pro Gly Gly Gly Val
 40 45 50
 gag gac agc gat tat ccc ttt atg ctc ccc cac cgc gat cag cac atg 307
 Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp Gln His Met
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 Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His Met Asp Ser
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 Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu Val Trp Glu
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 Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg Tyr Asp
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 135 140 145
 ctg cag cac cag cat caa acc acc gag gcc acc cat tct tat tgg gca 595
 Leu Gln His Gln His Gln Thr Thr Glu Ala Thr His Ser Tyr Trp Ala
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 act gca gaa gaa ctg ctc act caa tgg tca aca ggt cat ctc aac ctg 643
 Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His Leu Asn Leu
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 185 190 195
 cta aac cag ctg tat agc ttt gcc cag cgt acc cat aat ccg cag cac 739
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 act cca ccc aca gtg ttt gct aac tgg act gca ccg gct gat gag gcc 787
 Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala Asp Glu Ala
 215 220 225
 gcc atg cag cac tat ggg ttc cct gat ccc gat cgc tac ttt gac cat 835
 Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr Phe Asp His
 230 235 240 245
 gcc act atc gca gga aaa cac cac aca ctc atc aca aga aag 877
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 Pro Gly Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His
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 Arg Asp Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg
 65 70 75 80
 Leu His Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg
 85 90 95
 Arg Glu Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His
 100 105 110
 Glu Leu Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe
 115 120 125
 Arg Arg Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp
 130 135 140
 Ser Thr Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr
 145 150 155 160
 His Ser Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr
 165 170 175

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Gly His Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu
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Asn His Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr
195 200 205

His Asn Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala
210 215 220

Pro Ala Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp
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Ala Tyr Phe Asp His Ala Thr Ile Ala Gly Lys His His Thr Leu Ile
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Thr Arg Lys

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Ala Arg Glu Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln																	
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144																	
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Arg Gln Ser Thr Met Ala Tyr Ala Ala Asn Ala Val Val Phe Pro Gly																	
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192																	
ggc ggt gtt gag gac agc gat tat ccc ttt atg ctc ccc cac cgc gat	192																
Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp																	
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Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His																	
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Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu																	
85 90 95																	
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Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His Glu Leu																	
100 105 110																	
384																	
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Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg																	
115 120 125																	

THE 2000

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aac gca gct ctg cag cac cag cat caa acc acc gag gcc acc cat tct 480
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 Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His
 165 170 175

ctc aac ctg ttg tta cca acg tgg tgg cat atc aac cag ctc aat cac 576
 Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu Asn His
 180 185 190

ctc cac acg cta aac cag ctg tat agc ttt gcc cag cgt acc cat aat 624
 Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr His Asn
 195 200 205

ccg cag cac act cca ccc aca gtg ttt gct aac tgg act gca ccg gct 672
 Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala
 210 215 220

gat gag gcc gcc atg cag cac tat ggg ttc cct gat ccc gat gcg tac 720
 Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr
 225 230 235 240

ttt gac cat gcc act atc gca gga aaa cac cac aca ctc atc aca aga 768
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 35 40 45

Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp
 50 55 60

Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His
 65 70 75 80

Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu
 85 90 95

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Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His Glu Leu
 100 105 110
 Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg
 115 120 125
 Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp Ser Thr
 130 135 140
 Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr His Ser
 145 150 155 160
 Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His
 165 170 175
 Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu Asn His
 180 185 190
 Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr His Asn
 195 200 205
 Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala
 210 215 220
 Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr
 225 230 235 240
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 245 250 255
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 Met Gly Ile Ser Leu
 1 5
 ttg tca tca ctg ttg aaa atc cat ggt ttt cca gtc gtc gca gat ttc 163
 Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro Val Val Ala Asp Phe
 10 15 20
 ttc ttc gcg tta gct gtt gtg gtg gca att gtc att att ggc ggt tgg 211
 Phe Phe Ala Leu Ala Val Val Val Ala Ile Val Ile Ile Gly Gly Trp
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 cta atc tac cgc tct cct tca ttc aaa act gaa gtc atg ccg gca tgg 259

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Ala	Met	Leu	Ser	Met	Gly	Leu	Ile	Ala	Leu	Gly	Thr	Ala	Ser	Pro	Val	
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gtt	tgt	ggt	gat	gat	ctg	tgg	gga	ttt	atg	ttt	gtg	tgc	tgg	tct	att	355
Val	Leu	Gly	Asp	Asp	Leu	Trp	Gly	Phe	Met	Phe	Val	Cys	Trp	Ser	Ile	
	70				75					80					85	
ggc	aca	gcc	gtg	gga	ctt	gtt	gcc	tat	tcc	tta	tat	ata	acg	gcc	att	403
Gly	Thr	Ala	Val	Gly	Leu	Val	Ala	Tyr	Ser	Leu	Tyr	Ile	Thr	Ala	Ile	
				90					95					100		
tgt	cga	tct	aag	gcg	ggc	aca	cca	act	ttt	gcg	tgg	ggt	ctt	cct	ctt	451
Leu	Arg	Ser	Lys	Ala	Gly	Thr	Pro	Thr	Phe	Ala	Trp	Gly	Leu	Pro	Leu	
			105					110					115			
gtc	acg	ccg	atg	gtt	gct	tcc	acc	tcg	gca	gca	caa	ctc	cat	gag	cac	499
Val	Thr	Pro	Met	Val	Ala	Ser	Thr	Ser	Ala	Ala	Gln	Leu	His	Glu	His	
			120				125					130				
ttt	gaa	ctt	ccg	gcg	atg	ctg	tgg	gtt	tct	ttc	ggg	ctc	ttc	ctt	tta	547
Phe	Glu	Leu	Pro	Ala	Met	Leu	Trp	Val	Ser	Phe	Gly	Leu	Phe	Leu	Leu	
	135					140				145						
act	tgt	gcg	tct	gca	cca	gca	gtt	ttt	acc	cga	gtg	tat	ttc	tac	tat	595
Thr	Leu	Ala	Ser	Ala	Pro	Ala	Val	Phe	Thr	Arg	Val	Tyr	Phe	Phe	Tyr	
	150				155					160					165	
ttc	ggc	ccc	aag	gcg	cag	ggc	atc	cca	ctg	atg	gca	aca	cca	aca	tca	643
Phe	Gly	Pro	Lys	Ala	Gln	Gly	Ile	Pro	Leu	Met	Ala	Thr	Pro	Thr	Ser	
			170						175					180		
tgg	att	cct	tgt	ggt	atg	gtg	ggc	caa	tcc	act	gca	gca	gct	cag	ctc	691
Trp	Ile	Pro	Leu	Gly	Met	Val	Gly	Gln	Ser	Thr	Ala	Ala	Ala	Gln	Leu	
			185					190					195			
atc	ggt	gcg	tcc	ttt	gga	tcc	aag	aca	gca	atc	aca	atg	ggc	att	att	739
Ile	Gly	Ala	Ser	Phe	Gly	Ser	Lys	Thr	Ala	Ile	Thr	Met	Gly	Ile	Ile	
		200					205					210				
tac	ggc	atc	atc	atg	gga	att	ttt	acg	att	cct	ctg	gga	gcc	atc	gct	787
Tyr	Gly	Ile	Ile	Met	Gly	Ile	Phe	Thr	Ile	Pro	Leu	Gly	Ala	Ile	Ala	
	215					220				225						
cac	ttt	gtg	ttc	tac	aga	gct	gtt	ttc	aaa	ggg	gcg	aca	tac	agc	ccc	835
His	Phe	Val	Phe	Tyr	Arg	Ala	Val	Phe	Lys	Gly	Ala	Thr	Tyr	Ser	Pro	
	230				235					240					245	
aca	tgg	tgg	gcc	agt	acc	ttc	cca	gtt	ggc	act	ttg	agt	ttg	ggt	gcg	883
Thr	Trp	Trp	Ala	Ser	Thr	Phe	Pro	Val	Gly	Thr	Leu					

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 Gln Leu Ala
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 <213> *Corynebacterium glutamicum*

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 35 40 45
 Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly
 50 55 60
 Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe
 65 70 75 80
 Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu
 85 90 95
 Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala
 100 105 110
 Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala
 115 120 125
 Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe
 130 135 140
 Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg
 145 150 155 160
 Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met
 165 170 175
 Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr
 180 185 190
 Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile
 195 200 205
 Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro
 210 215 220
 Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly
 225 230 235 240

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Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr
245 250 255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp
260 265 270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val
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<212> DNA

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<222> (101)..(994)

<223> RXA00016

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Val Ile Arg Phe Arg 5
1

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Phe Val Asp Asp Ala Arg Lys Thr Tyr Ser Val Lys Arg Ile Cys Asp 20
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Val Leu Lys Leu Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Ser Thr Ala 35
25 30

ttc acg cgt gaa aaa cgc ctg etc agc gac gct att ctt ggg gtc cag 259
Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala Ile Leu Gly Val Gln 50
40 45

gtc aag act gta ttc acc act cac agt ggc tgt tat ggg gcc aaa cga 307
Val Lys Thr Val Phe Thr His Ser Gly Cys Tyr Gly Ala Lys Arg 65
55 60

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Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His Asp Leu Ala Asn His 85
70 75 80

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Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys Leu Phe Gly Tyr Thr 95
90 100

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Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp Lys Thr Lys Thr Val 115
105 110

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ctc tat gtc ggg gat atc acc tat ctg cca att cag gat ggg tcg aat 547
 Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Gln Asp Gly Ser Asn
 135 140 145

atg tac ctg gcc acg gtc att gac tgt tac tcc cgc agg ttg gtg ggc 595
 Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly
 150 155 160 165

ttt tct atc gca gat cac atg cgc acg agc ttg gtc cag gac gcg ctg 643
 Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Asp Ala Leu
 170 175 180

ctc atg gct aaa gac cag cgt gga aac ctc aaa ggt gcg att ttt cac 691
 Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys Gly Ala Ile Phe His
 185 190 195

tcc gac cac ggc agc gtt tac acg tct cat gcg ttt cag gag acg tgt 739
 Ser Asp His Gly Ser Val Tyr Thr Ser His Ala Phe Gln Glu Thr Cys
 200 205 210

aag aaa cta ggg atc agg cag tcg atg gga tca att ggc acc agt gct 787
 Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser Ile Gly Thr Ser Ala
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 265 270 275

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 Cys Arg Tyr Leu Ala Pro Val Val Phe Glu Glu Arg Gly Pro Ala Ile
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<210> 192
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 <212> PRT
 <213> Corynebacterium glutamicum

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Trp Lys Ser Thr Ala Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala
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 Ile Leu Gly Val Gln Val Lys Thr Val Phe Thr Thr His Ser Gly Cys
 50 55 60
 Tyr Gly Ala Lys Arg Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His
 65 70 75 80
 Asp Leu Ala Asn His Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys
 85 90 95
 Leu Phe Gly Tyr Thr Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp
 100 105 110
 Lys Thr Lys Thr Val Phe Pro Asp Leu Val Gly Arg Lys Phe Thr Ala
 115 120 125
 Asp Lys Pro Asn Gln Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile
 130 135 140
 Gln Asp Gly Ser Asn Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser
 145 150 155 160
 Arg Arg Leu Val Gly Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu
 165 170 175
 Val Gln Asp Ala Leu Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys
 180 185 190
 Gly Ala Ile Phe His Ser Asp His Gly Ser Val Tyr Thr Ser His Ala
 195 200 205
 Phe Gln Glu Thr Cys Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser
 210 215 220
 Ile Gly Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala
 225 230 235 240
 Met Lys Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Glu Asn Gln Leu
 245 250 255
 Cys Cys Arg Arg Asp Val Phe Arg Trp Cys Thr Arg Tyr Asn Thr Val
 260 265 270
 Arg Arg His Ser Trp Cys Arg Tyr Leu Ala Pro Val Val Phe Glu Glu
 275 280 285
 Arg Gly Pro Ala Ile Leu Arg Ser Ala Ser
 290 295

<210> 193
 <211> 573
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> {101}..{550}

00602833.062300

<400> 193

cccagcacca actgcacgac cagaaacgag aattgattaa atg cgc tcc gct cac 115

ggc cca tac att gat aag ttc ttc ccc gag cca tac aag aac atg ctc 163
Gly Pro Tyr Ile Asp Lys Phe Phe Pro Glu Pro Tyr Lys Asn Met Leu
10 15 20

gag ctc acc aag act ctg cga aag atc tac ccg gac gtt gat ctg cct 211
Glu Leu Thr Lys Thr Leu Arg Lys Ile Tyr Pro Asp Val Asp Leu Pro
25 30 35

acc tca ttg att gag ctg gtc aat gtc cgc gtt tct caa atc aac gga 259
Thr Ser Leu Ile Glu Leu Val Asn Val Arg Val Ser Gln Ile Asn Gly
40 45 50

tgt ggc acc tgc tta agt tta cat gtt ccc gct gct cgc cgt gcc ggc 307
Cys Gly Thr Cys Leu Ser Leu His Val Pro Ala Ala Arg Arg Ala Gly
55 60 65

ggt cca gag aag aaa ctc gat gct ctg gca gcg tgg caa atg gtg gat 355
Val Pro Glu Lys Lys Leu Asp Ala Leu Ala Ala Trp Gln Met Val Asp
70 75 80 85

gaa ttc acc gtg gag gaa aag gca gca cta cag cta gca gaa tcc tta 403
Glu Phe Thr Val Glu Glu Lys Ala Ala Leu Gln Leu Ala Glu Ser Leu
90 95 100

acc ttg ctg gaa tcc cgc gaa ggt cac ctg gct gca cgc aca gcc tgc 451
Thr Leu Leu Glu Ser Arg Glu Gly His Leu Ala Ala Arg Thr Ala Cys
105 110 115

agt gtg ttt gcc gaa gag cag gta gct gcc ctg gaa tgg gct atc att 49
Ser Val Phe Ala Glu Glu Gln Val Ala Ala Leu Glu Trp Ala Ile Ile
120 125 130

gcg atc aat gct ttc aac cgc att tct att gcc agt ggg cac cca ctg 54
Ala Ile Asn Ala Phe Asn Arg Ile Ser Ile Ala Ser Gly His Pro Leu
135 140 145

ctc tagtaatcag gcagcaaaaa act 57
Leu
150

<210> 194

<211> 150

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 194

Met Arg Ser Ala His Gly Pro Tyr Ile Asp Lys Phe Phe Pro Glu Pro
1 5 10 15

Tyr Lys Asn Met Leu Glu Leu Thr Lys Thr Leu Arg Lys Ile Tyr Pro
20 25 30

Asp Val Asp Leu Pro Thr Ser Leu Ile Glu Leu Val Asn Val Arg Val
35 40 45

Ser Gln Ile Asn Gly Cys Gly Thr Cys Leu Ser Leu His Val Pro Ala
50 55 60

Ala Arg Arg Ala Gly Val Pro Glu Lys Lys Leu Asp Ala Leu Ala Ala
65 70 75 80

Trp Gln Met Val Asp Glu Phe Thr Val Glu Glu Lys Ala Ala Leu Gln
85 90 95

Leu Ala Glu Ser Leu Thr Leu Leu Glu Ser Arg Glu Gly His Leu Ala
100 105 110

Ala Arg Thr Ala Cys Ser Val Phe Ala Glu Glu Gln Val Ala Ala Leu
115 120 125

Glu Trp Ala Ile Ile Ala Ile Asn Ala Phe Asn Arg Ile Ser Ile Ala
130 135 140

Ser Gly His Pro Leu Leu
145 150

<210> 195

<211> 381

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (358)

<223> RXA00938

<400> 195

atgatctacc gctgggtcca gaaatacgcc cctgagctgg acaagcaaac acggtggtac 60

cggcaggtgc ctgactggca ggccagttcc tggcggggtgg atg aga cct ata tcc 115
Met Arg Pro Ile Ser
1 5

ggg tgg gcg gca ggt ggt gct acc tct gat ctg gcg atc acc gcc ggt 163
Gly Ser Ala Ala Gly Gly Ala Thr Ser Asp Leu Ala Ile Thr Ala Gly
10 15 20

ggc cag acc ctg gac ttt tac ctc tct ccg aag cgg aac gtg gcc gca 211
Gly Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala
25 30 35

gcg aag cgt ttc ctg gcc aag gcc ctc aga tcc aat gcg tca gcc ggg 259
Ala Lys Arg Phe Leu Ala Lys Ala Leu Arg Ser Asn Ala Ser Ala Gly
40 45 50

tat ccc aga gtg atc aac acc gat aaa gca ccc tcc cta gcc agg gca 307
Tyr Pro Arg Val Ile Asn Thr Asp Lys Ala Pro Ser Leu Ala Arg Ala
55 60 65

atc acc gag ttg aag tca gag gga atc tgc ccg cca aca gtg gaa cac 355
Ile Thr Glu Leu Lys Ser Glu Gly Ile Cys Pro Pro Thr Val Glu His

[illegible]

70	75	80	85	
cgg taggtgaaat acctcaacaa cat				381
Arg				

<210> 196
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Met Arg Pro Ile Ser Gly Ser Ala Ala Gly Gly Ala Thr Ser Asp Leu
1 5 10 15

Ala Ile Thr Ala Gly Gly Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys
20 25 30

Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Ala Leu Arg Ser
35 40 45

Asn Ala Ser Ala Gly Tyr Pro Arg Val Ile Asn Thr Asp Lys Ala Pro
50 55 60

Ser Leu Ala Arg Ala Ile Thr Glu Leu Lys Ser Glu Gly Ile Cys Pro
65 70 75 80

Pro Thr Val Glu His Arg
85

<210> 197
<211> 339
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(316)
<223> RXA01264
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<400> 197
atcaagacat gattgcgcg tatggaatc cgtagaaatc agaggaaaag aagctgatga 60
gaagggggac aacagcctgc gcaaaaggcct accagcgaga atg gac gag ctt gcc 115
                                     Met Asp Glu Leu Ala
                                     1             5

```

caa ctg ggg cac acc ttg tgg cgt cgg cgt aag aac gtg ttg gcg tcc 163
Gln Leu Gly His Thr Leu Trp Arg Arg Arg Lys Asn Val Leu Ala Ser
10 15 20

ttc aat atc ggt gca tcc aac gga cct gtc gag gcc atc aac ggc aga 21
Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg
25 30 35

ctt gag cac ctg cgc ggg atc acc ttg ggg ttc agg aac ctc aac cac 25
Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe Arg Asn Leu Asn His
40 45 50

0160-4085/96/0005-0000\$05.00/0

tac atc ttg cgg tgc ttg atc caa gcc gga caa ctg cag agg aag atc 307
 Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln Leu Gln Arg Lys Ile
 55 60 65
 aat gta ctc taaatccgaa gagttggcaa aga 339
 Asn Val Leu
 70

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<210> 198
<211> 72
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 198
Met Asp Glu Leu Ala Gln Leu Gly His Thr Leu Trp Arg Arg Lys
  1          5          10          15
Asn Val Leu Ala Ser Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu
  20          25          30
Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe
  35          40          45
Arg Asn Leu Asn His Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln
  50          55          60
Leu Gln Arg Lys Ile Asn Val Leu
  65          70

```

```
<210> 199
<211> 273
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(250)  
<223> RXA01265
```

```

400> 199
tacgaggaag atcttcacaca aatcctgtac tgcgcgggatg actgatccaa gttcaaccac 60
cgggggcactg ctagatcttg cagcgcttgg tgattgacgg      atg agt gtg tct gcc 115
                                   Met Ser Val Ser Ala
                                   1          5

acg gct aaa gca ctg aag atc ggc tgg gaa cta gtc aac cag gtt gca 163
Thr Ala Lys Ala Leu Lys Ile Gly Trp Glu Leu Val Asn Gln Val Ala
              10              15              20

ctc gat gct tgc cga cag ctc att tac aac gac ccg cgc cac ctt gaa 211
Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp Pro Arg His Leu Glu
              25              30              35

gtc gat gaa cat gta tgg aag tat act cga aag cca ggt tagccgtcga 260
Val Asp Glu His Val Trp Lys Tyr Thr Arg Lys Pro Gly
              40              45              50

acctggtgac cat 273

```

```

<210> 200
<211> 50
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Met Ser Val Ser Ala Thr Ala Lys Ala Leu Lys Ile Gly Trp Glu Leu
 1             5             10             15
Val Asn Gln Val Ala Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp
          20             25             30
Pro Arg His Leu Glu Val Asp Glu His Val Trp Lys Tyr Thr Arg Lys
          35             40             45
Pro Gly
 50

```

```

<210> 201
<211> 267
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> {101}..(244)
<223> RXA01327

<400> 201
gaaatccaaa tatcctctac gaacgcaatg gtcacacagt tttcaaactc gaaatcgcc 60
tatctgacaa catcgattgt aacgcctcga catcgaccgt atg agt atc gca gca 115
                                     Met Ser Ile Ala Ala
                                     1 5
acc gcg aaa gcc ctc ggt cta ggc tgg gat ctc acc tgc caa cta gcc 163
Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala
                10 15 20
cta gat atg tgc cac gaa ctc atc tac tac gac ccc acc cac cta gaa 211
Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp Pro Thr His Leu Glu
                25 30 35
att gtg cac gtt att ggc gtc gat gag cac aaa tgatctcata accgattaaa 264
Ile Val His Val Ile Gly Val Asp Glu His Lys
                40 45
aca 267

```

```
<210> 202
<211> 48
<212> PRT
<213> Corynebacterium glutamicum

<400> 202
Met Ser Ile Ala Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu
  1             5             10             15
```

[illegible]

```

Thr Cys Gln Leu Ala Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp
      20                      25                      30
Pro Thr His Leu Glu Ile Val His Val Ile Gly Val Asp Glu His Lys
      35                      40                      45

```

<210> 203
 <211> 498
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> {101}..(475)
 <223> RXA01328

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<400> 203
cacaaatgat ctcataacog attaaaacat ggtgatggct atgtcacctt cattgttaat 60

atgaccagcc ttccaccgag atgccacgtc cccagcggagg ttg ctt gat gta gtc 115
                        Leu Leu Asp Val Val
                        1                      5

gaa ggc cgc agt gct gat gcg ttg cgg gcg tgg ctt gca cgc cga agc 163
Glu Gly Arg Ser Ala Asp Ala Leu Arg Ala Trp Leu Ala Arg Arg Ser
                        10                      15                      20

cca gca ttt cga cac caa gta cgc att gta act atg gat gga ttc caa 211
Pro Ala Phe Arg His Gln Val Arg Ile Val Thr Met Asp Gly Phe Gln
                        25                      30                      35

ggc tat gcc aca acc agc aaa caa ctt ctg ccc gcc gca cgc cga gtc 259
Gly Tyr Ala Thr Thr Ser Lys Gln Leu Leu Pro Ala Ala Arg Arg Val
                        40                      45                      50

atg gat cct ttc cac gtg gta ctc ctc gcc ggc gat aaa ctc acc cga 307
Met Asp Pro Phe His Val Val Leu Leu Ala Gly Asp Lys Leu Thr Arg
                        55                      60                      65

tgc cga caa cgt ttg cag cag gaa aaa tac cac cgg cgg ggt ttg cat 355
Cys Arg Gln Arg Leu Gln Gln Lys Tyr His Arg Arg Gly Leu His
                        70                      75                      80                      85

gat gac cgg ttg tat aag aac cgg aaa acc ttg ctg acc acg caa aaa 403
Asp Asp Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr Gln Lys
                        90                      95                      100

tgg ttg agt aag aaa aag caa agc gtc ttg atg agt tgt tta gct ttg 451
Trp Leu Ser Lys Lys Lys Gln Ser Val Leu Met Ser Cys Leu Ala Leu
                        105                      110                      115

ata aag act acg cgg cac tgc aac tgatgtggca ggcgtatcaa ggc 498
Ile Lys Thr Thr Arg His Cys Asn
                        120                      125

```

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<210> 204
 <211> 125
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 204
 Leu Leu Asp Val Val Glu Gly Arg Ser Ala Asp Ala Leu Arg Ala Trp
 1 5 10 15
 Leu Ala Arg Arg Ser Pro Ala Phe Arg His Gln Val Arg Ile Val Thr
 20 25 30
 Met Asp Gly Phe Gln Gly Tyr Ala Thr Thr Ser Lys Gln Leu Leu Pro
 35 40 45
 Ala Ala Arg Arg Val Met Asp Pro Phe His Val Val Leu Leu Ala Gly
 50 55 60
 Asp Lys Leu Thr Arg Cys Arg Gln Arg Leu Gln Gln Glu Lys Tyr His
 65 70 75 80
 Arg Arg Gly Leu His Asp Asp Pro Leu Tyr Lys Asn Arg Lys Thr Leu
 85 90 95
 Leu Thr Thr Gln Lys Trp Leu Ser Lys Lys Lys Gln Ser Val Leu Met
 100 105 110
 Ser Cys Leu Ala Leu Ile Lys Thr Thr Arg His Cys Asn
 115 120 125

<210> 205
 <211> 414
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXA01329

<400> 205
 aaaagcaaaag cgtcttgatg agttgtttg ctttgataaa gactacgcgg cactgcaact 60
 gatgtggcag gcgtatcaag gcattattga ctgatacaac atg gcc gat aaa cgc 115
 Met Ala Asp Lys Arg
 1 5
 cgc gca aag acc atg atg cgc gag att gtt gac cag atg cgg cta ctg 163
 Arg Ala Lys Thr Met Met Arg Glu Ile Val Asp Gln Met Arg Leu Leu
 10 15 20
 aaa gga caa gcg aat cga gaa ctt gca caa cta gcc cgc agc cta cac 211
 Lys Gly Gln Ala Asn Arg Glu Leu Ala Gln Leu Gly Arg Ser Leu His
 25 30 35
 aaa cgc ctc ggt gac atc ctg gcg tat ttc gat gtc gga atc tct aac 259
 Lys Arg Leu Gly Asp Ile Leu Ala Tyr Phe Asp Val Gly Ile Ser Asn
 40 45 50
 gga ccc gta gaa gca atc aac gga cga ctc gaa cac ctc cgc gga atc 307

00602839.062300

Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile
 55 60 65

gcc cta gga ttt cgc aac ctc aac cac tac atc ctg cac tgt ctc atc 355
 Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu His Cys Leu Ile
 70 75 80 85

cac tcc gga caa ctc acc cac aaa atc aac gca ctc taaaaccgga 401
 His Ser Gly Gln Leu Thr His Lys Ile Asn Ala Leu
 90 95

agagcccgat tgc 414

<210> 206
 <211> 97
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 206
 Met Ala Asp Lys Arg Arg Ala Lys Thr Met Met Arg Glu Ile Val Asp
 1 5 10 15

Gln Met Arg Leu Leu Lys Gly Gln Ala Asn Arg Glu Leu Ala Gln Leu
 20 25 30

Gly Arg Ser Leu His Lys Arg Leu Gly Asp Ile Leu Ala Tyr Phe Asp
 35 40 45

Val Gly Ile Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu
 50 55 60

His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile
 65 70 75 80

Leu His Cys Leu Ile His Ser Gly Gln Leu Thr His Lys Ile Asn Ala
 85 90 95

Leu

<210> 207
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXA01443

<400> 207
 gaaagctgct aaatatttcc cggaagaga caaactgggtg agctgcttcc ggtttggtga 60

cgagctgcga aaaacctatc cggttaagcg gttatgcgaa gtg ttg aaa atc aac 115
 Val Leu Lys Ile Asn
 1 5

cgc tcc tcg tac tac aaa tgg aaa aag act gcc ccg acc agg agc aac 163
 Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala Pro Thr Arg Ser Asn

00603030 062300

	10	15	20	
cgc ctg ctc agc gac gca gtc tta gga gcg aag atc aag tcc atc ttc				211
Arg Leu Leu Ser Asp Ala Val Leu Gly Ala Lys Ile Lys Ser Ile Phe				
	25	30	35	
acg aaa gaa cgc ggc tgc tac ggc tca aaa cgc atc acg gct gag ctc				259
Thr Lys Glu Arg Gly Cys Tyr Gly Ser Lys Arg Ile Thr Ala Glu Leu				
	40	45	50	
aac gat gat cct ggc agc act ccg gtt aac cat aaa cga gtc gcc cgg				307
Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His Lys Arg Val Ala Arg				
	55	60	65	
atc atg gca tca tta aag ctg ttt ggt ttc acg aag aaa cgc agg gtc				355
Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr Lys Lys Arg Arg Val				
	70	75	80	85
atc acg acc gtg tct gat aaa aag aag cct gtc ttc cct gac ctg gtc				403
Ile Thr Thr Val Ser Asp Lys Lys Lys Pro Val Phe Pro Asp Leu Val				
	90	95	100	
aaa cgt cat ttt aac gca cta gca gca aat gaa gtt tac gtc ggg gat				451
Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu Val Tyr Val Gly Asp				
	105	110	115	
att act tac cta ccg atc gca gat ggc acg aac atg tat ctg gct acg				499
Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn Met Tyr Leu Ala Thr				
	120	125	130	
gtc att gat tgc tat tcc cgt agg ctg gtg ggt ttt gcg att gcg gat				547
Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly Phe Ala Ile Ala Asp				
	135	140	145	
cat atg cgc acg tca ttg gtg cag gag gca ttg ctg atg gcg aag agt				595
His Met Arg Thr Ser Leu Val Gln Glu Ala Leu Leu Met Ala Lys Ser				
	150	155	160	165
cag cga ggc agc ctg aag ggt gcg gtg ttt cat tcg gat cac gcc agt				643
Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His Ser Asp His Gly Ser				
	170	175	180	
gtg tac acc tcg cag gcg ttt cag gac act tgt aaa aag ttg ggt gtt				691
Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys Lys Lys Leu Gly Val				
	185	190	195	
cgt cag tcg atg ggt gct gtt ggt acc agt gcg gat aat tcg ctg gcg				739
Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala Asp Asn Ser Leu Ala				
	200	205	210	
gag tcg ttt aat gcc gcc ctc aag cga gag gtg ctg cag gat tcc aag				787
Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val Leu Gln Asp Ser Lys				
	215	220	225	
acg ttt gcc aat cag ttg gtg tgc cgc cgg gag gta ttt cgc tgg tgt				835
Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu Val Phe Arg Trp Cys				
	230	235	240	245
acc agg tac agc aca aat cgc agg cat tct tgg tgt gcc tat gtg gtg				883
Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp Cys Gly Tyr Val Val				
	250	255	260	

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cct gcg gtg ttc gag agt aga aat tta gct att ctg aaa tct gtt tcc 931
 Pro Ala Val Phe Glu Ser Arg Asn Leu Ala Ile Leu Lys Ser Val Ser
 265 270 275

tgattaaatc gcctgtgttt cca 954

<210> 208

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Val Leu Lys Ile Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala
 1 5 10 15

Pro Thr Arg Ser Asn Arg Leu Leu Ser Asp Ala Val Leu Gly Ala Lys
 20 25 30

Ile Lys Ser Ile Phe Thr Lys Glu Arg Gly Cys Tyr Gly Ser Lys Arg
 35 40 45

Ile Thr Ala Glu Leu Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His
 50 55 60

Lys Arg Val Ala Arg Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr
 65 70 75 80

Lys Lys Arg Arg Val Ile Thr Thr Val Ser Asp Lys Lys Lys Pro Val
 85 90 95

Phe Pro Asp Leu Val Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu
 100 105 110

Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn
 115 120 125

Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly
 130 135 140

Phe Ala Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu
 145 150 155 160

Leu Met Ala Lys Ser Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His
 165 170 175

Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys
 180 185 190

Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala
 195 200 205

Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val
 210 215 220

Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu
 225 230 235 240

Val Phe Arg Trp Cys Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp
 245 250 255

00602030 062300

Cys Gly Tyr Val Val Pro Ala Val Phe Glu Ser Arg Asn Leu Ala Ile
260 265 270

Leu Lys Ser Val Ser
275

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<210> 209
<211> 390
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(367)
<223> RXA01444
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400> 209	ttttaccacac ctctcctgtt tgtcgttaaa gggacctggc cctctgtttg tagacaccta	60
acatcccaac attctgggat agaaaggtaa cctaccgac	atg cca acc aag acc	115
	Met Pro Thr Lys Thr	
	1 5	
tat tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc		163
Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser		
	10 15 20	
gac ggg gcc tca ctc caa cag atc gcc aac gat ctc ggc atc aac cga		211
Asp Gly Ala Ser Leu Lys Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg		
	25 30 35	
gta acc ctg aaa aac tgg atc atc aaa tac gga tcc aac cac aac gta		259
Val Thr Leu Lys Asn Trp Ile Lys Tyr Gly Ser Asn His Asn Val		
	40 45 50	
caa ggg aca acc cca tct gcg gca gtc tct gaa gct gaa caa atc cgg		307
Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu Ala Glu Gln Ile Arg		
	55 60 65	
cag ctg aag aag gaa aac gcg cta caa cgc gca aga acg cga cat cct		355
Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala Arg Thr Arg His Pro		
	70 75 80 85	
gcg gaa agc tgc taaatatttc ccggcaagag aca		390
Ala Glu Ser Cys		

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<210> 210
<211> 89
<212> PRT
<213> Corynebacterium glutamicum
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```

<400> 210
Met  Pro  Thr  Lys  Thr  Tyr  Ser  Glu  Glu  Phe  Lys  Arg  Asp  Ala  Val  Ala
 1          5          10         15
Leu  Tyr  Glu  Asn  Ser  Asp  Gly  Ala  Ser  Leu  Gln  Gln  Ile  Ala  Asn  Asp
          20          25          30

```

Leu Gly Ile Asn Arg Val Thr Leu Lys Asn Trp Ile Ile Lys Tyr Gly
 35 40 45

Ser Asn His Asn Val Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu
 50 55 60

Ala Glu Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala
 65 70 75 80

Arg Thr Arg His Pro Ala Glu Ser Cys
 85

<210> 211
 <211> 492
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(469)
 <223> RXA01648

<400> 211
 ccaatgaagt ttacgtcgagg gatattactt atctgccgat tgctgatggg tcgaatatgt 60

atttgaacgac gggtcattgat tgctattctt agcacgggttg gtg ggt ttt gcc ttt 115
 Val Gly Phe Ala Phe
 1 5

gcg gat cat atg cgc acg tca ttg gtg cag gag gcg ttg atg atg gcg 163
 Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu Met Met Ala
 10 15 20

aag agt cag cga ggc agt cta cag ggt gct gtt ttt cat tcg gat cac 211
 Lys Ser Gln Arg Gly Ser Leu Gln Gly Ala Val Phe His Ser Asp His
 25 30 35

ggc agt gtg tac acc tcg cag gcg ttt cag gac act tgt aaa aag ttg 259
 Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys Lys Lys Leu
 40 45 50

ggg gtt cgt cag tcg atg ggt gct gtt ggt acc agt gcg gat aat tcg 307
 Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala Asp Asn Ser
 55 60 65

cta gcg gag tcg ttt aat gcc gcg ctc aag cgg gaa gtg ctg cag gat 355
 Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val Leu Gln Asp
 70 75 80 85

tcc aag acg ttt gct aat cag ttg gtg tgc cgt cgg gag gta ttt cgg 403
 Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu Val Phe Arg
 90 95 100

tgg tgt gac cta gta caa cac ggt gcg cag aca ttc ttg gtg tgg cta 451
 Trp Cys Asp Leu Val Gln His Gly Ala Gln Thr Phe Leu Val Trp Leu
 105 110 115

tgt ggc gcc tgc ggt gtt tgaggtccag gggtctctgcta ttc 492
 Cys Gly Ala Cys Gly Val

00602879.062300

120

<210> 212

<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Val Gly Phe Ala Phe Ala Asp His Met Arg Thr Ser Leu Val Gln Glu
 1 5 10 15

Ala Leu Met Met Ala Lys Ser Gln Arg Gly Ser Leu Gln Gly Ala Val
 20 25 30

Phe His Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp
 35 40 45

Thr Cys Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr
 50 55 60

Ser Ala Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg
 65 70 75 80

Glu Val Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg
 85 90 95

Arg Glu Val Phe Arg Trp Cys Asp Leu Val Gln His Gly Ala Gln Thr
 100 105 110

Phe Leu Val Trp Leu Cys Gly Ala Cys Gly Val
 115 120

<210> 213

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA01649

<400> 213

ggctgctaaa tattttcccg gcaagaggca agacttatga cccgctttctg gttttgttgac 60

gacgtgcgaa aaacctactg aagttaagcg gttatgcgaa gtg ttg aaa att aac 115
 Val Leu Lys Ile Asn
 1 5

cgt tcc tcg tat tac aaa tgg aaa aag act gct ctg acg agg aag aaa 163
 Arg Ser Ser Tyr Trp Lys Lys Thr Ala Leu Thr Arg Lys Lys
 10 15 20

ctc ctg etc agc gac gca gtc ctg gga gcg aag atc aag tcc atc ttc 211
 Leu Leu Leu Ser Asp Ala Val Leu Gly Ala Lys Ile Lys Ser Ile Phe
 25 30 35

act aaa gaa cgc ggc tgt tat ggt gcg aaa cgt att acg gcc gag ctt 259
 Thr Lys Glu Arg Gly Cys Tyr Gly Ala Lys Arg Ile Thr Ala Glu Leu

00602239.0622060

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      40              45              50
aat gac ggg cca ggt aca aca act ccg gtt aac cac aag cga gtc gct 307
Asn Asp Gly Pro Gly Thr Thr Thr Pro Val Asn His Lys Arg Val Ala
      55              60              65

cga gtg atg tct tcg atg aag ctt gtt ggt ttt acg aag aaa cgc aag 355
Arg Val Met Ser Ser Met Lys Leu Val Gly Phe Thr Lys Lys Arg Lys
      70              75              80              85

gtc atc acc aca atc cca gca gct gtc aag ccg gtg ttc ccg gac ttg 403
Val Ile Thr Thr Ile Pro Ala Ala Val Lys Pro Val Phe Pro Asp Leu
      90              95              100

gtg aag cgt caa ttc aac gct ttg gct gcc aat gaa gtt tac gtc ggg 451
Val Lys Arg Gln Phe Asn Ala Leu Ala Ala Asn Glu Val Tyr Val Gly
      105              110              115

gat att act tat ctg ccg att gct gat ggg tcg aat atg tat ttg acg 499
Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Ser Asn Met Tyr Leu Thr
      120              125              130

acg gtc att gat tgc tat tct tagcacgggtt ggtgggtttt gcc 543
Thr Val Ile Asp Cys Tyr Ser
      135              140

<210> 214
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 214
Val Leu Lys Ile Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala
      1              5              10              15

Leu Thr Arg Lys Lys Leu Leu Leu Ser Asp Ala Val Leu Gly Ala Lys
      20              25              30

Ile Lys Ser Ile Phe Thr Lys Glu Arg Gly Cys Tyr Gly Ala Lys Arg
      35              40              45

Ile Thr Ala Glu Leu Asn Asp Gly Pro Gly Thr Thr Thr Pro Val Asn
      50              55              60

His Lys Arg Val Ala Arg Val Met Ser Ser Met Lys Leu Val Gly Phe
      65              70              75              80

Thr Lys Lys Arg Lys Val Ile Thr Thr Ile Pro Ala Ala Val Lys Pro
      85              90              95

Val Phe Pro Asp Leu Val Lys Arg Gln Phe Asn Ala Leu Ala Ala Asn
      100              105              110

Glu Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Ser
      115              120              125

Asn Met Tyr Leu Thr Thr Val Ile Asp Cys Tyr Ser
      130              135              140

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002290.6582360

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<210> 215
<211> 237
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(214)  
<223> RXA01650
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<400>	215
cagatcgcca acgatctcgg catcaacoga gtaacctga aaaacttcga tcaataaaata	60
cggtgcat gccacaacca acaccaaaga agcaacagca atg tcg gaa gct gaa	115
	Met Ser Glu Ala Glu
	1 5
caa atc aga cag cta aag aag gaa aac gca cta ctg cgt gaa gaa cgc	163
Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu Leu Arg Glu Glu Arg	
	10 15 20
gac att ttg cgc aag gct gct aaa tat ttt ccc gcc aag agg caa gac	211
Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Pro Gly Lys Arg Gln Asp	
	25 30 35
tta tgaccogctt ctgggttgtt gac	237
Leu	

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<210> 216
<211> 38
<212> PRT
<213> Corynebacterium glutamicum
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```
<400> 216
Met Ser Glu Ala Glu Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu
  1              5              10              15
Leu Arg Glu Glu Arg Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Pro
              20              25              30
Gly Lys Arg Gln Asp Leu
      35
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<210> 217
<211> 258
<212> DNA
<213> Corynebacterium glutamicum
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```
<220>  
<221> CDS  
<222> (101)..(235)  
<223> RXA01651
```

<400> 217
caatctcttaa ggagaaagt tatgacaaat aggaacctgac cctgtttgg tagacaccta 60
acatcccaac attctgggac agaaaggtaa cctacctatc atg cca acc aag acc 115
Met Pro Thr Lys Thr

09602839-066300

1 5

tac tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc 163
Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
 10 15 20

gat ggg gcc tca ctg caa cag atc gcc aac gat ctg ggc atc aac cga 211
Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg
 25 30 35

gta acc ctg aaa aac ttc gat caa taaatacggt gcgcatgcct caa 258
Val Thr Leu Lys Asn Phe Asp Gln
 40 45

<210> 218
<211> 45
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Pro Thr Lys Thr Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala
 1 5 10 15

Leu Tyr Glu Asn Ser Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp
 20 25 30

Leu Gly Ile Asn Arg Val Thr Leu Lys Asn Phe Asp Gln
 35 40 45

<210> 219
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXN01680

<400> 219
aagagtctcta cotcaccttac ggggactgcc ttaacgaacg cacctaacgc gctgatgtac 60

caggcacatgc catcccga aa catatccgcc ccaatoagaa atg gca ggt cac acc 115
 1 Met Ala Gly His Thr 5

cac aaa acc cac cgg act gct tat aag cag ttg gaa gcc ttg gcc cgc 163
His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu Glu Ala Leu Ala Arg
 10 15 20

aat ggg cat ttg ttt acc tat att gat cca cca gca gag gtt gac ggg 211
Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro Ala Glu Val Asp Gly
 25 30 35

gtg gtg aaa tca aca acg aac tgt ttg gaa ggt ggt atc aac gct cag 259
Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly Gly Ile Asn Ala Gln
 40 45 50

att aaa gcq ttg qcq aqa aac cat ccq qqg atg ttt gat qaa cat caa 307

[illegible]

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<210> 220
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 220
Met Ala Gly His Thr His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu
  1              5              10              15
Glu Ala Leu Ala Arg Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro
          20              25              30
Ala Glu Val Asp Gly Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly
          35              40              45
Gly Ile Asn Ala Gln Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met
          50              55              60
Phe Asp Glu His Gln Arg Ile Ala Val Asp Trp Trp Leu Leu Met His
          65              70              75              80
Thr Gln Leu Pro Gly Asp Pro Val Glu Ile Ala Arg Gln Gln Asn Trp
          85              90              95
Gly Gln Asp Gly Leu Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln
          100             105             110
Pro His Asp His Tyr Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp
          115             120             125
Ala Thr Thr Thr Arg Arg Lys Ser Lys
          130             135

<210> 221
<211> 534
<212> DNA

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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> FRXA01680

<400> 221

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aagagttcta cctcacctac ggggactggc ttaacgaacg cacctaccgc gctgatgtac 60
cagcacatgc catcccgaaa catatccgcc ccaatcagaa atg gca ggt cac acc 115
                                     Met Ala Gly His Thr
                                     1 5
cac aaa acc cac cgg act gct tat aag cag ttg gaa gcc ttg gcc cgc 163
His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu Glu Ala Leu Ala Arg
                                     10 15 20
aat ggg cat ttg ttt acc tat att gat cca cca gca gag gtt gac ggg 211
Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro Ala Glu Val Asp Gly
                                     25 30 35
gtg gtg aaa tca aca acg aac tgt ttg gaa ggt ggt atc aac gct cag 259
Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly Gly Ile Asn Ala Gln
                                     40 45 50
att aaa cgg ttg cgg aga aac cat cgg ggg atg ttt gat gaa cat caa 307
Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met Phe Asp Glu His Gln
                                     55 60 65
cgt atc cgg gtg gat tgg tgg tta ttg atg cat acg cag ttg cct gcc 355
Arg Ile Ala Val Asp Trp Trp Leu Leu Met His Thr Gln Leu Pro Gly
                                     70 75 80 85
gat ccg gat gag atc gcc agg caa caa aac tgg ggt caa gac gga ctc 403
Asp Pro Asp Glu Ile Ala Arg Gln Gln Asn Trp Gly Gln Asp Gly Leu
                                     90 95 100
gcc aac gtc ccc gac ttg atc caa caa gaa caa cca cac gac cac tac 451
Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln Pro His Asp His Tyr
                                     105 110 115
ggg cgc ccg gtt acc tat gac acc gga atc gat gcc aca acg aca cgc 499
Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp Ala Thr Thr Thr Arg
                                     120 125 130
cgt aaa agc aag taaaaatccc ggcccaccaa caa 534
Arg Lys Ser Lys
                                     135

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<210> 222

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

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Met Ala Gly His Thr His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu
1 5 10 15
Glu Ala Leu Ala Arg Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro

```

002290*6620960

ttc ctg gcc aag acg ctg cga tgg aat acg aca gcc ggg tcc ccg cgg 403
 Phe Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg
 90 95 100

gtc atc aac acc gac aag gca cca gct ctg gcc aag gca ata tcc gag 451
 Val Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu
 105 110 115

ctg aag gcg gag gga atc tgc cct cag acg gtg gag cac cgg cag gtg 499
 Leu Lys Ala Glu Gly Ile Cys Pro Gln Thr Val Glu His Arg Gln Val
 120 125 130

aaa tac ctc aac aac gtt atc gag gga gat cat ggc cga ctt aaa aga 547
 Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys Arg
 135 140 145

atc ctg ggg ccg aag gga gcg ttc aaa aac cga att tcc gcc tac cgg 595
 Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg
 150 155 160 165

acg ttg aaa ggg atg gaa gcg atg cat tca tta cgg aaa ggc cag ggc 643
 Thr Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Gln Gly
 170 175 180

acg atg ttt gac ctc acg ggc acc cga acc cag acg cgg tgatogtcag 692
 Thr Met Phe Asp Leu Thr Gly Thr Arg Thr Gln Thr Arg
 185 190

ccggatattc gag 705

<210> 224
 <211> 194
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 224
 Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg
 1 5 10 15

Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys Gln Thr Arg Trp Tyr
 20 25 30

Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp Arg Val Asp Glu Thr
 35 40 45

Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu Tyr Arg Ala Ile Thr
 50 55 60

Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser Pro Lys Arg Asn Val
 65 70 75 80

Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr
 85 90 95

Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala
 100 105 110

Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile Cys Pro Gln Thr Val
 115 120 125

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Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His
 130 135 140

Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg
 145 150 155 160

Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser Leu
 165 170 175

Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr Gly Thr Arg Thr Gln
 180 185 190

Thr Arg

<210> 225
 <211> 572
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1) .. (549)
 <223> FRXA01784

<400> 225
 acc acc atc tac cgc tgg gtc cag aaa tac gcc ctt gag ctg gat aag 48
 Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys
 1 5 10 15

cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg 96
 Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
 20 25 30

cgg gtg gat gag acc tat atc cgg gtc gcc gcc acg tgg tgc tat ctc 144
 Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
 35 40 45

tac cgg gct att acc gcg ggt ggg cag acc ctg gag ttt tat ctc tca 192
 Tyr Arg Ala Ile Thr Ala Gly Gln Thr Leu Glu Phe Tyr Leu Ser
 50 55 60

cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg 240
 Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
 65 70 75 80

cga tcg aat acg aca gcc ggg tcc ccg cgg gtc atc aac acc gac aag 288
 Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
 85 90 95

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc 336
 Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
 100 105 110

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt 384
 Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
 115 120 125

atc gag gga gat cat gcc cga ctt aaa aga atc ctg ggg ccg aag gga 432
 Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly

00602300 0062300

130 135 140

gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gaa 480
 Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
 145 150 155 160

gcg atg cat tca tta cgg aaa ggc cag ggc acg atg ttt gac ctc acg 528
 Ala Met His Ser Leu Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr
 165 170 175

ggc acc cga acc cag acg cgg tgatcgtag ccggatattc gag 572
 Gly Thr Arg Thr Gln Thr Arg
 180

<210> 226
 <211> 183
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 226
 Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys
 1 5 10 15
 Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
 20 25 30
 Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
 35 40 45
 Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser
 50 55 60
 Pro Lys Arg Asn Val Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
 65 70 75 80
 Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
 85 90 95
 Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
 100 105 110
 Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
 115 120 125
 Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly
 130 135 140
 Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
 145 150 155 160
 Ala Met His Ser Leu Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr
 165 170 175
 Gly Thr Arg Thr Gln Thr Arg
 180

<210> 227
 <211> 1329
 <212> DNA

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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1306)

<223> RXA01862

<400> 227

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ataatccaac tccctactca tcgctaggag gcacagactc atg gcc tat gac ttc 115
 Met Ala Tyr Asp Phe
 1 5

gtc att gga atg gac gtc ggc aaa tac ttc cac cac gcc tgc gtc ctc 163
 Val Ile Gly Met Asp Val Gly Lys Tyr Phe His His Ala Cys Val Leu
 10 15 20

gat ccc cag ggc aga caa gtc cta tcc aaa cgc atc aac caa cac gaa 211
 Asp Pro Gln Gly Arg Gln Val Leu Ser Lys Arg Ile Asn Gln His Glu
 25 30 35

ggc tcg cta cgc aag ctc ttc gac aaa ttc ctg gcc aat gac gcc gag 259
 Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu Ala Asn Asp Ala Glu
 40 45 50

gtc ctt gtc gtc gtc gat cag ccc aac aac atc gcc agg cta acc gtc 307
 Val Leu Val Val Val Asp Gln Pro Asn Asn Ile Gly Arg Leu Thr Val
 55 60 65

gca gtc gcc caa gca atg gga gcc gac gtt cgc tac ctc ccc ggg ctt 355
 Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg Tyr Leu Pro Gly Leu
 70 75 80 85

gcc atg cga caa ctt tca cgt atc cac gtc gcc aac tcc aag acc gat 403
 Ala Met Arg Gln Leu Ser Arg Ile His Val Gly Asn Ser Lys Thr Asp
 90 95 100

gta cgg gac gct tat gtc atc gcc cat gcc gcc ctc aac ctt ccg gat 451
 Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly Leu Asn Leu Pro Asp
 105 110 115

gcc ctg cgt agc gtc gac cgc gtt gag gaa gtc ttc ctc cag ctg aaa 499
 Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val Phe Leu Gln Leu Lys
 120 125 130

gtc ctc aac ggt atc gac gaa gac ctc gcc cgc gcc tac aca cgc ctg 547
 Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg Ala Tyr Thr Arg Leu
 135 140 145

atc aac cag atg caa tcc gcg ctc gtg gcc acc tac ccc gca ttc gaa 595
 Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr Tyr Pro Ala Phe Glu
 150 155 160 165

cat gtc ctg cgt ggg cag atg att cac cgc aag tgg att ctc cac ctt 643
 His Val Leu Arg Gly Gln Met Ile His Arg Lys Trp Ile Leu His Leu
 170 175 180

ctg gcg aaa tac ggt ggc ccc acc aag att cga cgc gtc gcc aaa gca 691
 Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg Arg Val Gly Lys Ala
 185 190 195

00602030 062200

cgg ctg gca gct ttc gca cgt ggt cac agg gca cgt aat cct gag cca 739
 Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala Arg Asn Pro Glu Pro
 200 205 210

gtt atc gat gcc atg ctt gct gcg atc cac ggc cag acg gta tcc atc 787
 Val Ile Asp Ala Met Leu Ala Ala Ile His Gly Gln Thr Val Ser Ile
 215 220 225

gcc ggc gca gaa tac gcg gaa ctt ggc gta gca atg tcc gcc aaa gat 835
 Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala Met Ser Ala Lys Asp
 230 235 240 245

gca cta gcc aag ctg gag cac cgc aaa gag att gaa ggc cag gta ctc 883
 Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile Glu Gly Gln Val Leu
 250 255 260

gag ctg atc cag gac att cct cag acc gag att ctc ttg tcc atg ccc 931
 Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile Leu Leu Ser Met Pro
 265 270 275

ggc atc ggc cca cgt agc gcc gcg caa atc ctt atg acc gtc ggc gat 979
 Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu Met Thr Val Gly Asp
 280 285 290

atg tcc gac ttt ccc gat gca gcg cac ctg gcg tcc tat gca ggc ctg 1027
 Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala Ser Tyr Ala Gly Leu
 295 300 305

tcg cgc cag aca aat cag tcg gga acg tcg atc atg tcg aat tcg ccc 1075
 Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile Met Ser Asn Ser Pro
 310 315 320 325

aac cgg gcc ggc aac aag aaa ttg aag aac gcc cta tgg cag tcg tct 1123
 Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala Leu Trp Gln Ser Ser
 330 335 340

ttt gca tcg atc aga ttc cac gag cgt tcc cgg caa ttc tat gaa cga 1171
 Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg Gln Phe Tyr Glu Arg
 345 350 355

aaa cgc aac gaa ggc aaa aga cac aac gcc gca gtc gtc gcg ctc gca 1219
 Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala Val Val Ala Leu Ala
 360 365 370

cgc cga cgc ctc aac gtc ctc ttc gcc atg atg cgc agc gga gag ctc 1267
 Arg Arg Arg Leu Asn Val Leu Phe Ala Met Met Arg Ser Gly Glu Leu
 375 380 385

tac aga gac atc ccc aca gcc cag gag gcc gca gcg gcc tagccctac 1316
 Tyr Arg Asp Ile Pro Thr Ala Gln Glu Ala Ala Ala Ala
 390 395 400

aagccccgaa gcc 1329

<210> 228
 <211> 402
 <212> PRT
 <213> Corynebacterium glutamicum

00602839.062300

<400> 228
 Met Ala Tyr Asp Phe Val Ile Gly Met Asp Val Gly Lys Tyr Phe His
 1 5 10 15
 His Ala Cys Val Leu Asp Pro Gln Gly Arg Gln Val Leu Ser Lys Arg
 20 25 30
 Ile Asn Gln His Glu Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu
 35 40 45
 Ala Asn Asp Ala Glu Val Leu Val Val Val Asp Gln Pro Asn Asn Ile
 50 55 60
 Gly Arg Leu Thr Val Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg
 65 70 75 80
 Tyr Leu Pro Gly Leu Ala Met Arg Gln Leu Ser Arg Ile His Val Gly
 85 90 95
 Asn Ser Lys Thr Asp Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly
 100 105 110
 Leu Asn Leu Pro Asp Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val
 115 120 125
 Phe Leu Gln Leu Lys Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg
 130 135 140
 Ala Tyr Thr Arg Leu Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr
 145 150 155 160
 Tyr Pro Ala Phe Glu His Val Leu Arg Gly Gln Met Ile His Arg Lys
 165 170 175
 Trp Ile Leu His Leu Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg
 180 185 190
 Arg Val Gly Lys Ala Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala
 195 200 205
 Arg Asn Pro Glu Pro Val Ile Asp Ala Met Leu Ala Ala Ile His Gly
 210 215 220
 Gln Thr Val Ser Ile Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala
 225 230 235 240
 Met Ser Ala Lys Asp Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile
 245 250 255
 Glu Gly Gln Val Leu Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile
 260 265 270
 Leu Leu Ser Met Pro Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu
 275 280 285
 Met Thr Val Gly Asp Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala
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 Ser Tyr Ala Gly Leu Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile
 305 310 315 320

00602830 0602300

Met Ser Asn Ser Pro Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala
 325 330 335

Leu Trp Gln Ser Ser Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg
 340 345 350

Gln Phe Tyr Glu Arg Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala
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Ala Ala

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 Met Ile Ala Ala Tyr
 1 5

cgc gag aag gac cga tcc ctc gcc cgc gcg gcg atg gag gcg ctc atc 163
 Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala Met Glu Ala Leu Ile
 10 15 20

gac gcc gtc agc caa gac gtc ccc gcc ggg ctg gac gag ttg cgc aag 211
 Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu Asp Glu Leu Arg Lys
 25 30 35

ctc ggt cgg acc ctg aag gct cgc gcc acc gac gtg ctg gcc tac ttc 259
 Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp Val Leu Ala Tyr Phe
 40 45 50

gag cgg cct gcc acc agc aat gcc ccc aca gag gcg atc aac gga cgc 307
 Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu Ala Ile Asn Gly Arg
 55 60 65

ctg gag cac ctg cgc gcc tcg gcc ctg gcc ttc cgc aac ctg acc aac 355
 Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe Arg Asn Leu Thr Asn
 70 75 80 85

tac atc gcc aga tcc ctg ctc gag ttc cgg cgg att cag acc tca act 403
 Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg Ile Gln Thr Ser Thr
 90 95 100

aca ccc tca tct gtg aag agc cgc ttt aga cat ccc tca tcg tca cgg 451

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Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His Pro Ser Ser Ser Arg
      105                      110                      115

acc act atg aac gat gtc ccg act cac cta tgaacgatgt cctgaacctta      501
Thr Thr Met Asn Asp Val Pro Thr His Leu
      120                      125

cac                                                                504

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Asp Glu Leu Arg Lys Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp
      35                      40                      45

Val Leu Ala Tyr Phe Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu
      50                      55                      60

Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe
      65                      70                      75                      80

Arg Asn Leu Thr Asn Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg
      85                      90                      95

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gttggggcag taggaagacc ggcgtggaat aatcaggtcc atg ggc atc ttc tcc      115
                      Met Gly Ile Phe Ser
                      1                      5

ggc cgg cag ttc cct cgt gaa atc atc ctg tgg ggc gtg cgg tgg tac      163
Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr
      10                      15                      20

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 cgg gga gtg ccg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa 259
 Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys
 40 45 50
 tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct 307
 Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro
 55 60 65
 gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355
 Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val
 70 75 80 85
 ggg gga aag tgg tgc tac ctc tat cgg gca atc acc gcc ggt agc cag 403
 Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Ser Gln
 90 95 100
 acc ctg gac ttc tac ctc tcc ccg aag aga aac gtc gcg gcg gcg aag 451
 Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys
 105 110 115
 cgt ttc ctg gcg aag acg ctg cgg tcg aat aaa tcg gca gcc tat ccg 499
 Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys Ser Ala Gly Tyr Pro
 120 125 130
 cgg gtg atc agc acc gac aag gcc ccc tca ctc gcc agg gca atc tct 547
 Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu Ala Arg Ala Ile Ser
 135 140 145
 gag ctg aag gcg gaa gcc gtc tgt cca tcg acg gtc gag cat cgt cgg 595
 Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr Val Glu His Arg Arg
 150 155 160 165
 gtg aaa tac ctc aac aac gtc att gaa gcc gac cat ggt cgg tta aag 643
 Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys
 170 175 180
 cgg atc ctg ggg ccg aaa gcc gca ttc aaa aac cga acg tct gcc tac 691
 Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Thr Ser Ala Tyr
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 cgg acg ttg aaa ggg atg gag gcg atg cac tca ttg cgg aag ggg cag 739
 Arg Thr Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Gln
 200 205 210
 ggc acg atg ttt gcc tat ggt cac ccg aat ccg gat gca gtg att gtt 787
 Gly Thr Met Phe Ala Tyr Gly His Pro Asn Pro Asp Ala Val Ile Val
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00602630.062300

<213> Corynebacterium glutamicum

<400> 232

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Glu Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr
 35           40           45

Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp
 50           55           60

Tyr Arg Gln Val Pro Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu
 65           70           75           80

Thr Tyr Ile Arg Val Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile
 85           90           95

Thr Ala Gly Ser Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn
100           105           110

Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys
115           120           125

Ser Ala Gly Tyr Pro Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu
130           135           140

Ala Arg Ala Ile Ser Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr
145           150           155           160

Val Glu His Arg Arg Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp
165           170           175

His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn
180           185           190

Arg Thr Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser
195           200           205

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 Met Asn Thr Lys Leu
 1 5

cat gct gtg acc gat gcg acg ggg cgt cca atc cgc ttc ttc atg acc 163
 His Ala Val Thr Asp Ala Thr Gly Arg Pro Ile Arg Phe Phe Met Thr
 10 15 20

gcc gga aag gtc agc gac tac atc gga gct atg gct ttg cta ggc agc 211
 Ala Gly Lys Val Ser Asp Tyr Ile Gly Ala Met Ala Leu Leu Gly Ser
 25 30 35

ctg ccc aag gcc ggc tgg ctt cta gcg gat cgg ggc tat gac gcg gac 259
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 Trp Phe Arg Asp Ala
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Gly Tyr Asp Ala Asp Trp Phe Arg Asp Ala
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cgaatcctgt ctccaaaatc acggcggggt caggggggtga atg cac cac gag caa 115
 Met His His Glu Gln
 1 5

ccc gaa ggg tgc gaa gtg ggc att cgt aga aca atc cca gag gaa agc 163
 Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr Ile Pro Glu Glu Ser
 10 15 20

00602639 062300

cgt acg gct ttc ctc gac atg atc aat caa ggt atg tca ggt ctt gct 211
 Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly Met Ser Gly Leu Ala
 25 30 35

gcg tct aca gcg gtc ggg gtc agt gaa ttc acc ggg cga aag tgg gcg 259
 Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr Gly Arg Lys Trp Ala
 40 45 50

aag gcc gcc ggg gtg aaa ctg acc cgc gcc ccg cga ggt gcc aat gct 307
 Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro Arg Gly Gly Asn Ala
 55 60 65

ttt gac acc gcc gag aaa ctt gag att gca gcc agc atg cta gag aaa 355
 Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala Ser Met Leu Glu Lys
 70 75 80 85

gga tgc cta ccc cga gaa atc gcc gag tat gtc gcc atg act cgg gcc 403
 Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val Gly Met Thr Arg Ala
 90 95 100

aat ata tcc cta tgg cgc aaa caa gcc cca gac aag ctt cgc caa cgc 451
 Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp Lys Leu Arg Gln Arg
 105 110 115

gca gcc acc ttg cgc acc gcc aag cga gca gct gaa ttc atc cac gcc 499
 Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala Glu Phe Ile His Ala
 120 125 130

ccg gtg atg gcc cct tat tat ggg cca cgc aca ctc cat caa gtg ttg 547
 Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr Leu His Gln Val Leu
 135 140 145

cgt gag gac tac aca aca ctg ttt gac gag tta tct gcg ttg ggg ttg 595
 Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu Ser Ala Leu Gly Leu
 150 155 160 165

cca gca cag gtg tgt ggg gcc tta ctt cat ett gct cca cca cca tca 643
 Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu Ala Pro Pro Pro Ser
 170 175 180

tta cgc ttt tct tat atg tgc tgt gta gtg ccg tta ttt gct gat gaa 691
 Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro Leu Phe Ala Asp Glu
 185 190 195

atc aaa gtc gta gga caa gcc aca cga tta tgc tta gaa gag aaa atg 739
 Ile Lys Val Val Gly Gln Gly Thr Arg Leu Ser Leu Glu Glu Lys Met
 200 205 210

atg atc caa cgt ttc cat gac acc ggg gtc agt gca gca gaa atc ggt 787
 Met Ile Gln Arg Phe His Asp Thr Gly Val Ser Ala Ala Glu Ile Gly
 215 220 225

cga cgc ctg ggt cgg tgt cgg caa aca att tcc agg gaa ctt cga cgt 835
 Arg Arg Leu Gly Arg Cys Arg Gln Thr Ile Ser Arg Glu Leu Arg Arg
 230 235 240 245

ggt caa gat gat gat gga cgt tat cgt gca cgc gac tcc tat gaa ggt 883
 Gly Gln Asp Asp Asp Gly Arg Tyr Arg Ala Arg Asp Ser Tyr Glu Gly
 250 255 260

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Ala Ile Arg Lys Leu Ala Arg Pro Lys Thr Pro Lys Leu Asp Ala Asn
265 270 275

cgt agg ctt cgg gct gtg gtg gtc gag cgc ttg aat aat aaa tta tct 979
Arg Arg Leu Arg Ala Val Val Val Glu Ala Leu Asn Asn Lys Leu Ser
280 285 290

ccg gag cag att tct ggt ctt tta gcc acc gag cat gct aac gat agc 1027
Pro Glu Gln Ile Ser Gly Leu Leu Ala Thr Glu His Ala Asn Asp Ser
295 300 305

tct atg cag att agt cat gaa act att tac cag cgc tta tat gtt caa 1075
Ser Met Gln Ile Ser His Glu Thr Ile Tyr Gln Ala Leu Tyr Val Gln
310 315 320 325

ggt aaa ggg cgc ttg cgt gat gaa ttg aag gtg gag aaa ttt ctt cgt 1123
Gly Lys Gly Ala Leu Arg Asp Glu Leu Lys Val Glu Lys Phe Leu Arg
330 335 340

acc ggt cgg aag gga cgt aaa ccg cag tcg aag ttg cca tcg aga ggt 1171
Thr Gly Arg Lys Gly Arg Lys Pro Gln Ser Lys Leu Pro Ser Arg Gly
345 350 355

aag ccg tgg gtg gag ggt cgc ttg att agt caa cgc cca gca gaa gtt 1219
Lys Pro Trp Val Glu Gly Ala Leu Ile Ser Gln Arg Pro Ala Glu Val
360 365 370

gct gat cgt gct gtg cct ggg cac tgg gag ggc gat tta gta att ggt 1267
Ala Asp Arg Ala Val Pro Gly His Trp Glu Gly Asp Leu Val Ile Gly
375 380 385

ggt gaa aac caa cgc aca cgc ttg gtg acg ttg gtg gag cgc acg agc 1315
Gly Glu Asn Gln Ala Thr Ala Leu Val Thr Leu Val Glu Arg Thr Ser
390 395 400 405

cgg ttg acg ttg att aag ccg ttg ggg gtt aat cat gag cgc tcg act 1363
Arg Leu Thr Leu Ile Lys Arg Leu Gly Val Asn His Glu Ala Ser Thr
410 415 420

gtg acg gat cgc ttg gtg gag atg atg ggt gat ttg ccg cag cgc ttg 1411
Val Thr Asp Ala Leu Val Glu Met Met Gly Asp Leu Pro Gln Ala Leu
425 430 435

cgt ccg agt ttg acg tgg gat cag ggt gtg gag atg gca gag cat cgc 1459
Arg Arg Ser Leu Thr Trp Asp Gln Gly Val Glu Met Ala Glu His Ala
440 445 450

cgg ttt agc gtg gtg acc aag tgt ccg gtg ttt ttc tgt gat cct cat 1507
Arg Phe Ser Val Val Thr Lys Cys Pro Val Phe Phe Cys Asp Pro His
455 460 465

tcg ccg tgg cag cgt ggg tcg aat gag aat acg aat gga ttg gtc agg 1555
Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr Asn Gly Leu Val Arg
470 475 480 485

gat ttt ttc ccg aag ggc act aat ttt gct aaa gta agt gac gaa gaa 1603
Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys Val Ser Asp Glu Glu
490 495 500

gtt cag cgg gca cag gat ctg ctg aat tac ccg ccg cgg aaa atg cat 1651

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Val Gln Arg Ala Gln Asp Leu Leu Asn Tyr Arg Pro Arg Lys Met His
 505 510 515 1699

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 Ser Thr Asp
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 35 40 45

Gly Arg Lys Trp Ala Lys Ala Gly Val Lys Leu Thr Arg Gly Pro
 50 55 60

Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala
 65 70 75 80

Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val
 85 90 95

Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp
 100 105 110

Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala
 115 120 125

Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr
 130 135 140

Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu
 145 150 155 160

Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu
 165 170 175

Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro
 180 185 190

Leu Phe Ala Asp Glu Ile Lys Val Val Gly Gln Gly Thr Arg Leu Ser
 195 200 205

Leu Glu Glu Lys Met Met Ile Gln Arg Phe His Asp Thr Gly Val Ser
 210 215 220

Ala Ala Glu Ile Gly Arg Arg Leu Gly Arg Cys Arg Gln Thr Ile Ser

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<210> 237

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 <212> DNA
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 Met Pro Arg Lys Thr
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 Tyr Thr Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
 10 15 20
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 Ala Gly Thr Ser Ile Gln Lys Ile Ala Asn Asp Leu Gly Ile Asn Arg
 25 30 35
 atg acc ctt aaa aac tgg att act aaa tac ggg gcc aac tca act cca 259
 Met Thr Leu Lys Asn Trp Ile Thr Lys Tyr Gly Ala Asn Ser Thr Pro
 40 45 50
 cat gcc gct aac acg gcc acc gcg ctg tcc gaa gct gaa cgg atc cgc 307
 His Gly Ala Asn Thr Ala Thr Ala Leu Ser Glu Ala Glu Arg Ile Arg
 55 60 65
 caa ctt gaa aag gaa aat gca ctc ctc cgc gaa gag cgt gac atc ctg 355
 Gln Leu Glu Lys Glu Asn Ala Leu Leu Arg Glu Glu Arg Asp Ile Leu
 70 75 80 85
 cgg aaa gcg gcc aaa tat ttc gcg gaa gag acg aac tgg tgatccgctt 404
 Arg Lys Ala Ala Lys Tyr Phe Ala Glu Glu Thr Asn Trp
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 ccgattcggt gat 417

<210> 238
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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
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 35 40 45
 Ala Asn Ser Thr Pro His Gly Ala Asn Thr Ala Thr Ala Leu Ser Glu
 50 55 60

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Ala Glu Arg Ile Arg Gln Leu Glu Lys Glu Asn Ala Leu Leu Arg Glu
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85 90 95

Asn Trp

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<212> DNA
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Leu Gly Ser Ile Gly
1 5
acc agt gct gac aac gcg tta gcg gag tcg ttc aac gcc gca ctc agg 163
Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala Leu Arg
10 15 20
cgg gaa gtc ctc caa gat tct aag act ttt gcg aac tagttgatct 209
Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Ala Asn
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gccgccggga tgt 222

<210> 240
<211> 33
<212> PRT
<213> Corynebacterium glutamicum

<400> 240
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Asn

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Met Val Met Gln Gly
1 5
att ggt ggt agg aag ctg gcg gcg acg gtg ctg ttg gtt cgg gat ggg 163
Ile Gly Gly Arg Lys Leu Ala Ala Thr Val Leu Leu Val Arg Asp Gly
10 15 20
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Ile Ile Asn Gly Arg Pro Asp Val Glu Val Tyr Ile Gln Glu Arg Val
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Ser Thr Met Ala Asn Phe Pro Arg Ala Thr Val Phe Pro Gly Gly Gly
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Val Asp Ser Arg Asp Phe Ala Asp Gly His Gly Lys Glu Val Trp Arg
55 60 65
gga cct agc gcg gag gag tgg ggt gtg cgt tta gcc gtg gag cct cat 355
Gly Pro Ser Ala Glu Glu Trp Gly Val Arg Leu Gly Val Glu Pro His
70 75 80 85
gtt gcg tat gcg ttg gtt ttt gct gcg gtt cgt gag ttg ttt gaa gag 403
Val Ala Tyr Ala Leu Val Phe Ala Ala Val Arg Glu Leu Phe Glu Glu
90 95 100
gcc ggt acg ttg ctt gcg gag cat acg gat ggt tct ggt ttg gtg aag 451
Ala Gly Thr Leu Leu Ala Glu His Thr Asp Gly Ser Gly Leu Val Lys
105 110 115
aat gct ggt cag tat cac gga tat cgg gag ttg ttg gag act cat gag 499
Asn Ala Gly Gln Tyr His Gly Tyr Arg Glu Leu Leu Glu Thr His Glu
120 125 130
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Met Ser Leu Thr Asp Met Leu Gln Ser Glu Asn Leu Ala Ile Arg Ser
135 140 145
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Asp Leu Ile Val Pro Phe Ala Arg Trp Ala Ser Pro Glu Gly Asn Arg
150 155 160 165
gag cag ttt gat acg ttt tct ttt gtt gct gtg gag ccg gag ggg cag 643
Glu Gln Phe Asp Thr Phe Ser Phe Val Ala Val Glu Pro Glu Gly Gln
170 175 180
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Cys Ala Asp Gly Asn Thr Ser Glu Ala Ser Ser Thr Gly Tyr Phe Pro
185 190 195
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Ala Arg Leu Ile Leu Asp Gly Trp Arg Ala Gly Leu Leu Arg Leu Val
200 205 210

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 215 220 225

gag gaa ttg ctg gag tac agc gcg cag gtt gat atg tct cct gtg ttg 835
 Glu Glu Leu Leu Glu Tyr Ser Ala Gln Val Asp Met Ser Pro Val Leu
 230 235 240 245

gat gat gcg gtg gat aat ccg agg tat gcg gag ttt tat cag gcg atg 883
 Asp Asp Ala Val Asp Asn Pro Arg Tyr Ala Glu Phe Tyr Gln Ala Met
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<210> 242

<211> 266

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 242

Met Val Met Gln Gly Ile Gly Gly Arg Lys Leu Ala Ala Thr Val Leu
 1 5 10 15

Leu Val Arg Asp Gly Ile Ile Asn Gly Arg Pro Asp Val Glu Val Tyr
 20 25 30

Ile Gln Glu Arg Val Ser Thr Met Ala Asn Phe Pro Arg Ala Thr Val
 35 40 45

Phe Pro Gly Gly Gly Val Asp Ser Arg Asp Phe Ala Asp Gly His Gly
 50 55 60

Lys Glu Val Trp Arg Gly Pro Ser Ala Glu Glu Trp Gly Val Arg Leu
 65 70 75 80

Gly Val Glu Pro His Val Ala Tyr Ala Leu Val Phe Ala Ala Val Arg
 85 90 95

Glu Leu Phe Glu Glu Ala Gly Thr Leu Leu Ala Glu His Thr Asp Gly
 100 105 110

Ser Gly Leu Val Lys Asn Ala Gly Gln Tyr His Gly Tyr Arg Glu Leu
 115 120 125

Leu Glu Thr His Glu Met Ser Leu Thr Asp Met Leu Gln Ser Glu Asn
 130 135 140

Leu Ala Ile Arg Ser Asp Leu Ile Val Pro Phe Ala Arg Trp Ala Ser
 145 150 155 160

Pro Glu Gly Asn Arg Glu Gln Phe Asp Thr Phe Ser Phe Val Ala Val
 165 170 175

Glu Pro Glu Gly Gln Cys Ala Asp Gly Asn Thr Ser Glu Ala Ser Ser
 180 185 190

Thr Gly Tyr Phe Pro Ala Arg Leu Ile Leu Asp Gly Trp Arg Ala Gly

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195 200 205

Leu Leu Arg Leu Val Ile Pro Thr Trp Ala Ser Leu Phe Glu Leu Ser
210 215 220

Gln Phe Lys Thr Val Glu Glu Leu Leu Glu Tyr Ser Ala Gln Val Asp
225 230 235 240

Met Ser Pro Val Leu Asp Asp Ala Val Asp Asn Pro Arg Tyr Ala Glu
245 250 255

Phe Tyr Gln Ala Met Arg Thr Glu Arg Phe
260 265

<210> 243
<211> 570
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(547)
<223> RXA01819

<400> 243
ggttgggggtc atcaaaggat gcggacatcg ctgtgggggtt gtgtaataat tgcacctgtg 60
aggtgccttt ctggcaggtg aatcaggact ctaagcaagc ttg att ctt cca gtt 115
Leu Ile Leu Pro Val
1 5

cag gag ggc att tcc tat ttt ccc acg ccg tta cac ctg aat cac atc 163
Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu His Leu Asn His Ile
10 15 20

ggt gga tcc agg ttt aag aag ttc ctg gtc aag atc gac aag act gtt 211
Gly Gly Ser Arg Phe Lys Lys Phe Leu Val Lys Ile Asp Lys Thr Val
25 30 35

ccc cag gac ctt gat gtt cat gtt att tgt gac aac tac gcc acg cat 259
Pro Gln Asp Leu Asp Val His Val Ile Cys Asp Asn Tyr Ala Thr His
40 45 50

aaa cac ccg acc atc aat acc tgg ttg gtc aag cat cca cgg ttt cac 307
Lys His Pro Thr Ile Asn Thr Trp Leu Val Lys His Pro Arg Phe His
55 60 65

atg cac ttc acc ccg acg tat tgc tcc tgg atc aac cag gtt gaa cgg 355
Met His Phe Thr Pro Thr Tyr Ser Ser Trp Ile Asn Gln Val Glu Arg
70 75 80 85

ttg ttc gct gag gtg acc ccg gag tta ctc cag cgt tct gat cat cgg 403
Leu Phe Ala Glu Val Thr Arg Glu Leu Leu Gln Arg Ser Asp His Arg
90 95 100

agt gtc cag gcc ctg gag aaa gat tta cgc aac tgg gtg aaa gca tgg 451
Ser Val Gln Ala Leu Glu Lys Asp Leu Arg Asn Trp Val Lys Ala Trp
105 110 115

aac gag gat cct aag ccg ttt atc tgg acc aaa acc gcg gag gag atc 499

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Asn Glu Asp Pro Lys Pro Phe Ile Trp Thr Lys Thr Ala Glu Glu Ile
 120 125 130 547
 ctt tcc tct atc gcc cga tac tta aaa cga att aac ggc gca gga cac
 Leu Ser Ser Ile Ala Arg Tyr Leu Lys Arg Ile Asn Gly Ala Gly His
 135 140 145
 tagcagcagc gtaagaagaa aag 570

<210> 244
 <211> 149
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 244
 Leu Ile Leu Pro Val Gln Glu Gly Ile Ser Tyr Phe Pro Thr Pro Leu
 1 5 10 15
 His Leu Asn His Ile Gly Gly Ser Arg Phe Lys Lys Phe Leu Val Lys
 20 25 30
 Ile Asp Lys Thr Val Pro Gln Asp Leu Asp Val His Val Ile Cys Asp
 35 40 45
 Asn Tyr Ala Thr His Lys His Pro Thr Ile Asn Thr Trp Leu Val Lys
 50 55 60
 His Pro Arg Phe His Met His Phe Thr Pro Thr Tyr Ser Ser Trp Ile
 65 70 75 80
 Asn Gln Val Glu Arg Leu Phe Ala Glu Val Thr Arg Glu Leu Leu Gln
 85 90 95
 Arg Ser Asp His Arg Ser Val Gln Ala Leu Glu Lys Asp Leu Arg Asn
 100 105 110
 Trp Val Lys Ala Trp Asn Glu Asp Pro Lys Pro Phe Ile Trp Thr Lys
 115 120 125
 Thr Ala Glu Glu Ile Leu Ser Ser Ile Ala Arg Tyr Leu Lys Arg Ile
 130 135 140
 Asn Gly Ala Gly His
 145

<210> 245
 <211> 879
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(856)
 <223> RXN03052
 <400> 245
 ccgctttatc tactacggcc tcagccatag cgtggttgcc gaagtgtgtg ttgcaatagt 60
 tttttaaata tcccagcct tcattctgtg aacggtcata atg ccc ttt tct cac 115

002290.6520950

	Met	Pro	Phe	Ser	His	
	1				5	
gac aaa tct gaa ctc ggt ggg gaa acc ccc tac ggg ctt gta cat gtt						163
Asp Lys Ser Glu Leu Gly Gly Glu Thr Pro Tyr Gly Leu Val His Val						
	10				20	
aac cct atg gct gaa gtg cga cct gta aaa gca caa acc aac gag ccc						211
Asn Pro Met Ala Glu Val Arg Pro Val Lys Ala Gln Thr Asn Glu Pro						
	25				35	
caa gca ctg cag gtt gct gac att caa ccc ttt cac gct gtt att gcg						259
Gln Ala Leu Gln Val Ala Asp Ile Gln Pro Phe His Ala Val Ile Ala						
	40				50	
gcc tca aaa caa ttg act ctc atc gac gtt gtc gat gtc tgc ctt gga						307
Ala Ser Lys Gln Leu Thr Leu Ile Asp Val Val Asp Val Cys Leu Gly						
	55				65	
aca gtg ttg cga gca tgg gaa gca ctg agc ctg cga tgg gta gac gtg						355
Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu Arg Trp Val Asp Val						
	70				80	
gtg ctt gac gag gag cat cca aga atc ttt atc cga ggc acc att gtc						403
Val Leu Asp Glu Glu His Pro Arg Ile Phe Ile Arg Gly Thr Ile Val						
	90				100	
tac aac aaa gaa aaa ggt aac cac aga caa gat aaa aca aaa acg acc						451
Tyr Asn Lys Glu Lys Gly Asn His Arg Gln Asp Lys Thr Lys Thr Thr						
	105				115	
agc agt agg cgt gtc att cag ttg cca gaa att gcc tca gac gtc tta						499
Ser Ser Arg Arg Val Ile Gln Leu Pro Glu Ile Ala Ser Asp Val Leu						
	120				130	
cgc aaa aga cat gca ctc tac gcc gaa cat ctc gaa atg gtg ttc cct						547
Arg Lys Arg His Ala Leu Tyr Ala Glu His Leu Glu Met Val Phe Pro						
	135				145	
tcc gct aga ggc aca tat att tat gag tcc aat ttc aac aaa ttg ttg						595
Ser Ala Arg Gly Thr Tyr Ile Tyr Glu Ser Asn Phe Asn Lys Leu Leu						
	150				160	
cga aaa cac cga aag ggt act gca tat gat tgg gtg acc gtg cac agc						643
Arg Lys His Arg Lys Gly Thr Ala Tyr Asp Trp Val Thr Val His Ser						
	170				180	
atc agg aaa acc ctt gca tca att gtc tct gag aac ctt gat tcc aag						691
Ile Arg Lys Thr Leu Ala Ser Ile Val Ser Glu Asn Leu Asp Ser Lys						
	185				195	
gcc gca tca gac gta ctc ggc cat gct gac tca cga ctc aca gaa cgg						739
Ala Ala Ser Asp Val Leu Gly His Ala Asp Ser Arg Leu Thr Glu Arg						
	200				210	
gtc tac atc gct aaa act gac aaa gac gtt cgg att ggt gat gtc gtc						787
Val Tyr Ile Ala Lys Thr Asp Lys Asp Val Pro Ile Gly Asp Val Val						
	215				225	
aac caa gcg ctc aaa gag gca cga aaa gtc tcc aaa aag tct cca aat						835
Asn Gln Ala Leu Lys Glu Ala Arg Lys Val Ser Lys Lys Ser Pro Asn						

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230 235 240 245 879

aaa gaa gct aaa gaa gaa gaa tagacgcaat agttgcattt tta
Lys Glu Ala Lys Glu Glu Glu
250

<210> 246
<211> 252
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 246
Met Pro Phe Ser His Asp Lys Ser Glu Leu Gly Gly Glu Thr Pro Tyr
1 5 10 15
Gly Leu Val His Val Asn Pro Met Ala Glu Val Arg Pro Val Lys Ala
20 25 30
Gln Thr Asn Glu Pro Gln Ala Leu Gln Val Ala Asp Ile Gln Pro Phe
35 40 45
His Ala Val Ile Ala Ala Ser Lys Gln Leu Thr Leu Ile Asp Val Val
50 55 60
Asp Val Cys Leu Gly Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu
65 70 75 80
Arg Trp Val Asp Val Val Leu Asp Glu Glu His Pro Arg Ile Phe Ile
85 90 95
Arg Gly Thr Ile Val Tyr Asn Lys Glu Lys Gly Asn His Arg Gln Asp
100 105 110
Lys Thr Lys Thr Thr Ser Ser Arg Arg Val Ile Gln Leu Pro Glu Ile
115 120 125
Ala Ser Asp Val Leu Arg Lys Arg His Ala Leu Tyr Ala Glu His Leu
130 135 140
Glu Met Val Phe Pro Ser Ala Arg Gly Thr Tyr Ile Tyr Glu Ser Asn
145 150 155 160
Phe Asn Lys Leu Leu Arg Lys His Arg Lys Gly Thr Ala Tyr Asp Trp
165 170 175
Val Thr Val His Ser Ile Arg Lys Thr Leu Ala Ser Ile Val Ser Glu
180 185 190
Asn Leu Asp Ser Lys Ala Ala Ser Asp Val Leu Gly His Ala Asp Ser
195 200 205
Arg Leu Thr Glu Arg Val Tyr Ile Ala Lys Thr Asp Lys Asp Val Pro
210 215 220
Ile Gly Asp Val Val Asn Gln Ala Leu Lys Glu Ala Arg Lys Val Ser
225 230 235 240
Lys Lys Ser Pro Asn Lys Glu Ala Lys Glu Glu Glu
245 250

<210> 247
 <211> 478
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> {101}..(478)
 <223> RXN02915

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<400> 247
cacttaaagc catgacacctg tgcattgcata gtgtcatgac ctgtgcaca cccagacct 60
acaccacagg catagtcccta ggctgctcac aattgacatc atg cct aaa ccc cta 115
                                     Met Pro Lys Pro Leu
                                     1 5
ccc cca gaa acc cga cgc aag atc atc gat ttc gat ccg ttc gca ccg 163
Pro Pro Glu Thr Arg Arg Lys Ile Ile Asp Phe Ala Pro
                                     10 15 20
aac agc ccc tcg atc gaa gag ttc tgc agt cgg cta aaa ata tcg cgg 211
Asn Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg
                                     25 30 35
cgc agc ttc tac aac atc cgc aac cga tac caa caa gac gcc aac gca 259
Arg Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Asn Ala
                                     40 45 50
gca ctg cat tca cac tcc agc gcc cca atc acc gcc cgg cga acg tac 307
Ala Leu His Ser His Ser Ser Ala Pro Ile Thr Ala Arg Arg Thr Tyr
                                     55 60 65
gat gaa tcc atc acc agc acc ttg ctg tcc atc cgc gca cgc ctg aaa 355
Asp Glu Ser Ile Thr Ser Thr Leu Leu Ser Ile Arg Ala Arg Leu Lys
                                     70 75 80 85
gcc caa gga tgg gag tac ggc ccg atc tct att cga ttc gaa ggc atc 403
Ala Gln Gly Trp Glu Tyr Gly Pro Ile Ser Ile Arg Phe Glu Gly Ile
                                     90 95 100
ttc acc cgg gaa ctg act gca ccg att cca tct gtt tca acc att gct 451
Phe Thr Arg Glu Leu Thr Ala Pro Ile Pro Ser Val Ser Thr Ile Ala
                                     105 110 115
cgt ttg tta cgc gcc gca gga gct gtt 478
Arg Leu Leu Arg Ala Ala Gly Ala Val
                                     120 125

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<210> 248
 <211> 126
 <212> PRT
 <213> *Corynebacterium glutamicum*

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<400> 248
Met Pro Lys Pro Leu Pro Pro Glu Thr Arg Arg Lys Ile Ile Asp Phe
  1 5 10 15
Asp Pro Phe Ala Pro Asn Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg

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      20              25              30
Leu Lys Ile Ser Arg Arg Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln
   35              40              45
Gln Asp Ala Asn Ala Ala Leu His Ser His Ser Ser Ala Pro Ile Thr
   50              55              60
Ala Arg Arg Thr Tyr Asp Glu Ser Ile Thr Ser Thr Leu Leu Ser Ile
   65              70              75              80
Arg Ala Arg Leu Lys Ala Gln Gly Trp Glu Tyr Gly Pro Ile Ser Ile
   85              90              95
Arg Phe Glu Gly Ile Phe Thr Arg Glu Leu Thr Ala Pro Ile Pro Ser
   100             105             110
Val Ser Thr Ile Ala Arg Leu Leu Arg Ala Ala Gly Ala Val
   115             120             125

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<210> 249
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(634)
<223> RXN02919

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<400> 249
atttccctcg cgagatccat cctgtgggcg gtgcacaggt cactgccgct acgggctcag 60
ctgacctaag atctcgagga aatgatgact tcagcgcgga  gtg  cgg  gtc  gat  cac      115
                                         Val Pro Val Asp His
                                         1              5
acc acc atc tac cgc tgg gtc cag aaa tac gcc cct gag ctg gat aag      163
Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys
      10              15              20
cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg      211
Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
      25              30              35
cgg gtg gat gag acc tat atc cgg gtc gcc gcc acg tgg tgc tat ctc      259
Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
      40              45              50
tac cgg gct att acc gcg ggt ggg cag acc ctg gag ttt tat ctc toa      307
Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser
      55              60              65
cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg      355
Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
      70              75              80              85
cga tcg aat acg aca gcc ggg tcc cgg cgg gtc atc aac acc gac aag      403
Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
      90              95              100

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006290.65820960

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc 451
Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
105 110 115

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt 499
Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
120 125 130

atc gag gga gat cat ggc cga ctc aaa aga atc ctg ggg ccg aag gga 547
Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly
135 140 145

gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gag 595
Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
150 155 160 165

gcg atg cat tca ttg cgg aaa ggg tca ggg aac gat gtt tgacctcacg 644
Ala Met His Ser Leu Arg Lys Gly Ser Gly Asn Asp Val
170 175

ggcaccgcgaa ccc 657

<210> 250
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 250
Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala
1 5 10 15
Pro Glu Leu Asp Lys Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp
20 25 30
Gln Ala Ser Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly
35 40 45
Thr Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu
50 55 60
Glu Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Lys Arg Phe
65 70 75 80
Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val
85 90 95
Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu
100 105 110
Lys Ala Glu Gly Ile Cys Pro Gln Thr Val Glu His Arg Gln Val Lys
115 120 125
Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile
130 135 140
Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr
145 150 155 160
Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Ser Gly Asn

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175

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<210> 251
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1258)
<223> RXN03033
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400> 251	aagaccatca gaatcaa	atg gtgatcgata tcttgggaaa	agctatttggg accaggccca	60
atctcggcga gggcttagac	gaggaggacg ccaccta	aac gtg gat gag	caa cgc	115
		Val Asp Glu Gln	Arg	
gcc ttt gat	caa gga ctc	aag gaa gaa aac	acc ttg atc	aca gat ctc
Ala Phe Asp	Gln Gly Leu Lys	Glu Glu Asn Thr	Leu Ile Thr	Asp Leu
	10	15	20	163
acc acc tgt	gcc agg ctg	agc cat aac	aag gca tta	cgg ctg atc aag
Thr Thr Cys	Ala Arg Leu Ser	His Asn Lys	Ala Leu Arg	Leu Ile Lys
	25	30	35	211
ctg tcg aaa	tca acg gcg	tat tac cgc	aac aag ccg	cgt ccc cgt cct
Leu Ser Lys	Ser Thr Ala Tyr	Tyr Arg Asn Lys	Pro Arg Pro Arg	Pro
	40	45	50	259
gca ccg aaa	cct gtc ctg	cag gcc gtg	cca gca cca	aca gca cct ggt
Ala Pro Lys	Pro Val Leu Gln	Ala Val Pro	Ala Pro Thr	Ala Pro Gly
	55	60	65	307
gtg gaa ccc	aca cca gag	cct tgg cag	ggg aag gag	cca gca gtg tcg
Val Glu Pro	Thr Pro Glu Pro	Trp Gln Gly	Lys Glu Pro	Ala Val Ser
	70	75	80	85
tcg gtg cgt	caa gcg ttg	gca gaa cac	gaa cgc cag	ttc att gtt gat
Ser Val Arg	Gln Ala Leu Ala	Glu His Glu Arg	Gln Phe Ile Val	Asp
	90	95	100	403
gcg atc acc	gcg tac cca	caa ctg agc	ggt agt ggg	gtg ttt aac atg
Ala Ile Thr	Ala Tyr Pro Gln	Leu Ser Val Ser	Gly Val Phe	Asn Met
	105	110	115	451
ctg ttt aac	aaa ggc atc	tac cgc gca	tca cta cgt	aca tgg tgg cgt
Leu Phe Asn	Lys Gly Ile Tyr	Arg Ala Ser	Leu Arg Thr	Trp Trp Arg
	120	125	130	499
ggt gcc aag	cag cac aag	ttg tta cac	aaa gac cga	gtc agt gcc ctg
Val Ala Lys	Gln His Lys Leu	Leu Leu His Lys	Asp Arg Val	Ser Ala Leu
	135	140	145	547
ccc cgc ggg	aaa cga tca	cca acg cca	cgg gtt aag	ccg agg ttg gaa
Ser Pro Gly	Lys Arg Ser	Pro Thr Pro	Arg Val Lys	Pro Arg Leu Glu
	150	155	160	595

091023Z 060900Z

09503030

<400> 252

Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr

[illegible]

gcg atc acc gcg tac cca caa ctg agc gtt agt ggg gtg ttt aac atg 451
 Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser Gly Val Phe Asn Met
 105 110 115

ttg ttt aac aaa ggc atc tac cgc gca tca cta cgt aca tgg tgg cgt 499
 Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu Arg Thr Trp Trp Arg
 120 125 130

gtt gcc aag cag cac aag ttg tta cac aaa gac cga gtc agt gcc ctg 547
 Val Ala Lys Gln His Lys Leu Leu His Lys Asp Arg Val Ser Ala Leu
 135 140 145

tcc ccg ggg aaa cga tca cca acg cca cgg gtt aag ccg agg ttg gaa 595
 Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val Lys Pro Arg Leu Glu
 150 155 160 165

gca aca cag cct ggt cag gtg gtg tgt tgg gat gtg acg ttc ttg ccg 643
 Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp Val Thr Phe Leu Pro
 170 175 180

tcg ctg gta cgt ggt aag acc tat gcg ttg cat ctg gcg att gat ttg 691
 Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His Leu Ala Ile Asp Leu
 185 190 195

ttt tcc cgc aag att gtt ggg gcg aag gtc gcg ccg acg gaa aat acc 739
 Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala Pro Thr Glu Asn Thr
 200 205 210

tcc acc gcg gtg gag ttg tta acg cag gtg tta gcg gat aat ccg ggt 787
 Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu Ala Asp Asn Pro Gly
 215 220 225

gtg gtg acg gtg cat tcg gat aat ggg tcg gcg atg aca tcg acg agg 835
 Val Val Thr Val His Ser Asp Asn Gly Ser Ala Met Thr Ser Thr Arg
 230 235 240 245

gtg ccg ccg ttg tta gcg gat cat ggt gtg gcg ttg tcg ttg att ccg 883
 Val Arg Arg Leu Leu Ala Asp His Gly Val Ala Leu Ser Leu Ile Arg
 250 255 260

ccg ccg gtg agt gat gat aat gcg ttt gtg gag tcg gtg ttt cat acg 931
 Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu Ser Val Phe His Thr
 265 270 275

ttg aag tat ccg ccg ttt tat ccg aag gtg ttt gca tcg atg gat cag 979
 Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe Ala Ser Met Asp Gln
 280 285 290

gcc ccg gtg tgg gtg gag gag ttt gtg gtg tat tac aac acg gtt cat 1027
 Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr Tyr Asn Thr Val His
 295 300 305

ccg cat tct ggt gtg gct ggg cat act ccg cag tcg gtg ttt gat ggt 1075
 Pro His Ser Gly Val Ala Gly His Thr Pro Gln Ser Val Phe Asp Gly
 310 315 320 325

agt tgg agg gcg gct cat agg ttg cgt gtg cag gcg ttg gat gcc cat 1123
 Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln Ala Leu Asp Ala His
 330 335 340

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tac cgg cag ttc cgg cag cgg tat gtg ggg cgg cgg gtg gtt cag gaa 1171
Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg Pro Val Val Gln Glu
345 350 355

gtt gct ggt gtg gtg cgt ctt aat ggt gcg cgt gat gat ggg tct gta 1219
Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg Asp Asp Gly Ser Val
360 365 370

cag gag agg gtt ggt ggt gta gcg tcg ctg tta agt gct tgagtttagca 1268
Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu Ser Ala
375 380 385

tgtgttctta tcg 1281

<210> 254

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Val Asp Glu Gln Arg Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr
1 5 10 15

Leu Ile Thr Asp Leu Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala
20 25 30

Leu Arg Leu Ile Lys Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys
35 40 45

Pro Arg Pro Arg Pro Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala
50 55 60

Pro Thr Ala Pro Gly Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys
65 70 75 80

Glu Pro Ala Val Ser Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg
85 90 95

Gln Phe Ile Val Asp Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser
100 105 110

Gly Val Phe Asn Met Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu
115 120 125

Arg Thr Trp Trp Arg Val Ala Lys Gln His Lys Leu Leu His Lys Asp
130 135 140

Arg Val Ser Ala Leu Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val
145 150 155 160

Lys Pro Arg Leu Glu Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp
165 170 175

Val Thr Phe Leu Pro Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His
180 185 190

Leu Ala Ile Asp Leu Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala
195 200 205

Pro Thr Glu Asn Thr Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu

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210 215 220

Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala
225 230 235 240

Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala
245 250 255

Leu Ser Leu Ile Arg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu
260 265 270

Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe
275 280 285

Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr
290 295 300

Tyr Asn Thr Val His Pro His Ser Gly Val Ala Gly His Thr Pro Gln
305 310 315 320

Ser Val Phe Asp Gly Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln
325 330 335

Ala Leu Asp Ala His Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg
340 345 350

Pro Val Val Gln Glu Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg
355 360 365

Arg Asp Gly Ser Val Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu
370 375 380

Ser Ala
385

<210> 255
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXN03049

<400> 255
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Met Val His Met Val
1 5
ttc gcc gat atg aac act gac cgt gcg gcg cag gcc tac atc atc gtg 163
Phe Gly Asp Met Asn Thr Asp Arg Ala Ala Gln Ala Tyr Ile Ile Val
10 15 20
atc acc acc atc gtc atg gtg gtg ttg ttc tgg atc gtg ctc aga tat 211
Ile Thr Thr Ile Val Met Val Val Leu Phe Trp Ile Val Leu Arg Tyr
25 30 35

Trp	ctg	ctg	gct	gac	cgg	gcc	cgc	gcc	cag	cgg	ttc	acc	gcc	agc	atc	259
Ser	Leu	Ala	Asp	Arg	Ala	Ala	Arg	Ala	Gln	Arg	Phe	Thr	Ala	Ser	Ile	
	40						45					50				
acg	gag	atc	gga	cgc	aaa	atc	ttc	ctc	aac	cgg	ctg	cgt	ccc	cgg	atg	307
Thr	Glu	Ile	Gly	Arg	Lys	Ile	Phe	Leu	Asn	Arg	Leu	Arg	Pro	Arg	Met	
	55					60					65					
agc	agg	cag	aac	acc	tac	acg	gac	aag	gac	atc	tgc	cag	ttc	cac	tgg	355
Ser	Arg	Gln	Asn	Thr	Tyr	Thr	Asp	Lys	Asp	Ile	Ser	Gln	Phe	His	Trp	
	70				75					80					85	
acc	aat	ggc	ctg	ccg	ccg	acc	gat	gat	gaa	tcc	ccc	gag	tgg	atc	gcc	403
Thr	Asn	Gly	Leu	Pro	Pro	Thr	Asp	Asp	Glu	Ser	Pro	Glu	Trp	Ile	Ala	
				90					95					100		
gcc	cgc	gac	aac	gag	tgg	gag	gga	tac	acc	atc	acc	ctc	ggc	gac	gat	451
Ala	Arg	Asp	Asn	Glu	Trp	Glu	Gly	Thr	Thr	Ile	Thr	Leu	Gly	Asp	Asp	
			105				110						115			
ccc	aac	ggc	acc	gag	aaa	acc	atc	acc	ctc	gac	gat	ctg	cgg	gag	ctg	499
Pro	Asn	Gly	Thr	Glu	Lys	Thr	Ile	Thr	Leu	Asp	Asp	Leu	Arg	Glu	Leu	
		120					125					130				
ccg	cag	acc	tgc	tat	gtc	gcc	gtc	cac	acg	tgc	atg	cag	ggc	tgg	tca	547
Pro	Gln	Thr	Ser	Tyr	Val	Ala	Val	His	Thr	Cys	Met	Gln	Gly	Trp	Ser	
	135				140					145						
gct	acc	gcc	cgg	tgg	aca	ggg	gtg	cgg	tta	cgt	gat	gtt	ttg	tgt	cat	595
Ala	Thr	Ala	Arg	Trp	Thr	Gly	Val	Arg	Leu	Arg	Asp	Val	Leu	Cys	His	
	150				155				160					165		
gac	ctt	gtg	cac	acc	cta	gac	ctt	cac	cac	agg	cat	agt	cct	cgg	ctg	643
Asp	Leu	Val	His	Thr	Leu	Asp	Leu	His	His	Arg	His	Ser	Pro	Arg	Leu	
			170					175					180			
ctc	aca	att	gag	atc	ata	cct	aaa	ccc	ctg	ccc	cca	gaa	acc	cga	tgc	691
Leu	Thr	Ile	Glu	Ile	Ile	Pro	Lys	Pro	Leu	Pro	Pro	Glu	Thr	Arg	Cys	
			185					190					195			
aag	atc	atc	gat	ttc	gat	ctg	ttc	gca	cgg	aac	agt	ccc	tgc	atc	gaa	739
Lys	Ile	Ile	Asp	Phe	Asp	Leu	Phe	Ala	Pro	Asn	Ser	Pro	Ser	Ile	Glu	
	200						205					210				
gag	ttc	tgc	agt	cgg	ctt	aaa	ata	tgc	cgg	cgc	agc	ttc	tac	aac	atc	787
Glu	Phe	Cys	Ser	Arg	Leu	Lys	Ile	Ser	Arg	Arg	Ser	Phe	Tyr	Asn	Ile	
	215				220						225					
cgc	aac	cga	tac	caa	caa	gat	gcc	agt	gca	cgc	ctg	cat	cca	cgc	tcc	835
Arg	Asn	Arg	Tyr	Gln	Gln	Asp	Ala	Ser	Ala	Ala	Leu	His	Pro	Arg	Ser	
	230			235					240					245		
agc	gcc	cag	atc	acc	tcc	cgg	cga	aca	tac	gat	gaa	tcc	atc	acc	agt</	

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Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa His Arg Gly Thr Asp
 280 285 290
 tgc acc gat tcc atc cgt ctc aac tat cgc ttg ctt gtt acg cgc tgc 1027
 Cys Thr Asp Ser Ile Arg Leu Asn Tyr Arg Leu Leu Val Thr Arg Cys
 295 300 305
 agg agc agt cga aag taaccctaag aagcgaccaa agt 1065
 Arg Ser Ser Arg Lys
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 <212> PRT
 <213> Corynebacterium glutamicum
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 20 25 30
 Ile Val Leu Arg Tyr Trp Ser Leu Ala Asp Arg Ala Arg Ala Gln Arg
 35 40 45
 Phe Thr Ala Ser Ile Thr Glu Ile Gly Arg Lys Ile Phe Leu Asn Arg
 50 55 60
 Leu Arg Pro Arg Met Ser Arg Gln Asn Thr Tyr Thr Asp Lys Asp Ile
 65 70 75 80
 Ser Gln Phe His Trp Thr Asn Gly Leu Pro Pro Thr Asp Asp Glu Ser
 85 90 95
 Pro Glu Trp Ile Ala Ala Arg Asp Asn Glu Trp Glu Gly Tyr Thr Ile
 100 105 110
 Thr Leu Gly Asp Asp Pro Asn Gly Thr Glu Lys Thr Ile Thr Leu Asp
 115 120 125
 Asp Leu Arg Glu Leu Pro Gln Thr Ser Tyr Val Ala Val His Thr Cys
 130 135 140
 Met Gln Gly Trp Ser Ala Thr Ala Arg Trp Thr Gly Val Arg Leu Arg
 145 150 155 160
 Asp Val Leu Cys His Asp Leu Val His Thr Leu Asp Leu His His Arg
 165 170 175
 His Ser Pro Arg Leu Leu Thr Ile Glu Ile Ile Pro Lys Pro Leu Pro
 180 185 190
 Pro Glu Thr Arg Cys Lys Ile Ile Asp Phe Asp Leu Phe Ala Pro Asn
 195 200 205
 Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg Arg
 210 215 220
 Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Ser Ala Ala

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<211> 951
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(928)
<223> RXN03070
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cgaattcgac caagaaaacg taacacaccc aggagtactc	gtg cct gcc ctt cca Val Pro Ala Leu Pro	115
tca tct atc atc gac ccc ctc tgg cgc cag ttc tcc gcc tta atc cca	1 15	163
Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe Ser Ala Leu Ile Pro	10 20	
cgg gtt atc atc acc cac cca cta ggg tgc cac cgt gea cgc att gct	25	211
Pro Val Ile Ile Thr His Pro Leu Gly Cys His Arg Ala Arg Ile Ala	30 35	
gac cgg atc atc gtc gac aaa etc atc gea gtg ctt gtc ctc ggt gtc	40	259
Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val Leu Val Leu Gly Val	45 50	
tcc tat atc aag att tcc gat tcc acc tgc tca gcc acc acg ata cgc	55	307
Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser Ala Thr Thr Ile Arg	60 65	
acc cgc cga gac gag tgg atc act gcc ggg att ttc aag aat tta gaa	70	355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Lys Asn Leu Glu	75 80 85	
cag atc tgt ctg gag tcc tac gac cgt ttc ttc aag tta gac cta gaa	90	403
Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile Gly Leu Asp Leu Glu	95 100	
aac tta aat gtt gat ggc tgc att gtt aaa gct ccc tgc gcc gga gga		451
Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala Pro Cys Gly Gly Glu		

105 110 115
 gta gcc ggc aga ttc ccg gtt gac cgg gaa aaa ggc acc aaa cgc tgc 499
 Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys Gly Thr Lys Arg Ser
 120 125 130
 tta atg gtc gat gga cat gga atc ccg atc ggg tgc gtg gtc gcc gga 547
 Leu Met Val Asp Gly His Gly Ile Pro Ile Gly Cys Val Val Ala Gly
 135 140 145
 gcc aat cgg cat gat tta ccg ttg tta gct gca acc ttg gac acg ctc 595
 Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala Thr Leu Asp Thr Leu
 150 155 160 165
 ggc cgg ttt ggg ggc tct ctt ccc gat cag atc acg gtg cat ctc gat 643
 Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile Thr Val His Leu Asp
 170 175 180
 gct ggg tat gac tgc aag aaa acc cgc agg cta ctc agc gaa ttt ggt 691
 Ala Gly Tyr Asp Ser Lys Lys Thr Arg Arg Leu Leu Ser Glu Phe Gly
 185 190 195
 tat agc tgg gtg atc agc att aaa ggt gag cgg ctg cag gct ggg act 739
 Tyr Ser Trp Val Ile Ser Ile Lys Gly Glu Pro Leu Gln Ala Gly Thr
 200 205 210
 cgg tgg gtg gtg gag cgt act aac tct tgg cat aac cgg ggt ttt aag 787
 Arg Trp Val Val Glu Arg Thr Asn Ser Trp His Asn Arg Gly Phe Lys
 215 220 225
 aaa ctt agt atc tgc acc gaa cgt tgt acc cgg gtt gtg gaa gcg ttt 835
 Lys Leu Ser Ile Cys Thr Glu Arg Cys Thr Val Val Glu Ala Phe
 230 235 240 245
 atc gct tta gcc aac gcg gtg att att ctg cgt cgg ctt atc aaa cag 883
 Ile Ala Leu Ala Asn Ala Val Ile Ile Leu Arg Arg Leu Ile Lys Gln
 250 255 260
 gcc tgg act agt tac cgc tgg gac acc cga cgg gcc cac aga cct 928
 Ala Trp Thr Ser Tyr Arg Trp Asp Thr Arg Pro Gly His Arg Pro
 265 270 275
 taatctatcc gcgcaatctc taa 951

 <210> 258
 <211> 276
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 258
 Val Pro Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe
 1 5 10 15
 Ser Ala Leu Ile Pro Pro Val Ile Ile Thr His Pro Leu Gly Cys His
 20 25 30
 Arg Ala Arg Ile Ala Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val
 35 40 45
 Leu Val Leu Gly Val Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser

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50 55 60
 Ala Thr Thr Ile Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
 65 70 75 80
 Phe Lys Asn Leu Glu Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile
 85 90 95
 Gly Leu Asp Leu Glu Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala
 100 105 110
 Pro Cys Gly Gly Glu Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys
 115 120 125
 Gly Thr Lys Arg Ser Leu Met Val Asp Gly His Gly Ile Pro Ile Gly
 130 135 140
 Cys Val Val Ala Gly Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala
 145 150 155 160
 Thr Leu Asp Thr Leu Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile
 165 170 175
 Thr Val His Leu Asp Ala Gly Tyr Asp Ser Lys Lys Thr Arg Arg Leu
 180 185 190
 Leu Ser Glu Phe Gly Tyr Ser Trp Val Ile Ser Ile Lys Gly Glu Pro
 195 200 205
 Leu Gln Ala Gly Thr Arg Trp Val Val Glu Arg Thr Asn Ser Trp His
 210 215 220
 Asn Arg Gly Phe Lys Lys Leu Ser Ile Cys Thr Glu Arg Cys Thr Arg
 225 230 235 240
 Val Val Glu Ala Phe Ile Ala Leu Ala Asn Ala Val Ile Ile Leu Arg
 245 250 255
 Arg Leu Ile Lys Gln Ala Trp Thr Ser Tyr Arg Trp Asp Thr Arg Pro
 260 265 270
 Gly His Arg Pro
 275

<210> 259

<211> 742

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(742)

<223> RXN03121

<400> 259

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cgaatctttg cgctaactgt agggcggggt caggggggtga atg cac cac gag caa 115

 Met His His Glu Gln
 1 5

002200.062300

ccc gaa ggg tgc gaa gtg ggc att cgt aga aca atc cca gag gaa agc 163
 Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr Ile Pro Glu Glu Ser
 10 15 20

cgt acg gct ttc ctc gac atg atc aat caa ggt atg tca ggt ctt gct 211
 Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly Met Ser Gly Leu Ala
 25 30 35

gcg tct aca gcg gtc ggg gtc agt gaa ttc acc ggg cga aag tgg gcg 259
 Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr Gly Arg Lys Trp Ala
 40 45 50

aag gcc gcc ggg gtg aaa ctg acc cgc ggc cgg cga ggt ggc aat got 307
 Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro Arg Gly Gly Asn Ala
 55 60 65

ttt gac acc gcc gag aaa ctt gag att gca gcc agc atg cta gag aaa 355
 Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala Ser Met Leu Glu Lys
 70 75 80 85

gga tgc cta ccc cga gaa atc ggc gag tat gtc ggc atg act cgg gcc 403
 Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val Val Gly Met Thr Arg Ala
 90 95 100

aat ata tcc cta tgg cgc aaa caa ggc cca gac aag ctt cgc caa cgc 451
 Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp Lys Leu Arg Gln Arg
 105 110 115

gca gcc acc ttg cgc acc ggc aag cga gca gct gaa ttc atc cac gcc 499
 Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala Glu Phe Ile His Ala
 120 125 130

ccg gtg atg ggc cct tat tat ggg cca cgc aca ctc cat caa gtg ttg 547
 Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr Leu His Gln Val Leu
 135 140 145

cgt gag gac tac aca aca ctg ttt gag gag tta tct gcg ttg ggg ttg 595
 Arg Glu Asp Tyr Thr Leu Phe Asp Glu Leu Ser Ala Leu Gly Leu
 150 155 160 165

cca gca cag gtg tgt ggg gcc tta ctt cat ctt gct cca cca cca tca 643
 Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu Ala Pro Pro Pro Ser
 170 175 180

tta cgc ttt tct tat atg tog tgt gta gtg ccg tta ttt gct gat gaa 691
 Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro Leu Phe Ala Asp Glu
 185 190 195

atc aaa atc gta gga caa ggc aca cga tta tcg tta gaa gag aaa atg 739
 Ile Lys Ile Val Gly Gln Gly Thr Arg Leu Ser Leu Glu Glu Lys Met
 200 205 210

atg 742
 Met

<210> 260

<211> 214

<212> PRT

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<213> *Corynebacterium glutamicum*

<400> 260

Met His His Glu Gln Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr
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Ile Pro Glu Glu Ser Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly
20 25 30

Met Ser Gly Leu Ala Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr
35 40 45

Gly Arg Lys Trp Ala Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro
50 55 60

Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala
65 70 75 80

Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val
85 90 95

Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp
100 105 110

Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala
115 120 125

Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr
130 135 140

Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu
145 150 155 160

Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu
165 170 175

Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro
180 185 190

Leu Phe Ala Asp Glu Ile Lys Ile Val Gly Gln Gly Thr Arg Leu Ser
195 200 205

Leu Glu Glu Lys Met Met
210

<210> 261

<211> 484

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101) .. (484)

<223> RXN03161

<400> 261

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gttggggcag taggaagacc ggcgtggaat aatcaggtcc atg ggc atc ttc tcc 115
Met Gly Ile Phe Ser

1

5

ggt cgg cag ttc cct cgt gaa atc atc ctg tgg gcg gtg cgg tgg tac 163
 Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr
 10 15 20

tgc cgc tac gcc gtg agc tat cgc gac ctc gaa gag atg atg acc gag 211
 Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu
 25 30 35

cgg gga gtg cgg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa 259
 Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys
 40 45 50

tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct 307
 Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro
 55 60 65

gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355
 Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val
 70 75 80 85

ggg gga aag tgg tgc tac ctc tat cgg gca atc acc gcc ggt agc cag 403
 Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Ser Gln
 90 95 100

acc ctg gac ttc tac ctc tcc cgg aag aga aac gtc gcg gcg gcg aag 451
 Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys
 105 110 115

cgt ttc ctg gcg aag acg ctg cgg tgg aat aat 484
 Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Asn
 120 125

<210> 262

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Gly Ile Phe Ser Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp
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Ala Val Arg Trp Tyr Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu
 20 25 30

Glu Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr
 35 40 45

Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp
 50 55 60

Tyr Arg Gln Val Pro Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu
 65 70 75 80

Thr Tyr Ile Arg Val Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile
 85 90 95

Thr Ala Gly Ser Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn
 100 105 110

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Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Asn
 115 120 125

<210> 263

<211> 393

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (50)..(370)

<223> RXN03165

<400> 263

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 Met Gly Asn
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ttg ccg cag gcg ttg cgt cat agt ttt acg tgg gat cag ggt gtg cag 106
 Leu Pro Gln Ala Leu Arg His Ser Phe Thr Trp Asp Gln Gly Val Gln
 5 10 15

atg gca gag cat gcc cgg tta agc gtg gtg acc aag tgc ccg gtg ttt 154
 Met Ala Glu His Ala Arg Leu Ser Val Val Thr Lys Cys Pro Val Phe
 20 25 30 35

ttc tgt gat cct cat tcg ccg tgg cag cgt ggg tgg aat gag aat acg 202
 Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr
 40 45 50

aat gga ttg gtc agg gat ttt ttc ccg aag ggc act aat ttt gct aaa 250
 Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys
 55 60 65

gta agt gac gaa gaa gtt cag ccg gca cag gat atg ctg aat tac cga 298
 Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Met Leu Asn Tyr Arg
 70 75 80

ccg ccg aaa atg cat ggt ttt aaa agc gcg acg cag gta tat gaa ata 346
 Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Ile
 85 90 95

atc gta gtt ggt gca tcc acg gat tgaattcgcc taggagattg tgc 393
 Ile Val Val Gly Ala Ser Thr Asp
 100 105

<210> 264

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Gly Asn Leu Pro Gln Ala Leu Arg His Ser Phe Thr Trp Asp Gln
 1 5 10 15

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Gly Val Gln Met Ala Glu His Ala Arg Leu Ser Val Val Thr Lys Cys
20 25 30

Pro Val Phe Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn
35 40 45

Glu Asn Thr Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn
50 55 60

Phe Ala Lys Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Met Leu
65 70 75 80

Asn Tyr Arg Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val
85 90 95

Tyr Glu Ile Ile Val Val Gly Ala Ser Thr Asp
100 105

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<210> 265
<211> 423
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(400)
<223> RXN00083

<400> 265
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cggattcgac caagaaaacg tacaccactc aggagcactc gtg ctt gcc ctt cca 115
Val Leu Ala Leu Pro
1 5

tcc tct atc atc gac ccc ctc tgg tgc cag ttc gcc gcg ctg atc cca 163
Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe Ala Ala Leu Ile Pro
10 20

ccc gtg acc gac acc cac cca ctt cgg tgc cac cgc cca cgc atc ccg 211
Pro Val Thr Asp Thr His Pro Leu Arg Cys His Arg Pro Arg Ile Pro
25 30 35

gac cgg atc atc ttc gac aag ctc atc cag gtc ctc gtc ctc ggc gcc 259
Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val Leu Val Leu Gly Ala
40 45 50

tcc tat gcc aag atc gcc gac acg aca tgc tgc gcc acc acc ttg cgc 307
Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser Ala Thr Thr Leu Arg
55 60 65

acc cgc cgg gac gag tgg atc acc gct ggc atc ttc gag cag ctg gaa 355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Glu Gln Leu Glu
70 75 80 85

cag atc tgt ttg gaa ttc tac gac cgt atc gtc gga ctc gat ctc 400
Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val Gly Leu Asp Leu
90 95 100

taacttcgga ttgactcgaa ttg 423

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<210> 266
 <211> 100
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 266
 Val Leu Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe
 1 5 10 15

 Ala Ala Leu Ile Pro Pro Val Thr Asp Thr His Pro Leu Arg Cys His
 20 25 30

 Arg Pro Arg Ile Pro Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val
 35 40 45

 Leu Val Leu Gly Ala Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser
 50 55 60

 Ala Thr Thr Leu Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
 65 70 75 80

 Phe Glu Gln Leu Glu Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val
 85 90 95

 Gly Leu Asp Leu
 100

<210> 267
 <211> 230
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(207)
 <223> RXN02004

<400> 267
 cgc gtc ggc cgt ctg atg cgt cag aac ggc att ctc atc atc cgc agc 48
 Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
 1 5 10 15

 cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96
 Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
 20 25 30

 ccg aac ttt ctg cag cag gac ttt atg gcg agc agg ccg aac cag aag 144
 Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
 35 40 45

 tgg gcg ggc gac atc acc tat gtc tgg acg cgc gag ggc ctg ggt cta 192
 Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
 50 55 60

 tct ggc cga cat tct tgacctttat cccgcgcggg tga 230
 Ser Gly Arg His Ser
 65

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<210> 268
<211> 69
<212> PRT
<213> Corynebacterium glutamicum
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400> 268
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
  1          5          10          15
Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
          20          25          30
Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
          35          40          45
Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
          50          55          60
Ser Gly Arg His Ser
  65

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<210> 269
<211> 675
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(652)
<223> RXN02287
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acatctggcc ctcaaaattt tccttttact ggagaccact	gtg tac tca att tca Val Tyr Ser Ile Ser	115
gaa act atc gcc cga act ctt atg ccc cgc acc gat cac gtt ttc gac	1 5	163
Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp	10 15 20	
ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc		211
Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu	25 30 35	
ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc		259
Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala	40 45 50	
gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc		307
Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr	55 60 65	
acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc		355
Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val	70 75 80 85	
gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg gcc act gcc ccg agc		403

Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser
90 95 100

gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc 451
Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala
105 110 115

gta ggt gtg gaa acc ttc acc gtg cat gca gat gac gtt gct gcg gta 499
Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val
120 125 130

act ctt cag gct tgg aat aat acg cgg gaa aac aca cac gtg atc ctg 547
Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu
135 140 145

gaa atc ccc tat gac cta gca gct gcc aca gcc acc gat cca aca gtg 595
Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val
150 155 160 165

act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc cgg atg tca cgg 643
Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro
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Thr Leu Ser

<210> 270
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<212> PRT
<213> Corynebacterium glutamicum

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Asp His Val Phe Asp Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp
20 25 30

Ala Leu Glu Arg Leu Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val
35 40 45

Glu Thr Val Ala Ala Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro
50 55 60

Ala Val Ala Thr Thr Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr
65 70 75 80

Thr Leu Ala Asp Val Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val
85 90 95

Gly Thr Ala Pro Ser Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln
100 105 110

Gly Leu Ala Arg Ala Val Gly Val Glu Thr Phe Thr Val His Ala Asp
115 120 125

Asp Val Ala Ala Val Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn
130 135 140

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Thr His Val Ile Leu Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala
145 150 155 160

Thr Asp Pro Thr Val Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys
165 170 175

Leu Pro Met Ser Pro Thr Leu Ser
180

<210> 271

<211> 1431

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1408)

<223> RXN02963

<400> 271

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ggtatctaag ctaaccaaac accaacaataa ggctctaccc atg aag tct acc ggc 115
Met Lys Ser Thr Gly
1 5

aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc 163
Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr
10 15 20

atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211
Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp
25 30 35

gca ctc gac tac acc tcc acc tgc cca gaa tgc tcc caa cct ggg gtg 259
Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val
40 45 50

ttt cgt cat cac acc cac cgg atg ctc att gat tta ccc atc gtc ggg 307
Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly
55 60 65

ttt ccc acc aaa ctg ttt atc cgt cta cct cgc tac cgc tgc acc aac 355
Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn
70 75 80 85

ccc aca tgt aag caa aag tat ttc caa gca gaa cta agc tgc gct gac 403
Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp
90 95 100

cac ggt aaa aag gtc acc cac cgg gtc acc cgc tgg att tta caa cgc 451
His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg
105 110 115

ctt gct att gac cgg atg agt gtt cac gca acc gcg aaa gca ctt ggg 499
Leu Ala Ile Asp Arg Met Ser Val His Ala Thr Ala Lys Ala Leu Gly
120 125 130

cta ggg tgg gat tta acc tgc caa cta gcc ctc gat atg tgc cgt gag 547
Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu Asp Met Cys Arg Glu

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ctg gtc tat aac gat cct cac cat ctt gat gga gtg tat gtc att ggg 595			
Leu Val Tyr Asn Asp Pro His His Leu Asp Gly Val Tyr Val Ile Gly 165			
150	155	160	
gtg gat gag cat aag tgg tca cat aat agg gct aag cat ggt gat ggg 643			
Val Asp Glu His Lys Trp Ser His Asn Arg Ala Lys His Gly Asp Gly 180			
170	175	180	
ttt gtc acc gtg att gtc gat atg acc ggg cat cgg tat gac tca cgg 691			
Phe Val Thr Val Ile Val Asp Met Thr Gly His Arg Tyr Asp Ser Arg 195			
185	190	195	
tgt cct gcc cgg tta tta gat gtc gtc cca ggt cgt agt gct gat gct 739			
Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly Arg Ser Ala Asp Ala 210			
200	205	210	
tta cgg tcc tgg ctt ggc tcc cgc ggt gaa cag ttc cgc aat cag ata 787			
Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Phe Arg Asn Gln Ile 225			
215	220	225	
cgg atc gtg tcc atg gat gga ttc caa ggc tac gcc aca gca agt aaa 835			
Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr Ala Thr Ala Ser Lys 245			
230	235	240	
gaa ctc att cct tct gct cgt cgc gtg atg gat cca ttc cat gtt gtg 883			
Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp Pro Phe His Val Val 260			
250	255	260	
cgg ctt gct ggt gac aag ctc acc gcc tgc cgg caa cgc ctc cag cgg 931			
Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg Gln Arg Leu Gln Arg 275			
265	270	275	
gag aaa tac cag cgt cgt ggt tta agc cag gat cgg ttg tat aaa aac 979			
Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn 290			
280	285	290	
cgg aag acc ttg ttg acc acg cac aag tgg ttg agt cct cgt cag caa 1027			
Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu Ser Pro Arg Gln Gln 305			
295	300	305	
gaa agc ttg gag cag ttg tgg gcg tat gac aaa gac tac ggg gcg tta 1075			
Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Asp Tyr Gly Ala Leu 325			
310	315	320	
aag ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg 1123			
Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Asp Cys Tyr Gln Met 340			
330	335	340	
ggt aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag 1171			
Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln 355			
345	350	355	
ctt cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt 1219			
Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg 370			
360	365	370	
agt ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt 1267			
Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly 385			
375	380	385	

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gtc tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg 1315
 Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu
 390 395 400 405

cgt ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg 1363
 Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg
 410 415 420

tgc ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc 1408
 Cys Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu
 425 430 435

taaaacagga agagccagta aac 1431

<210> 272

<211> 436

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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Glu Leu Gly Leu Thr Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr
 20 25 30

Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys
 35 40 45

Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp
 50 55 60

Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg
 65 70 75 80

Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu
 85 90 95

Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg
 100 105 110

Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr
 115 120 125

Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu
 130 135 140

Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly
 145 150 155 160

Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala
 165 170 175

Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His
 180 185 190

Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly
 195 200 205

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Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln
 210 215 220
 Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr
 225 230 235 240
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp
 245 250 255
 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg
 260 265 270
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp
 275 280 285
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu
 290 295 300
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys
 305 310 315 320
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile
 325 330 335
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg
 340 345 350
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu
 355 360 365
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala
 370 375 380
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly
 385 390 395 400
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn
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 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys
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 Ile Asn Ala Leu
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<210> 273
 <211> 2787
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(2764)
 <223> RXA02788

<400> 273
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 cgctaaaaca ttctgagaag ttctaaggca ggataccgct gtg cag acc cat gag 115
 Val Gln Thr His Glu

002290.062300

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5

atc agg gag cgt ttt acc aat cac ttc gtc aat gcc ggt cac cag gcg	163
Ile Arg Glu Arg Phe Thr Asn His Phe Val Asn Ala Gly His Gln Ala	
10 15 20	
gta cct agc gcg tca ctg att ctc gac gac cct aac ctg ctg ttc gtt	211
Val Pro Ser Ala Ser Leu Ile Leu Asp Asp Pro Asn Leu Leu Phe Val	
25 30 35	
aac gca ggc atg gtt cca ttc aag cgc tac ttc ctg ggc cag cag acc	259
Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe Leu Gly Gln Gln Thr	
40 45 50	
cca cct ttt gaa aac ggc act gcg act tcc att cag aag tgt gtt cgt	307
Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile Gln Lys Cys Val Arg	
55 60 65	
acc ctg gat atc gaa gaa gtg ggt atc acc act cgc cac aat acc ttc	355
Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr Arg His Asn Thr Phe	
70 75 80 85	
ttc cag atg gca ggt aac ttc tcc ttc ggc cag tac ttc aaa gaa ggc	403
Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln Tyr Phe Lys Glu Gly	
90 95 100	
gca att acc cac gca tgg ggc ctt ctg act ggt tcc gta gca gac gga	451
Ala Ile Thr His Ala Trp Gly Leu Thr Thr Gly Ser Val Ala Asp Gly	
105 110 115	
ggc ttt ggc ctt gat cca gag cgc ctc tgg gtc act gtg tac ctc gat	499
Gly Phe Gly Leu Asp Pro Glu Arg Leu Trp Val Thr Val Tyr Leu Asp	
120 125 130	
gat gac gag gct gca gag atc tgg gaa aag aag atc ggc gtc cca tca	547
Asp Asp Glu Ala Ala Glu Ile Trp Glu Lys Lys Ile Gly Val Pro Ser	
135 140 145	
gag cgc atc cag cgc ctg ggt atg gct gac aac tac tgg tcc atg ggt	595
Glu Arg Ile Gln Arg Leu Gly Met Ala Asp Asn Tyr Trp Ser Met Gly	
150 155 160 165	
gta cca gga cct tgt ggc cct tgc tcc gag atc tac tac gac cgc ggc	643
Val Pro Gly Pro Cys Gly Pro Cys Ser Glu Ile Tyr Tyr Asp Arg Gly	
170 175 180	
gag aag tac ggc aag gaa ggc ggc cct gtc gct gac gac aac cgc tac	691
Glu Lys Tyr Gly Lys Glu Gly Gly Pro Val Ala Asp Asp Asn Arg Tyr	
185 190 195	
atg gag atc tgg aac ctg gtc ttc atg gag aag gaa cgc gga cag ggt	739
Met Glu Ile Trp Asn Leu Val Phe Met Glu Lys Glu Arg Gly Gln Gly	
200 205 210	
att ggc aag gac aac ttc gac atc ctt ggc gat ctt cca aag aag aac	787
Ile Gly Lys Asp Asn Phe Asp Ile Leu Gly Asp Leu Pro Lys Lys Asn	
215 220 225	
atc gat acc ggc atg ggc gtc gag cgc gtt gcc tgc atc ctc cag gat	835
Ile Asp Thr Gly Met Gly Val Glu Arg Val Ala Cys Ile Leu Gln Asp	
230 235 240 245	

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gtt gaa aac gtc tac gaa acc gac ctg ctg cgc cca gtc atc gac gtt 883
Val Glu Asn Val Tyr Glu Thr Asp Leu Leu Arg Pro Val Ile Asp Val
250 255 260

gca gag acc ctg acc gga acc aag tat ggt tct gac aac acc tct gac 931
Ala Glu Thr Leu Thr Gly Thr Lys Tyr Gly Ser Asp Asn Thr Ser Asp
265 270 275

att cgc ttc cgc gtt atc gcc gac cac tct cgt acc ggc atg atg ctc 979
Ile Arg Phe Arg Val Ile Ala Asp His Ser Arg Thr Gly Met Met Leu
280 285 290

atc ctc gat ggt gtt acc cca ggc aac gaa ggc cgt gga tac atc ctg 1027
Ile Leu Asp Gly Val Thr Pro Gly Asn Glu Gly Gly Tyr Ile Leu
295 300 305

cgc cgc ctg ctt cgc cgc att atc cgt tcc gca cgt ctg ctc ggt gct 1075
Arg Arg Leu Leu Arg Arg Ile Ile Arg Ser Ala Arg Leu Leu Gly Ala
310 315 320 325

act ggt gag acc atg gag cag ttc atg aac acc atc atg gac acc atg 1123
Thr Gly Glu Thr Met Glu Gln Phe Met Asn Thr Ile Met Asp Thr Met
330 335 340

acc ccg tcc tac cca gaa atc gcc gac aac cgt gag cgc atc atg cgt 1171
Thr Pro Ser Tyr Pro Glu Ile Ala Asp Asn Arg Glu Arg Ile Met Arg
345 350 355

gtg gct gtc acc gaa gag cgc gct ttc ttg aag act ctg gtc tct gga 1219
Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys Thr Leu Val Ser Gly
360 365 370

acc cac ctc ttc gaa gag gct gca acc tcc atc aag gct gca gga tcc 1267
Thr His Leu Phe Glu Glu Ala Ala Thr Ser Ile Lys Ala Ala Gly Ser
375 380 385

acc aag gtt gcc ggt gct cag gca ttc gca ctg cac gac acc tac ggt 1315
Thr Lys Val Ala Gly Ala Gln Ala Phe Ala Leu His Asp Thr Tyr Gly
390 395 400 405

ttc ccc atc gac ctc acc ctc gaa atg gct gca gaa gca ggc ctt gag 1363
Phe Pro Ile Asp Leu Thr Leu Glu Met Ala Ala Glu Ala Gly Leu Glu
410 415 420

gtt gac gtt gaa ggc ttt gat tcc ctc atg gca gag cag cgc tcc cgt 1411
Val Asp Val Glu Gly Phe Asp Ser Leu Met Ala Glu Gln Arg Ser Arg
425 430 435

gca aag gct gac agc cag gca aag aag cac ggc cac acc gac ttg agc 1459
Ala Lys Ala Asp Ser Gln Ala Lys Lys His Gly His Thr Asp Leu Ser
440 445 450

atc tac cgc gaa tgg gtc gac aac aac cca acc gta ttc acc ggc ttt 1507
Ile Tyr Arg Glu Trp Val Asp Asn Asn Pro Thr Val Phe Thr Gly Phe
455 460 465

gag gaa ctg gat tcc cag tcc aag gtc ctc gga cta ctt tcc gat ggt 1555
Glu Glu Leu Asp Ser Gln Ser Lys Val Leu Gly Leu Leu Ser Asp Gly
470 475 480 485

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gcc aag att tct gaa gcc aca gaa ggt caa gaa gtt gag gtc atc ctc 1603
Ala Lys Ile Ser Glu Ala Thr Glu Gly Gln Glu Val Glu Val Ile Leu
490 495 500

gac cag tca cct ctg tac gca gaa tca ggt gga cag ctc gcc gat cgt 1651
Asp Gln Ser Pro Leu Tyr Ala Glu Ser Gly Gly Gln Leu Gly Asp Arg
505 510 515

ggt cag atc ctg ctc gga gac acc gtg ctt gat gtc cat gac gtg cag 1699
Gly Gln Ile Leu Leu Gly Asp Thr Val Leu Asp Val His Asp Val Gln
520 525 530

aag atc ggt aag aaa ctg tgg gtt cac aag gca ctc gtg gca aac ggt 1747
Lys Ile Gly Lys Lys Leu Trp Val His Lys Ala Leu Val Ala Asn Gly
535 540 545

gga ctt gcg gta ggt gat gaa gtg gtg gca agc gtc gat aag caa tgg 1795
Gly Leu Ala Val Gly Asp Glu Val Val Ala Ser Val Asp Lys Gln Trp
550 555 560 565

cgc cat gct gca cgc cag gca cac acc gca acc cac ctg att cat gcc 1843
Arg His Ala Ala Arg Gln Ala His Thr Ala Thr His Leu Ile His Ala
570 575 580

gct ctg cgg cag gtt ctt gga cca act gcc ctc cag gca gga tcc atg 1891
Ala Leu Arg Gln Val Leu Gly Pro Thr Ala Leu Gln Ala Gly Ser Met
585 590 595

aac aag cca gcc tac ctg cgc ttc gac ttc aac tac acc gag cag ctc 1939
Asn Lys Pro Gly Tyr Leu Arg Phe Asp Phe Asn Tyr Thr Glu Gln Leu
600 605 610

acc cca gca caa gtc gag caa atc cag gcg atc acc aac gaa gcc gtg 1987
Thr Pro Ala Gln Val Glu Gln Ile Gln Ala Ile Thr Asn Glu Ala Val
615 620 625

gac acc gac tgg gct gtc aac acc gtg gaa acc tca ctc gag gaa gcc 2035
Asp Thr Asp Trp Ala Val Asn Thr Val Glu Thr Ser Leu Glu Glu Ala
630 635 640 645

aag gca atg ggt gcg atg gcg ctc ttc gcc gaa aac tac gga agc acc 2083
Lys Ala Met Gly Ala Met Ala Leu Phe Gly Glu Asn Tyr Gly Ser Thr
650 655 660

gtg cgc gtt gtg gaa atc ggc gga cct ttc tcc atg gaa ctc tgt gcc 2131
Val Arg Val Val Glu Ile Gly Gly Pro Phe Ser Met Glu Leu Cys Gly
665 670 675

ggt acg cac gtt gcg cac tcc tca cag atc gcc cca gtg gca ctg ttg 2179
Gly Thr His Val Ala His Ser Ser Gln Ile Gly Pro Val Ala Leu Leu
680 685 690

ggt gaa tca tcc atc gcc tcc gcc gtg cgc cgc atc gag gcc tac tcc 2227
Gly Glu Ser Ser Ile Gly Ser Gly Val Arg Arg Ile Glu Ala Tyr Ser
695 700 705

ggc ctg aac tcc ttc aac tac ctg tcc aag gaa cgc gca ctc gcc gag 2275
Gly Leu Asn Ser Phe Asn Tyr Leu Ser Lys Glu Arg Ala Leu Ala Glu
710 715 720 725

ggt ttg gca agc tcc ctg aag gct cca tcc gag gaa ctt cca gag cgc 2323

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Gly Leu Ala Ser Ser Leu Lys Ala Pro Ser Glu Glu Leu Pro Glu Arg
 730 735 740
 gtc gca cag ctg gta gac aag ctg aag gca gca gag aag gaa atc gaa 2371
 Val Ala Gln Leu Val Asp Lys Leu Lys Ala Ala Glu Lys Glu Ile Glu
 745 750 755
 gcc ctg cac cgt cag cag ctc atg gca caa acc gca gac ctg ttg aac 2419
 Ala Leu His Arg Gln Gln Leu Met Ala Gln Thr Ala Asp Leu Leu Asn
 760 765 770
 aac gct caa gag atc ggt ggc gtc acc acc ttg ctg ctg cgc gtc aag 2467
 Asn Ala Gln Glu Ile Gly Gly Val Thr Thr Leu Leu Leu Arg Val Lys
 775 780 785
 gac aac acc aac gcc ggt gac ctg cgc acc atc gca acc acc ctg aag 2515
 Asp Asn Thr Asn Ala Gly Asp Leu Arg Thr Ile Ala Thr Thr Leu Lys
 790 795 800 805
 gac aag ctc ggc gac cgc gaa ggc gtc ttg gtt att gcc tcc gac aac 2563
 Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val Ile Ala Ser Asp Asn
 810 815 820
 gcc ggc aag gtt cca ttc gtg gta gct gca acc aag gcc gct gtg gct 2611
 Ala Gly Lys Val Pro Phe Val Val Ala Ala Thr Lys Ala Ala Val Ala
 825 830 835
 cgc gga gct cac tcc ggc aac ctg gtt aag ctc gtt ggt tcc tac atc 2659
 Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu Val Gly Ser Tyr Ile
 840 845 850
 gac ggt cgc ggt ggc ggc aag gct gac ctc gca caa gga tcc ggc gcc 2707
 Asp Gly Arg Gly Gly Lys Ala Asp Leu Ala Gln Gly Ser Gly Ala
 855 860 865
 aac att gct ggc ctg gaa tcc gca ttc ggc gca gtc cgc gct gag atc 2755
 Asn Ile Ala Gly Leu Glu Ser Ala Phe Gly Ala Val Arg Ala Glu Ile
 870 875 880 885
 gag gca ctc taagccttca gtctaggccc taa 2787
 Glu Ala Leu

<210> 274

<211> 888

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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 Ala Gly His Gln Ala Val Pro Ser Ala Ser Leu Ile Leu Asp Asp Pro
 20 25 30
 Asn Leu Leu Phe Val Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe
 35 40 45
 Leu Gly Gln Gln Thr Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile
 50 55 60

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Gln Lys Cys Val Arg Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr
 65 70 75 80
 Arg His Asn Thr Phe Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln
 85 90 95
 Tyr Phe Lys Glu Gly Ala Ile Thr His Ala Trp Gly Leu Leu Thr Gly
 100 105 110
 Ser Val Ala Asp Gly Gly Phe Gly Leu Asp Pro Glu Arg Leu Trp Val
 115 120 125
 Thr Val Tyr Leu Asp Asp Asp Glu Ala Ala Glu Ile Trp Glu Lys Lys
 130 135 140
 Ile Gly Val Pro Ser Glu Arg Ile Gln Arg Leu Gly Met Ala Asp Asn
 145 150 155 160
 Tyr Trp Ser Met Gly Val Pro Gly Phe Cys Gly Pro Cys Ser Glu Ile
 165 170 175
 Tyr Tyr Asp Arg Gly Glu Lys Tyr Gly Lys Glu Gly Gly Pro Val Ala
 180 185 190
 Asp Asp Asn Arg Tyr Met Glu Ile Trp Asn Leu Val Phe Met Glu Lys
 195 200 205
 Glu Arg Gly Gln Gly Ile Gly Lys Asp Asn Phe Asp Ile Leu Gly Asp
 210 215 220
 Leu Pro Lys Lys Asn Ile Asp Thr Gly Met Gly Val Glu Arg Val Ala
 225 230 235 240
 Cys Ile Leu Gln Asp Val Glu Asn Val Tyr Glu Thr Asp Leu Leu Arg
 245 250 255
 Pro Val Ile Asp Val Ala Glu Thr Leu Thr Gly Thr Lys Tyr Gly Ser
 260 265 270
 Asp Asn Thr Ser Asp Ile Arg Phe Arg Val Ile Ala Asp His Ser Arg
 275 280 285
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 Glu Arg Ile Met Arg Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys
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Ala Thr Thr Leu Lys Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val
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Lys Ala Ala Val Ala Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu
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Val Gly Ser Tyr Ile Asp Gly Arg Gly Gly Gly Lys Ala Asp Leu Ala
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 Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala Val Gly Asp Ser
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ctt gca gcg gcg aag ggc gag cca acg cca gaa gac ggt tat ggc ggc 691
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gaa tac att aag gaa att gcg gag gca atc gtc gaa aag cat cct gaa 739
 Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val Glu Lys His Pro Glu
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Asp	Lys	Asp	Arg	Val	Val	Ile	Lys	Ser	Asp	Gly	Asp	Ala	Ala	Tyr	Ile	
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Arg	Met	Ser	Lys	Arg	Ala	Gly	Thr	Val	Val	Thr	Leu	Asp	Asp	Leu	Val	
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Glu	Ala	Ile	Gly	Ile	Asp	Ala	Ala	Arg	Tyr	Ser	Leu	Ile	Arg	Ser	Ser	
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Pro	His	Arg	Ile	Ala	Arg	Tyr	Ala	Glu	Glu	Leu	Ala	Gly	Thr	Phe	His	
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 Val Thr Arg Glu Tyr Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg
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 Asp Gly Tyr Gly Gly Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val
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 465 470 475 480
 Ala Asp Leu Arg Glu Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu
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 Ala Gly Thr Phe His Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys
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 Val Asp Glu Asp Thr Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala
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 Leu Ala Leu Glu Pro
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 gcc gca acc caa gag ctt ttc cgc gct gaa ggc gtg gag atg atg ttc 163
 Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu Gly Val Glu Met Met Phe
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 gag cac atc aaa tct tcc ctg cat gag ttc ggc acc gat ttc gat gtc 211
 Glu His Ile Lys Ser Ser Leu His Glu Phe Gly Thr Asp Phe Asp Val
 25 30 35
 tac tac cac gag aac tcc ctg ttc gag tcc ggt cgc gtg gac aag gcc 259
 Tyr Tyr His Glu Asn Ser Leu Phe Glu Ser Gly Ala Val Asp Lys Ala
 40 45 50
 gtg cag gtg ctg aag gac aac ggc aac ctg tac gaa aac gag ggc gct 307
 Val Gln Val Leu Lys Asp Asn Gly Asn Leu Tyr Glu Asn Glu Gly Ala
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 Ile Lys Ser Asp Gly Asp Ala Ala Tyr Ile Ala Gly Asp Ile Ala Tyr
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 ggt gct gac cac cat ggt tac atc cgc cgc ctg aag gca ggc ggc ggc 499
 Gly Ala Asp His His Gly Tyr Ile Ala Arg Leu Lys Ala Ala Ala Ala
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 Ala Leu Gly Tyr Lys Pro Glu Gly Val Glu Val Leu Ile Gly Gln Met
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 gtg aac ctg ctt cgc gac ggc aag gca gtg cgt atg tcc aag cgt gca 595
 Val Asn Leu Leu Arg Asp Gly Lys Ala Val Arg Met Ser Lys Arg Ala
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Tyr Val Gln Tyr Gly His Ala Arg Leu Cys Ser Ile Ala Arg Lys Ala
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gag acc ttg ggt gtc acc gag gaa ggc gca gac cta tct cta ctg acc 835
Glu Thr Leu Gly Val Thr Glu Glu Gly Ala Asp Leu Ser Leu Leu Thr
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Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr Glu Phe Gly Asp Asp
65 70 75 80

Lys Asp Arg Val Val Ile Lys Ser Asp Gly Asp Ala Ala Tyr Ile Ala
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Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser Arg Gly His Asn Leu
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Asn Ile Tyr Met Leu Gly Ala Asp His His Gly Tyr Ile Ala Arg Leu
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Met Ser Lys Arg Ala Gly Thr Val Val Thr Leu Asp Asp Leu Val Glu
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Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val Val Glu Arg Pro
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Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn Ile Ala Leu Gln Val
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Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu Ala Thr Trp Leu Ala
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gag gca ttg gct gca gat gac gcc att gat tct gct gaa att gct ggc 355
Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser Ala Glu Ile Ala Gly
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cca ggc ttt ttg aac att cgc ctt gct gca gca gca cag ggt gaa att 403
Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala Gln Gly Glu Ile
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gtg gcc aag att ctg gca cag gcc gag act ttc gga aac tcc gat cac 451

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 Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala Val Gly Asp Ser
 135 140 145
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 Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys Val Thr Arg Glu Tyr
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 Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg Phe Ala Leu Ser Ser
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 Ile Ala Leu Gln Val Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu
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 Ala Thr Trp Leu Ala Glu Ala Leu Ala Ala Asp Ala Ile Asp Ser
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 Ala Glu Ile Ala Gly Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala
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 Ala Gln Gly Glu Ile Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe
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 Ser Ala Asn Pro Thr Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala
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Val Leu Arg Thr His
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ctc tca ggc gag ctt cgt aaa gaa aac gca ggc cag tca gtt act ctg 163
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Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly Gly Val Ile Phe Ile
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gat ctt cgc gac cgt act ggc att gcc cag gtt gtt ttc cgc aat gag 259
Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val Val Phe Arg Asn Glu
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gac gtt gct gag cgt gca cac gca ctg cgc agc gaa ttc gtc cta cgc 307
Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser Glu Phe Val Leu Arg
55 60 65

gtc acc ggc gtc gtc gaa gag cgc cca gaa ggc tct caa aac cct aac 355
Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly Ser Gln Asn Pro Asn
70 75 80 85

ctt gca tcc ggc gac att gaa gtc agc gtc acc gaa ttt gag gta ctc 403
Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr Glu Phe Glu Val Leu
90 95 100

aac gag tcc gct cca ctt cct ttc cag atc gag gat tcc tcc tct gct 451
Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu Asp Ser Ser Ser Ala
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aag gct gca cgc acc gtg ctg gac agc cac gat ttc acc gag atc gag Lys Ala Ala Arg Thr Val Leu Asp Ser His Asp Phe Thr Glu Ile Glu 150 155 160 165	595
acc cca acc ttg act cgt tcc acc cca gaa ggc gca cgt gac ttc ctg Thr Pro Thr Leu Thr Arg Ser Thr Pro Glu Gly Ala Arg Asp Phe Leu 170 175 180	643
gtg cca gct cgt ctg cgc cca ggc act ttc tac gca ttg cca cag tcc Val Pro Ala Arg Leu Arg Pro Gly Thr Phe Tyr Ala Leu Pro Gln Ser 185 190 195	691
cca cag ctg ttc aag cag ctg ctg cag gtt gct ggc atg gag cgc tac Pro Gln Leu Phe Lys Gln Leu Leu Gln Val Ala Gly Met Glu Arg Tyr 200 205 210	739
tac cag atc gct cgt tgc tac cgc gat gag gat ttc cgt gca gac cgt Tyr Gln Ile Ala Arg Cys Tyr Arg Asp Glu Asp Phe Arg Ala Asp Arg 215 220 225	787
cag cca gag ttc acc cag ctg gac gtt gaa atg tcc ttc gtg gac cag Gln Pro Glu Phe Thr Gln Leu Asp Val Glu Met Ser Phe Val Asp Gln 230 235 240 245	835
gat gat gtc atc gca ctg ggc gag gag atc atc tct gag gtg tgg aag Asp Asp Val Ile Ala Leu Gly Glu Glu Ile Ile Ser Glu Val Trp Lys 250 255 260	883
ttg atc gga tat gag atc aag act cca atc cca cgc atg acc tac gcc Leu Ile Gly Tyr Glu Ile Lys Thr Pro Ile Pro Arg Met Thr Tyr Ala 265 270 275	931
gat gca atg cgt cgc tac ggc tcc gac aag cca gac ctg cgc ttc gac Asp Ala Met Arg Arg Tyr Gly Ser Asp Lys Pro Asp Leu Arg Phe Asp 280 285 290	979
atc gaa atc acc gag tgc acc gag ttc ttc cag gac acc aca ttc cgt Ile Glu Ile Thr Glu Cys Thr Glu Phe Phe Gln Asp Thr Thr Phe Arg 295 300 305	1027
gtg ttc aag aac gaa tat gtc ggc gca gtt gtc atg acc ggt ggt gct Val Phe Lys Asn Glu Tyr Val Gly Ala Val Val Met Thr Gly Gly Ala 310 315 320 325	1075
tcc cag cct cgc cgt cag ctc gac gca tgg cag gaa tgg gcc aag cag Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln Glu Trp Ala Lys Gln 330 335 340	1123
cgc ggt gct aag gga ctt gct tac atc ctc gtt ggt gaa gac ggc gag Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val Gly Glu Asp Gly Glu 345 350 355	1171
ctg tcc gga cct gtg gct aag aac atc acc gac gct gag cgc gca gga Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp Ala Glu Arg Ala Gly 360 365 370	1219

00602039 062300

atc gca gct cac gtt ggc gca cag cca ggc gac tgc atc ttc ttc gca 1267
 Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp Cys Ile Phe Phe Ala
 375 380 385

gca gga gac acc aag tct tcc ctc gca ctg ctc ggt gca gct cgt ggc 1315
 Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu Gly Ala Ala Arg Gly
 390 395 400 405

gag atc gct aag aag ctc gac ctg atc aag gaa ggc gac tgg gca ttc 1363
 Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu Gly Asp Trp Ala Phe
 410 415 420

acc tgg atc gtt gac gct cca atg ttc gag cca gca gca gac gcc acc 1411
 Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro Ala Ala Asp Ala Thr
 425 430 435

gca tcc ggt gac gtt gca ctg ggt aac tcc aag tgg acc gca gtc cac 1459
 Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys Trp Thr Ala Val His
 440 445 450

cac gcc ttc acc tca cct aag cca gag ttc ctg gac aac ttt gac acc 1507
 His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu Asp Asn Phe Asp Thr
 455 460 465

aac cca ggt gac gca ctt gct tat gca tac gac atc gtg tgc aac ggc 1555
 Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp Ile Val Cys Asn Gly
 470 475 480 485

aat gaa atc ggt ggc ggt tcc atc cgt atc cac cag cgc gac gtt cag 1603
 Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His Gln Arg Asp Val Gln
 490 495 500

gaa cgc gtt ttc gag gtt atg ggc atc acc ggt gaa gaa gca cgc gag 1651
 Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly Glu Glu Ala Arg Glu
 505 510 515

aag ttc ggc ttc ctg ctt gac gcc ttc gca ttc ggc gca cct cca cac 1699
 Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe Gly Ala Pro Pro His
 520 525 530

ggc gga atc gca ttc ggc tgg gac cgc atc gtg tcc ctg ctg ggc ggc 1747
 Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val Ser Leu Leu Gly Gly
 535 540 545

ttt gac tcc atc cgc gac gtc atc cgc ttc cct aag tcc ggt ggc gga 1795
 Phe Asp Ser Ile Arg Asp Val Ile Ala Phe Pro Lys Ser Gly Gly Gly
 550 555 560 565

atc gac ccc 1804
 Ile Asp Pro

<210> 282

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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5

10

15

00602039.062300

06300

Glu Trp Ala Lys Gln Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val
 340 345 350
 Gly Glu Asp Gly Glu Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp
 355 360 365
 Ala Glu Arg Ala Gly Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp
 370 375 380
 Cys Ile Phe Phe Ala Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu
 385 390 395 400
 Gly Ala Ala Arg Gly Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu
 405 410 415
 Gly Asp Trp Ala Phe Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro
 420 425 430
 Ala Ala Asp Ala Thr Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys
 435 440 445
 Trp Thr Ala Val His His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu
 450 455 460
 Asp Asn Phe Asp Thr Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp
 465 470 475 480
 Ile Val Cys Asn Gly Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His
 485 490 495
 Gln Arg Asp Val Gln Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly
 500 505 510
 Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe
 515 520 525
 Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val
 530 535 540
 Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe Pro
 545 550 555 560
 Lys Ser Gly Gly Gly Ile Asp Pro
 565

<210> 283
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 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1777)
 <223> FRXA01730

<400> 283
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 catcgactga tcaaaaccaa gcggaaggac ttccaccaac gtg ctg cgc act cat 115
 Val Leu Arg Thr His

00602339.062300

	1	5	
ctc tca ggc gag ctt cgt aaa gaa aac gca ggc cag tca gtt act ctg			163
Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly Gln Ser Val Thr Leu	10	20	
acc ggc tgg gtc aat cgt cgc cgt gac cac ggt ggc gtg atc ttc atc			211
Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly Gly Val Ile Phe Ile	25	35	
gat ctt cgc gac cgt act ggc att gcc cag gtt gtt ttc cgc aat gag			259
Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val Val Phe Arg Asn Glu	40	50	
gac gtt gct gag cgt gca cac gca ctg cgc agc gaa ttc gtc cta cgc			307
Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser Glu Phe Val Leu Arg	55	65	
gtc acc ggc gtc gtc gaa gag cgc cca gaa ggc tct caa aac cct aac			355
Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly Ser Gln Asn Pro Asn	70	80	85
ctt gca tcc ggc gac att gaa gtc agc gtc acc gaa ttt gag gta ctc			403
Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr Glu Phe Glu Val Leu	90	95	100
aac gag tcc gct cca ctt cct ttc cag atc gag gat tcc tcc tct gct			451
Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu Asp Ser Ser Ser Ala	105	110	115
ggt gaa gtc ggc gaa gag acc cgt ctg aag tac cgc tac ctg gac ctg			499
Gly Glu Val Gly Glu Glu Thr Arg Leu Lys Tyr Arg Tyr Leu Asp Leu	120	125	130
cgt cgc cca gtt cag gcg aac gcc ctg cgt ctg cgt tct gct gcc aac			547
Arg Arg Pro Val Gln Ala Asn Ala Leu Arg Leu Arg Ser Ala Ala Asn	135	140	145
aag gct gca cgc acc gtg ctg gac agc cac gat ttc acc gag atc gag			595
Lys Ala Ala Arg Thr Val Leu Asp Ser His Asp Phe Thr Glu Ile Glu	150	155	160
acc cca acc ttg act cgt tcc acc cca gaa ggc gca cgt gac ttc ctg			643
Thr Pro Thr Leu Thr Arg Ser Thr Pro Glu Gly Ala Arg Asp Phe Leu	170	175	180
gtg cca gct cgt ctg cgc cca ggc act ttc tac gca ttg cca cag tcc			691
Val Pro Ala Arg Leu Arg Pro Gly Thr Phe Tyr Ala Leu Pro Gln Ser	185	190	195
cca cag ctg ttc aag cag ctg ctg cag gtt gct ggc atg gag cgc tac			739
Pro Gln Leu Phe Lys Gln Leu Leu Gln Val Ala Gly Met Glu Arg Tyr	200	205	210
tac cag atc gct cgt tgc tac cgc gat gag gat ttc cgt gca gac cgt			787
Tyr Gln Ile Ala Arg Cys Tyr Arg Asp Glu Asp Phe Arg Ala Asp Arg	215	220	225
cag cca gag ttc acc cag ctg gac gtt gaa atg tcc ttc gtg gac cag			835
Gln Pro Glu Phe Thr Gln Leu Asp Val Glu Met Ser Phe Val Asp Gln	230	235	240
			245

005290-6522960

gat gat gtc atc gca ctg ggc gag gag atc atc tct gag gtg tgg aag 883
 Asp Asp Val Ile Ala Leu Gly Glu Glu Ile Ile Ser Glu Val Trp Lys
 250 255 260

ttg atc gga tat gag atc aag act cca atc cca cgc atg acc tac gcc 931
 Leu Ile Gly Tyr Glu Ile Lys Thr Pro Ile Pro Arg Met Thr Tyr Ala
 265 270 275

gat gca atg cgt cgc tac ggc tcc gac aag cca gac ctg cgc ttc gac 979
 Asp Ala Met Arg Arg Tyr Gly Ser Asp Lys Pro Asp Leu Arg Phe Asp
 280 285 290

atc gaa atc acc gag tgc acc gag ttc ttc cag gac acc aca ttc cgt 1027
 Ile Glu Ile Thr Glu Cys Thr Glu Phe Phe Gln Asp Thr Thr Phe Arg
 295 300 305

gtg ttc aag aac gaa tat gtc ggc gca gtt gtc atg acc ggt ggt gct 1075
 Val Phe Lys Asn Glu Tyr Val Gly Ala Val Val Met Thr Gly Gly Ala
 310 315 320 325

tcc cag cct cgc cgt cag ctc gac gca tgg cag gaa tgg gcc aag cag 1123
 Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln Glu Trp Ala Lys Gln
 330 335 340

cgc ggt gct aag gga ctt gct tac atc ctc gtt ggt gaa gac ggc gag 1171
 Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val Gly Glu Asp Gly Glu
 345 350 355

ctg tcc gga cct gtg gct aag aac atc acc gac gct gag cgc gca gga 1219
 Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp Ala Glu Arg Ala Gly
 360 365 370

atc gca gct cac gtt ggc gca cag cca ggc gac tgc atc ttc ttc gca 1267
 Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp Cys Ile Phe Phe Ala
 375 380 385

gca gga gac acc aag tct tcc ctc gca ctg ctc ggt gca gct cgt ggc 1315
 Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu Gly Ala Ala Arg Gly
 390 395 400 405

gag atc gct aag aag ctc gac ctg atc aag gaa ggc gac tgg gca ttc 1363
 Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu Gly Asp Trp Ala Phe
 410 415 420

acc tgg atc gtt gac gct cca atg ttc gag cca gca gca gac gcc acc 1411
 Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro Ala Ala Asp Ala Thr
 425 430 435

gca tcc ggt gac gtt gca ctg ggt aac tcc aag tgg acc gca gtc cac 1459
 Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys Trp Thr Ala Val His
 440 445 450

cac gcc ttc acc tca cct aag cca gag ttc ctg gac aac ttt gac acc 1507
 His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu Asp Asn Phe Asp Thr
 455 460 465

aac cca ggt gac gca ctt gct tat gca tac gac atc gtg tgc aac ggc 1555
 Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp Ile Val Cys Asn Gly
 470 475 480 485

00602379.062300

aat gaa atc ggt ggc ggt tcc atc cgt atc cac cag cgc gac gtt cag 1603
 Asn Glu Ile Gly Gly Ser Ile Arg Ile His Gln Arg Asp Val Gln
 490 495 500

gaa cgc gtt ttc gag gtt atg ggc atc acc ggt gaa gaa gca cgc gag 1651
 Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly Glu Glu Ala Arg Glu
 505 510 515

aag ttc ggc ttc ctg ctt gac gcc ttc gca ttc ggc gca cct cca cac 1699
 Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe Gly Ala Pro Pro His
 520 525 530

ggc gga atc gca ttc ggc tgg gac cgc atc gtg tcc ctg ctg ggc ggc 1747
 Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val Ser Leu Leu Gly Gly
 535 540 545

ttt gac tcc atc cgc gac gtc atc gcg ttc 1777
 Phe Asp Ser Ile Arg Asp Val Ile Ala Phe
 550 555

<210> 284
 <211> 559
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 284
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Gln Ser Val Thr Leu Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly
 20 25 30

Gly Val Ile Phe Ile Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val
 35 40 45

Val Phe Arg Asn Glu Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser
 50 55 60

Glu Phe Val Leu Arg Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly
 65 70 75 80

Ser Gln Asn Pro Asn Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr
 85 90 95

Glu Phe Glu Val Leu Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu
 100 105 110

Asp Ser Ser Ser Ala Gly Glu Val Gly Glu Glu Thr Arg Leu Lys Tyr
 115 120 125

Arg Tyr Leu Asp Leu Arg Arg Pro Val Gln Ala Asn Ala Leu Arg Leu
 130 135 140

Arg Ser Ala Ala Asn Lys Ala Ala Arg Thr Val Leu Asp Ser His Asp
 145 150 155 160

Phe Thr Glu Ile Glu Thr Pro Thr Leu Thr Arg Ser Thr Pro Glu Gly
 165 170 175

Ala Arg Asp Phe Leu Val Pro Ala Arg Leu Arg Pro Gly Thr Phe Tyr

00602839.062300

180										185										190										
Ala	Leu	Pro	Gln	Ser	Pro	Gln	Leu	Phe	Lys	Gln	Leu	Leu	Gln	Val	Ala															
		195					200								205															
Gly	Met	Glu	Arg	Tyr	Tyr	Gln	Ile	Ala	Arg	Cys	Tyr	Arg	Asp	Glu	Asp															
	210					215					220																			
Phe	Arg	Ala	Asp	Arg	Gln	Pro	Glu	Phe	Thr	Gln	Leu	Asp	Val	Glu	Met															
	225				230					235					240															
Ser	Phe	Val	Asp	Gln	Asp	Asp	Val	Ile	Ala	Leu	Gly	Glu	Glu	Ile	Ile															
			245					250						255																
Ser	Glu	Val	Trp	Lys	Leu	Ile	Gly	Tyr	Glu	Ile	Lys	Thr	Pro	Ile	Pro															
		260						265					270																	
Arg	Met	Thr	Tyr	Ala	Asp	Ala	Met	Arg	Arg	Tyr	Gly	Ser	Asp	Lys	Pro															
	275						280					285																		
Asp	Leu	Arg	Phe	Asp	Ile	Glu	Ile	Thr	Glu	Cys	Thr	Glu	Phe	Phe	Gln															
	290				295						300																			
Asp	Thr	Thr	Phe	Arg	Val	Phe	Lys	Asn	Glu	Tyr	Val	Gly	Ala	Val	Val															
	305				310					315					320															
Met	Thr	Gly	Gly	Ala	Ser	Gln	Pro	Arg	Arg	Gln	Leu	Asp	Ala	Trp	Gln															
			325					330						335																
Glu	Trp	Ala	Lys	Gln	Arg	Gly	Ala	Lys	Gly	Leu	Ala	Tyr	Ile	Leu	Val															
		340						345					350																	
Gly	Glu	Asp	Gly	Glu	Leu	Ser	Gly	Pro	Val	Ala	Lys	Asn	Ile	Thr	Asp															
		355					360					365																		
Ala	Glu	Arg	Ala	Gly	Ile	Ala	Ala	His	Val	Gly	Ala	Gln	Pro	Gly	Asp															
	370				375						380																			
Cys	Ile	Phe	Phe	Ala	Ala	Gly	Asp	Thr	Lys	Ser	Ser	Leu	Ala	Leu	Leu															
	385				390					395					400															
Gly	Ala	Ala	Arg	Gly	Glu	Ile	Ala	Lys	Lys	Leu	Asp	Leu	Ile	Lys	Glu															
			405					410					415																	
Gly	Asp	Trp	Ala	Phe	Thr	Trp	Ile	Val	Asp	Ala	Pro	Met	Phe	Glu	Pro															
		420					425						430																	
Ala	Ala	Asp	Ala	Thr	Ala	Ser	Gly	Asp	Val	Ala	Leu	Gly	Asn	Ser	Lys															
		435					440					445																		
Trp	Thr	Ala	Val	His	His	Ala	Phe	Thr	Ser	Pro	Lys	Pro	Glu	Phe	Leu															
		450				455					460																			
Asp	Asn	Phe	Asp	Thr	Asn	Pro	Gly	Asp	Ala	Leu	Ala	Tyr	Ala	Tyr	Asp															
	465				470					475					480															
Ile	Val	Cys	Asn	Gly	Asn	Glu	Ile	Gly	Gly	Gly	Ser	Ile	Arg	Ile	His															
			485					490					495																	
Gln	Arg	Asp	Val	Gln	Glu	Arg	Val	Phe	Glu	Val	Met	Gly	Ile	Thr	Gly															
			500					505					510																	

00602639 062300

Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe
515 520 525

Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val
530 535 540

Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe
545 550 555

<210> 285

<211> 1503

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1480)

<223> RXA00314

<400> 285

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tgaaaccttg agtggttcgca cacaggttag actaggggac gtg act cta cgc atc 115
Val Thr Leu Arg Ile
1 5

ttt gac acc ggt acc cgt acg ctt cga gat ttt aaa cct gtt caa cca 163
Phe Asp Thr Gly Thr Arg Thr Leu Arg Asp Phe Lys Pro Val Gln Pro
10 15 20

ggt cat gcc tcg gtg tac ctg tgt ggt gcc acc ccg caa tct tca ccc 211
Gly His Ala Ser Val Tyr Leu Cys Gly Ala Thr Pro Gln Ser Ser Pro
25 30 35

cac att gga cat gtt cgt tca gca gta cgc ttt gat att ttg cgc cgc 259
His Ile Gly His Val Arg Ser Ala Val Ala Phe Asp Ile Leu Arg Arg
40 45 50

tgg ctc atg gct aag gga ctt gat gtg gca ttt gtt cgc aat gtc act 307
Trp Leu Met Ala Lys Gly Leu Asp Val Ala Phe Val Arg Asn Val Thr
55 60 65

gat atc gat gac aag att ctc acc aag gca tct gaa aat ggt cgc cct 355
Asp Ile Asp Asp Lys Ile Leu Thr Lys Ala Ser Glu Asn Gly Arg Pro
70 75 80 85

tgg tgg gaa tgg gtg tcc acc tat gaa cgt gaa ttc acc tgg acg tac 403
Trp Trp Glu Trp Val Ser Thr Tyr Glu Arg Glu Phe Thr Trp Thr Tyr
90 95 100

aac acg ttg ggt gtg ctt cct cca tca acg gag cct cgt gca aca ggc 451
Asn Thr Leu Gly Val Leu Pro Pro Ser Thr Glu Pro Arg Ala Thr Gly
105 110 115

cac gtc act cag atg att aag tac atg cag cgc ttg att gat aac ggc 499
His Val Thr Gln Met Ile Lys Tyr Met Gln Arg Leu Ile Asp Asn Gly
120 125 130

ttt gct tac gcc gtt gat ggc tct gtg tac ttt gat gtc gca ggc tgg 547

006290-062900

Phe Ala Tyr Ala Val Asp Gly Ser Val Tyr Phe Asp Val Ala Ala Trp	
135 140 145	
tcc aag gct gaa gga tct gac tat ggt tct ttg tcc gga aac cgt gtt	595
Ser Lys Ala Glu Gly Ser Asp Tyr Gly Ser Leu Ser Gly Asn Arg Val	
150 155 160 165	
gaa gat atg gag cag ggc gag ccc gat aac ttt ggt aag cgg ggg cca	643
Glu Asp Met Glu Gln Gly Glu Pro Asp Asn Phe Gly Lys Arg Gly Pro	
170 175 180	
cag gac ttt gct ctg tgg aag gct gcc aaa ccg ggt gag ccg tca tgg	691
Gln Asp Phe Ala Leu Trp Lys Ala Ala Lys Pro Gly Glu Pro Ser Trp	
185 190 195	
cca acc cct tgg gga gac ggc cgg ccg ggt tgg cat ttg gaa tgc tct	739
Pro Thr Pro Trp Gly Asp Gly Arg Pro Gly Trp His Leu Glu Cys Ser	
200 205 210	
gcc atg gcc acc tac tat ttg ggt gag caa ttt gat att cac tgt ggt	787
Ala Met Ala Thr Tyr Tyr Leu Gly Glu Gln Phe Asp Ile His Cys Gly	
215 220 225	
ggt ttg gat ctg caa ttt cca cac cat gaa aat gaa att gcc cag gca	835
Gly Leu Asp Leu Gln Phe Pro His His Glu Asn Glu Ile Ala Gln Ala	
230 235 240 245	
cat gcg gct ggc gat aaa ttt gcc aac tac tgg atg cac aat cac tgg	883
His Ala Ala Gly Asp Lys Phe Ala Asn Tyr Trp Met His Asn His Trp	
250 255 260	
gta aca atg gcc ggc gag aaa atg tcc aag tct ttg ggc aat gtt ttg	931
Val Thr Met Ala Gly Glu Lys Met Ser Lys Ser Leu Glu Asn Val Leu	
265 270 275	
gct gtg ccg gaa atg cta aag cag gtt cgt cct gtc gag ctt cgt tat	979
Ala Val Pro Glu Met Leu Lys Gln Val Arg Pro Val Glu Leu Arg Tyr	
280 285 290	
tac ctt ggg tct gcc cat tac cgt tcc gtc ctt gag tat tcc gag agc	1027
Tyr Leu Gly Ser Ala His Tyr Arg Ser Val Leu Glu Tyr Ser Glu Ser	
295 300 305	
gct ttg agt gaa gct gcg gtg ggt tac cgt cgc att gag tet ttc ctt	1075
Ala Leu Ser Glu Ala Ala Val Gly Tyr Arg Arg Ile Glu Ser Phe Leu	
310 315 320 325	
gag cgt gtg ggg gat gtt gag gta ggc gag tgg acg cca ggt ttt gaa	1123
Glu Arg Val Gly Asp Val Glu Val Gly Glu Trp Thr Pro Gly Phe Glu	
330 335 340	
gtt gcg atg gat gag gat att gca gtt cct aag gct ttg gct gaa atc	1171
Val Ala Met Asp Glu Asp Ile Ala Val Pro Lys Ala Leu Ala Glu Ile	
345 350 355	
cat aac gct gtc cgc gag ggc aat gct gcc ttg gat aag ggt gat cgt	1219
His Asn Ala Val Arg Glu Gly Asn Ala Ala Leu Asp Lys Gly Asp Arg	
360 365 370	
gag gca gcg gag aag ctt gct tcc tgc gtt cgt gcg atg act ggc gtt	1267
Glu Ala Ala Glu Lys Leu Ala Ser Ser Val Arg Ala Met Thr Gly Val	

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375	380	385	
ttg ggc ttc gac ccc gtt gaa tgg ggt tca gat gca ggc gct gat ggc			1315
Leu Gly Phe Asp Pro Val Glu Trp Gly Ser Asp Ala Gly Ala Asp Gly			
390	395	400	405
aag gca gat aag gcg ctt gat gtg ctg att tct tcg gag ctt gag cgt			1363
Lys Ala Asp Lys Ala Leu Asp Val Leu Ile Ser Ser Glu Leu Glu Arg			
410	415		420
cgt gca act gct cgt gct gag aag aat tgg gcg gtt gct gat gag gtt			1411
Arg Ala Thr Ala Arg Ala Glu Lys Asn Trp Ala Val Ala Asp Glu Val			
425	430		435
cga gat cgt ctt gcc gat gct ggt att gag gtt gtg gat acc gca gat			1459
Arg Asp Arg Leu Ala Asp Ala Gly Ile Glu Val Val Asp Thr Ala Asp			
440	445		450
ggc gct aca tgg aaa ttg cag taattacaga cacttttaag gag			1503
Gly Ala Thr Trp Lys Leu Gln			
455	460		
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<400> 286			
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Lys Pro Val Gln Pro Gly His Ala Ser Val Tyr Leu Cys Gly Ala Thr			
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Pro Gln Ser Ser Pro His Ile Gly His Val Arg Ser Ala Val Ala Phe			
35	40		45
Asp Ile Leu Arg Arg Trp Leu Met Ala Lys Gly Leu Asp Val Ala Phe			
50	55		60
Val Arg Asn Val Thr Asp Ile Asp Asp Lys Ile Leu Thr Lys Ala Ser			
65	70		75
Glu Asn Gly Arg Pro Trp Trp Glu Trp Val Ser Thr Tyr Glu Arg Glu			
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Phe Thr Trp Thr Tyr Asn Thr Leu Gly Val Leu Pro Pro Ser Thr Glu			
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Pro Arg Ala Thr Gly His Val Thr Gln Met Ile Lys Tyr Met Gln Arg			
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Leu Ile Asp Asn Gly Phe Ala Tyr Ala Val Asp Gly Ser Val Tyr Phe			
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Asp Val Ala Ala Trp Ser Lys Ala Glu Gly Ser Asp Tyr Gly Ser Leu			
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Ser Gly Asn Arg Val Glu Asp Met Glu Gln Gly Glu Pro Asp Asn Phe			
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 Gly Glu Pro Ser Trp Pro Thr Pro Trp Gly Asp Gly Arg Pro Gly Trp
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 His Leu Glu Cys Ser Ala Met Ala Thr Tyr Tyr Leu Gly Glu Gln Phe
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 Asp Ile His Cys Gly Gly Leu Asp Leu Gln Phe Pro His His Glu Asn
 225 230 235 240
 Glu Ile Ala Gln Ala His Ala Ala Gly Asp Lys Phe Ala Asn Tyr Trp
 245 250 255
 Met His Asn His Trp Val Thr Met Ala Gly Glu Lys Met Ser Lys Ser
 260 265 270
 Leu Gly Asn Val Leu Ala Val Pro Glu Met Leu Lys Gln Val Arg Pro
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 Val Glu Leu Arg Tyr Tyr Leu Gly Ser Ala His Tyr Arg Ser Val Leu
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 Glu Tyr Ser Glu Ser Ala Leu Ser Glu Ala Ala Val Gly Tyr Arg Arg
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 Ile Glu Ser Phe Leu Glu Arg Val Gly Asp Val Glu Val Gly Glu Trp
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 Thr Pro Gly Phe Glu Val Ala Met Asp Glu Asp Ile Ala Val Pro Lys
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 Ala Leu Ala Glu Ile His Asn Ala Val Arg Glu Gly Asn Ala Ala Leu
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 Asp Lys Gly Asp Arg Glu Ala Ala Glu Lys Leu Ala Ser Ser Val Arg
 370 375 380
 Ala Met Thr Gly Val Leu Gly Phe Asp Pro Val Glu Trp Gly Ser Asp
 385 390 395 400
 Ala Gly Ala Asp Gly Lys Ala Asp Lys Ala Leu Asp Val Leu Ile Ser
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Thr Pro Glu Val Pro Ala Leu Ala ggc Thr Pro Val Pro Leu Glu Leu																				
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Phe Asp Thr Ala Asp Gln Glu Val Arg Leu Val Glu Thr Pro Pro Ala																				
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Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr Leu Ala Phe Asp Leu																				
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Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp Val His Tyr Val Gln																				
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aac atc acc gat gtc gat gac cct ctg ttt gaa cgc gca gcc cgc gac															403					
Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu Arg Ala Ala Arg Asp																				
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Gly Val Asp Trp Arg Asp Leu Gly Thr Ser Gln Ile Asn Leu Phe Arg																				
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Ser Asp Met Glu Ala Leu Ser Ile Ile Pro Pro Lys Asp Tyr Ile Gly																				
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Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met Val Lys Thr Leu Leu																				
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Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly Tyr Glu Ser Asn Tyr																				
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Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu Arg Gly Gly Asp Pro																				
														185						
gag cgt ccc gcc aag aaa aac ccc atg gat gcc ctc ctg tgg cgc gca															733					

Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala Leu Leu Trp Arg Ala
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 gcc cgc gaa ggt gaa cca agc tgg gaa tcc cca ttc gcc gca ggt cgt 787
 Ala Arg Glu Gly Glu Pro Ser Trp Glu Ser Pro Phe Gly Ala Gly Arg
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 cct gcc tgg cac atc gag tgt tca gca atc gct acc aac cgc cta gga 835
 Pro Gly Trp His Ile Glu Cys Ser Ala Ile Ala Thr Asn Arg Leu Gly
 230 235 240 245
 cac agc ttt gat atc caa ggt gcc gcc tct gac ctg atc ttc cct cac 883
 His Ser Phe Asp Ile Gln Gly Gly Gly Ser Asp Leu Ile Phe Pro His
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 His Glu Phe Ser Ala Ala His Ala Ala His Gly Val Glu Arg
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 Met Ala Lys His Tyr Val His Ala Gly Met Ile Ser Gln Asp Gly Val
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 Lys Met Ser Lys Ser Leu Gly Asn Leu Glu Phe Val Ser Arg Leu Thr
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 gct gca gcc cac gag ccc gcc gcg atc cgc ctc ggt gtt ttt gcc aac 1075
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 cat tac cgt gcc aac cgt gat tgg aac gca gag agc ctc gcc acc gca 1123
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 Glu Gln Arg Leu Ala Thr Trp Arg Glu Ala Ala Arg Ala Ala Thr Asn
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 Ala Asp Leu Asp Thr Pro Gly Ala Leu Ala Ala Val Asp Asn Trp Ala
 375 380 385
 gcg ggt atc gac acc acg acc gat tca aaa gag ttc acc gag gta gga 1315
 Ala Gly Ile Asp Thr Thr Asp Ser Lys Glu Phe Thr Glu Val Gly
 390 395 400 405
 aac atc gtg gtc gca gcc att gat gcc ctc ctg gcc gtg cag ctc 1360
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<213> Corynebacterium glutamicum

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35 40 45Gly Ile Thr Pro Tyr Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr
50 55 60Leu Ala Phe Asp Leu Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp
65 70 75 80Val His Tyr Val Gln Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu
85 90 95Arg Ala Ala Arg Asp Gly Val Asp Trp Arg Asp Leu Gly Thr Ser Gln
100 105 110Ile Asn Leu Phe Arg Ser Asp Met Glu Ala Leu Ser Ile Ile Pro Pro
115 120 125Lys Asp Tyr Ile Gly Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met
130 135 140Val Lys Thr Leu Leu Asp Glu Gly Ala Ala Tyr Ile Val Glu Asp Ala
145 150 155 160Glu Tyr Pro Asp Val Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly
165 170 175Tyr Glu Ser Asn Tyr Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu
180 185 190Arg Gly Gly Asp Pro Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala
195 200 205Leu Leu Trp Arg Ala Ala Arg Glu Gly Glu Pro Ser Trp Glu Ser Pro
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245 250 255Leu Ile Phe Pro His His Glu Phe Ser Ala Ala His Ala Glu Ala Ala
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Arg	Phe	Cys	Pro	Ser	Pro	Thr	Gly	Thr	Pro	His	Val	Gly	Leu	Val	Arg			
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Thr	Ala	Leu	Phe	Asn	Trp	Ala	Tyr	Ala	Arg	His	Thr	Gly	Gly	Lys	Leu			
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Glu	Gly	Val	Glu	Lys	Gly	Gly	Pro	His	Glu	Pro	Tyr	Arg	Gln	Ser	Gln			
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cgc	aag	gac	atc	tat	cag	gat	gtg	ttg	aag	cag	ctt	atc	gac	gcc	ggt		336	
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Val	Asp	Asp	Ala	Leu	Met	Glu	Val	Thr	His	Val	Leu	Arg	Gly	Glu	Asp																	
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Val	Met	Gly	Glu	Gly	Asn	Lys	Lys	Leu	Ser	Lys	Arg	Asp	Pro	Gln	Ser																	
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Ser	Leu	Phe	Asn	His	Arg	Asp	Asn	Gly	Ile	Ile	Pro	Glu	Gly	Met	Leu																	
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gat	cac	atc	cga	ctt	ctg	gag	cct	aag	gat	ttc	gag	gct	cgc	ctg	cgc																1056	
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aag ttt gcc att gct gcg gag ctg gtt cag acc cgc atc aag gtg ctc 1152
Lys Phe Ala Ile Ala Ala Glu Leu Val Gln Thr Arg Ile Lys Val Leu
370 375 380

agc gag gcg tgg gat ctg ctg aag ttc ctg gtc acc gct gac gaa gat 1200
Ser Glu Ala Trp Asp Leu Lys Phe Leu Val Thr Ala Asp Glu Asp
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Leu Val Phe Asn Glu Lys Ala Ala Lys Lys Asn Leu Lys Glu Thr Ala
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gtt gag cct ctc aac gcc ggt atc gca gcg ctg gag gca gtg gag gag 1296
Val Glu Pro Leu Asn Ala Gly Ile Ala Ala Leu Glu Ala Val Glu Glu
420 425 430

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Trp Thr Thr Pro Asn Ile Glu Ala Ala Leu Asn Lys Ala Leu Ile Glu
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atc tcc ggc gag gct gta tcc cca cca ctg ttt gag tcc atg gag ctt 1440
Ile Ser Gly Glu Ala Val Ser Pro Pro Leu Phe Glu Ser Met Glu Leu
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Leu Gly Lys Glu Ser Thr Leu Val Arg Leu Lys Val Thr Arg Glu Gln
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Thr Ala Leu Phe Asn Trp Ala Tyr Ala Arg His Thr Gly Gly Lys Leu
35 40 45

Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser
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Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp

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Glu	Val	Tyr	Pro	Ala	Tyr	Ser	Thr 120	Ala	Glu	Glu	Val	Glu	Glu	Arg	His
Lys	Ala	Ala	Gly	Arg	Asp	Pro 135	Lys	Leu	Gly	Tyr	Asp 140	Asn	Phe	Asp	Arg
Asp	Leu	Thr	Glu	Glu	Gln	Val	Ala	Ala	Phe	Glu 155	Ala	Glu	Gly	Arg	Lys 160
Pro	Val	Trp	Arg	Leu 165	Arg	Met	Pro	Glu	Gln 170	Asp	Trp	Lys	Trp	Thr	Asp 175
Leu	Val	Arg	Gly 180	Glu	Val	Glu	Phe	Lys 185	Ser	Phe	Thr	Gln	Pro 190	Asp	Phe
Val	Val	Ala	Arg	Ser	Asn	Gly	Glu 200	Pro	Leu	Tyr	Thr	Leu 205	Val	Asn	Pro
Val	Asp	Asp	Ala	Leu	Met	Glu 215	Val	Thr	His	Val	Leu 220	Arg	Gly	Glu	Asp
Leu	Leu	Pro	Ser	Thr 230	Pro	Arg	Gln	Leu	Ala	Leu 235	Tyr	Glu	Ala	Leu	Lys 240
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Ser	Leu	Phe	Asn	His	Arg	Asp 280	Asn	Gly	Ile	Ile	Pro	Glu 285	Gly	Met	Leu
Asn	Tyr	Leu	Ala	Leu	Leu	Gly 295	Trp	Ser	Leu	Ser	Ala 300	Asp	Gln	Asp	Ile
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Gly	Asn	Pro	Ala	Arg 325	Phe	Asp	Gln	Lys	Lys 330	Leu	Glu	Ala	Ile	Asn 335	Ala
Asp	His	Ile	Arg	Leu 340	Leu	Glu	Pro	Lys 345	Asp	Phe	Glu	Ala	Arg 350	Leu	Arg
Ala	Tyr	Met	Thr	Glu 355	Tyr	Thr	Glu 360	Phe	Pro	Ala	Asp	Tyr 365	Pro	Ala	Glu
Lys	Phe	Ala	Ile	Ala	Ala	Glu 375	Leu	Val	Gln	Thr	Arg 380	Ile	Lys	Val	Leu
Ser	Glu	Ala	Trp	Asp 385	Leu	Leu	Lys	Phe	Leu	Val 395	Thr	Ala	Asp	Glu	Asp 400

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 Val Glu Pro Leu Asn Ala Gly Ile Ala Ala Leu Glu Ala Val Glu Glu
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 Asp Leu Gly Leu Lys Pro Arg Val Ala Phe Gly Ala Leu Arg Ile Gly
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 Met Ala Gly Arg Tyr
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 Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala
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 Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp
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 aaa cta gac acc tac gaa tgt tat tgc tcg cgc cgg gac atc caa gaa 403

002290.002290

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 Arg Gly Leu Lys Glu Glu Arg Val Glu Lys Arg Ala Thr Leu Ala
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 gcg caa aac cgg cac ccc gcc att cgc ctg cgc gcg cag gta acc tgc 547
 Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg Ala Gln Val Thr Ser
 135 140 145
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 Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln Thr Gly Pro Val Asp
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 Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro Gly Trp Ala Tyr Asn
 170 175 180
 tta act gtc gtc gtc gac gat gcc tac caa gcc gtt gac cag gta gtc 691
 Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly Val Asp Gln Val Val
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 cgc gcc gac gac cta ctc gaa ttc gcc gcg cgc caa gct acc ttg 736
 Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg Gln Ala Thr Leu
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 <212> PRT
 <213> Corynebacterium glutamicum
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 Asn Leu Arg Thr Ala Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly
 20 25 30
 Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Ser
 35 40 45
 Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu
 50 55 60
 Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg Tyr Asp Ala Tyr
 65 70 75 80
 Arg Ala Ala Leu Glu Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg
 85 90 95
 Arg Asp Ile Gln Glu Ala Ser Arg Ala Pro His Val Ala Pro Gly Val
 100 105 110
 Tyr Pro Gly Thr Cys Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys
 115 120 125

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Arg Ala Thr Leu Ala Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg
130 135 140

Ala Gln Val Thr Ser Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln
145 150 155 160

Thr Gly Pro Val Asp Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro
165 170 175

Gly Trp Ala Tyr Asn Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly
180 185 190

Val Asp Gln Val Val Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg
195 200 205

Gln Ala Thr Leu
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<210> 293

<211> 328

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(328)

<223> FRXA00458

<400> 293

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atccgaaaca tggcggaag tgaacatcta atctagaaac atg gca gga cga tac 115
Met Ala Gly Arg Tyr
1 5

gca cca tca cca agc ggc gac ctt cac ttt ggc aac ctc cgc aca gca 163
Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala
10 15 20

ctg ctg gcc tgg ctg ttc gcg cgc tcc gaa gga aaa aaa ttc ctc atg 211
Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met
25 30 35

cgg gtc gaa gac atc gat gaa caa cgc tca ttc aag gaa tcc gcc gaa 259
Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe Lys Glu Ser Ala Glu
40 45 50

agc caa ctc gca gac cta tcc gcc ctg ggt ctc gat tgg gat ggc gac 307
Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp
55 60 65

gtc ctc tac caa tcc aca cgc 328
Val Leu Tyr Gln Ser Thr Arg
70 75

<210> 294

<211> 76

<212> PRT

00602839 062300

<213> *Corynebacterium glutamicum*

<400> 294

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Asn Leu Arg Thr Ala Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly
 20 25 30

Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe
 35 40 45

Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu
 50 55 60

Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg
 65 70 75

<210> 295

<211> 1506

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1483)

<223> RXA00069

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acgggtattt ttctattcga cgtggaggag agcatccgac gtg gct cag caa tcg 115
 Val Ala Gln Gln Ser
 1 5

atc atc gac acc gtg gtt aac ctg tgt aaa cga cgt gga ctg gtg tac 163
 Ile Ile Asp Thr Val Val Asn Leu Cys Lys Arg Arg Gly Leu Val Tyr
 10 15 20

ccc tgt ggt gag atc tac gcc ggt acc cgc tct gcg tgg gac tac gcc 211
 Pro Cys Gly Glu Ile Tyr Gly Gly Thr Arg Ser Ala Trp Asp Tyr Gly
 25 30 35

cgc ctg ggt gtg gag ctg aag gaa aac atc aag cgc cag tgg tgg cgt 259
 Pro Leu Gly Val Glu Leu Lys Glu Asn Ile Lys Arg Gln Trp Trp Arg
 40 45 50

tct atg gtt act tcc cgc cca gat gtt gtg ggt gtt gat act tct gtc 307
 Ser Met Val Thr Ser Arg Pro Asp Val Val Gly Val Asp Thr Ser Val
 55 60 65

atc ett cct cgc cag gtg tgg gta act tcc gcc cac gtt gag gtc ttc 355
 Ile Leu Pro Arg Gln Val Trp Val Thr Ser Gly His Val Glu Val Phe
 70 75 80 85

act gac cca ctg gtt gag tct ttg aac acc cac aag cgt tac cgt gcg 403
 Thr Asp Pro Leu Val Glu Ser Leu Asn Thr His Lys Arg Tyr Arg Ala
 90 95 100

gac cac ctg ctg gag cag tac gaa gag aag cat ggt cac cca cct gta 451

002290 002290 002290

Asp His Leu Leu Glu Gln Tyr Glu Glu Lys His Gly His Pro Pro Val
 105 110 115
 aac ggc ttg gct gac atc aac gat cca gag acc ggc cag cca ggt aac 499
 Asn Gly Leu Ala Asp Ile Asn Asp Pro Glu Thr Gly Gln Pro Gly Asn
 120 125 130
 tgg act gag cct aag gcg ttc tct ggt ctt ctg aag act ttc ttg gga 547
 Trp Thr Glu Pro Lys Ala Phe Ser Gly Leu Lys Thr Phe Leu Gly
 135 140 145
 cct gtg gac gac gaa gag ggt ctg cac tac ctg cgc cct gaa act gct 595
 Pro Val Asp Asp Glu Glu Gly Leu His Tyr Leu Arg Pro Glu Thr Ala
 150 155 160 165
 cag ggt atc ttc gtg aac ttc aag aac gtg atg aac act tca cgt atg 643
 Gln Gly Ile Phe Val Asn Phe Lys Asn Val Met Asn Thr Ser Arg Met
 170 175 180
 aag cca cct ttc ggt atc gcg aac atc ggt aag tct ttc cgt aac gag 691
 Lys Pro Pro Phe Gly Ile Ala Asn Ile Gly Lys Ser Phe Arg Asn Glu
 185 190 195
 atc acc cca ggt aac ttc att ttc cgt act cgt gag ttc gag cag atg 739
 Ile Thr Pro Gly Asn Phe Ile Phe Arg Thr Arg Glu Phe Glu Gln Met
 200 205 210
 gag atg gag ttc ttc gtc aag cct ggt gag gac gaa gag tgg cac cag 787
 Glu Met Glu Phe Phe Val Lys Pro Gly Glu Asp Glu Glu Trp His Gln
 215 220 225
 cac tgg att gat act cgc ctg cag tgg tac atc aac ctg ggc att aag 835
 His Trp Ile Asp Thr Arg Leu Gln Trp Tyr Ile Asn Leu Gly Ile Lys
 230 235 240 245
 cct gag aac ctg cgt ctg tac gag cac cct cag gag aag ctg tct cac 883
 Pro Glu Asn Leu Arg Leu Tyr Glu His Pro Gln Glu Lys Leu Ser His
 250 255 260
 tac tcc aag cgc act gtt gat att gag tac gca ttc aac ttt gct aac 931
 Tyr Ser Lys Arg Thr Val Asp Ile Glu Tyr Ala Phe Asn Phe Ala Asn
 265 270 275
 acc aag tgg ggc gag ttg gag ggg atc gcg aac cgt act gat tac gat 979
 Thr Lys Trp Gly Glu Leu Glu Gly Ile Ala Asn Arg Thr Asp Tyr Asp
 280 285 290
 ctt cgc gtg cac tct gag ggc tct ggt gag gac ctg tca ttc ttc gat 1027
 Leu Arg Val His Ser Glu Gly Ser Gly Glu Asp Leu Ser Phe Phe Asp
 295 300 305
 cag gag acc aat gag cgt tgg att cct ttc gta atc gag cct gct gca 1075
 Gln Glu Thr Asn Glu Arg Trp Ile Pro Phe Val Ile Glu Pro Ala Ala
 310 315 320 325
 ggt ctt ggt cgc gca atg atg atg ttc ctg atg gat gct tat cac gag 1123
 Gly Leu Gly Arg Ala Met Met Met Phe Leu Met Asp Ala Tyr His Glu
 330 335 340
 gac gaa gca cca aac tca aag ggt ggc gtc gat aag cgt gtt gtt ctg 1171
 Asp Glu Ala Pro Asn Ser Lys Gly Gly Val Asp Lys Arg Val Val Leu

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0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

Gly 130	Gln	Pro	Gly	Asn	Trp	Thr	Glu	Pro	Lys	Ala	Phe	Ser	Gly	Leu	Leu
Lys 145	Thr	Phe	Leu	Gly	Pro	Val	Asp	Asp	Glu	Glu	Gly	Leu	His	Tyr	Leu
Arg	Pro	Glu	Thr	Ala	Gln	Gly	Ile	Phe	Val	Asn	Phe	Lys	Asn	Val	Met
Asn	Thr	Ser	Arg	Met	Lys	Pro	Pro	Phe	Gly	Ile	Ala	Asn	Ile	Gly	Lys
Ser	Phe	Arg	Asn	Glu	Ile	Thr	Pro	Gly	Asn	Phe	Ile	Phe	Arg	Thr	Arg
Glu	Phe	Glu	Gln	Met	Glu	Met	Glu	Phe	Phe	Val	Lys	Pro	Gly	Glu	Asp
Glu	Glu	Trp	His	Gln	His	Trp	Ile	Asp	Thr	Arg	Leu	Gln	Trp	Tyr	Ile
Asn	Leu	Gly	Ile	Lys	Pro	Glu	Asn	Leu	Arg	Leu	Tyr	Glu	His	Pro	Gln
Glu	Lys	Leu	Ser	His	Tyr	Ser	Lys	Arg	Thr	Val	Asp	Ile	Glu	Tyr	Ala
Phe	Asn	Phe	Ala	Asn	Thr	Lys	Trp	Gly	Glu	Leu	Glu	Gly	Ile	Ala	Asn
Arg	Thr	Asp	Tyr	Asp	Leu	Arg	Val	His	Ser	Glu	Gly	Ser	Gly	Glu	Asp
Leu	Ser	Phe	Phe	Asp	Gln	Glu	Thr	Asn	Glu	Arg	Trp	Ile	Pro	Phe	Val
Ile	Glu	Pro	Ala	Ala	Gly	Leu	Gly	Arg	Ala	Met	Met	Met	Phe	Leu	Met
Asp	Ala	Tyr	His	Glu	Asp	Glu	Ala	Pro	Asn	Ser	Lys	Gly	Gly	Val	Asp
Lys	Arg	Val	Val	Leu	Lys	Leu	Asp	Arg	Arg	Leu	Ala	Pro	Val	Lys	Val
Ala	Val	Leu	Pro	Leu	Ser	Lys	Lys	Asp	Thr	Leu	Thr	Pro	Leu	Ala	Glu
Lys	Leu	Ala	Ala	Glu	Leu	Arg	Glu	Phe	Trp	Asn	Val	Asp	Tyr	Asp	Thr
Ser	Gly	Ala	Ile	Gly	Arg	Arg	Tyr	Arg	Arg	Gln	Asp	Glu	Ile	Gly	Thr
Pro	Phe	Cys	Val	Thr	Val	Asp	Phe	Asp	Ser	Leu	Glu	Asp	Asn	Ala	Val
Thr	Val	Arg	Glu	Arg	Asp	Thr	Met	Glu	Gln	Val	Arg	Val	Pro	Leu	Asp
Glu	Leu	Gln	Gly	Tyr	Leu	Ala	Gln	Arg	Leu	Ile	Gly	Cys			

450

455

460

<210> 297
 <211> 1410
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1387)
 <223> RXA01852

<400> 297
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 agttccgtac tactttcttcg aataggtatc gttaataatc gtg agt caa aac aag 115
 Val Ser Gln Asn Lys
 1 5
 tcc aag tct gaa aag ctt cag tca ttt gct gca ccc aag ggt gtt cct 163
 Ser Lys Ser Glu Lys Leu Gln Ser Phe Ala Ala Pro Lys Gly Val Pro
 10 15 20
 gat tac gcc cca cca aaa tct gca gcg ttt tta gca gtc cgt gat gcc 211
 Asp Tyr Ala Pro Lys Ser Ala Ala Phe Leu Ala Val Arg Asp Ala
 25 30 35
 ttt gtt aat caa gca cat aag gcc ggg ttt gag cat att gag ctg cag 259
 Phe Val Asn Gln Ala His Lys Ala Gly Phe Glu His Ile Glu Leu Pro
 40 45 50
 atc ttt gaa gac acc gcc ttg ttt gcg cgt ggt gtt ggt gag tcc act 307
 Ile Phe Glu Asp Thr Gly Leu Phe Ala Arg Gly Val Gly Glu Ser Thr
 55 60 65
 gac gta gtg agc aag gaa atg tac acc ttc gct gat cgt ggc gag cgc 355
 Asp Val Val Ser Lys Glu Met Tyr Thr Phe Ala Asp Arg Gly Glu Arg
 70 75 80 85
 tct gtc acg ctg cgc cca gaa ggc act gca ggc gtg atg cgt gca gtt 403
 Ser Val Thr Leu Arg Pro Glu Gly Thr Ala Gly Val Met Arg Ala Val
 90 95 100
 att gaa cac agc ctg gac cgt gga cag ctt ccc gta aag ctg aac tac 451
 Ile Glu His Ser Leu Asp Arg Gly Gln Leu Pro Val Lys Leu Asn Tyr
 105 110 115
 gcc gga cca ttc ttc cgt tat gag cgt cct cag gca ggg cgt tac cgt 499
 Ala Gly Pro Phe Phe Arg Tyr Glu Arg Pro Gln Ala Gly Arg Tyr Arg
 120 125 130
 cag ctt cag caa gta ggc gta gag gca att ggt gtg gat gat cca gcg 547
 Gln Leu Gln Gln Val Gly Val Glu Ala Ile Gly Val Asp Asp Pro Ala
 135 140 145
 ctt gat gcg gag atc att gcg ctt gct gat cgt tct tac cgc agc ttg 595
 Leu Asp Ala Glu Ile Ile Ala Leu Ala Asp Arg Ser Tyr Arg Ser Leu
 150 155 160 165
 ggg ctg cag gat ttc cgt ctg gag ctc acc agc ttg ggt gat cgt cac 643

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Gly Leu Gln Asp Phe Arg Leu Glu Leu Thr Ser Leu Gly Asp Arg His	170	175	180	
tgc cgt ccc gag tat cgt cag aag ctg cag gat ttc ttg ttt gca ctt	691			
Cys Arg Pro Glu Tyr Arg Gln Lys Leu Gln Asp Phe Leu Phe Ala Leu	185	190	195	
cct ttg gat gag gaa acc cgc aag cgc gca gag atc aac cca ctt cgg	739			
Pro Leu Asp Glu Glu Thr Arg Lys Arg Ala Glu Ile Asn Pro Leu Arg	200	205	210	
gtg ttg gat gat aag cgt cct gaa gtc caa gag atg act gcg gat gca	787			
Val Leu Asp Asp Lys Arg Pro Glu Val Gln Glu Met Thr Ala Asp Ala	215	220	225	
cca ttg atg ctg gat cac ctt gat gca gag tgc cgt gag cac ttt gaa	835			
Pro Leu Met Leu Asp His Leu Asp Ala Glu Cys Arg Glu His Phe Glu	230	235	240	245
aca gtg act ggt ttg ctg gat gac atg ggt gtt cca tat gtg att aac	883			
Thr Val Thr Gly Leu Leu Asp Asp Met Gly Val Pro Tyr Val Ile Asn	250	255	260	
cca cgc atg gtt cgt ggt ttg gat tac tac acc aag act tgt ttt gag	931			
Pro Arg Met Val Arg Gly Leu Asp Tyr Tyr Thr Lys Thr Cys Phe Glu	265	270	275	
ttc gtt cac gat gcc ctg gcc gca cag tct gcc att ggt gcc gcc gga	979			
Phe Val His Asp Gly Leu Gly Ala Gln Ser Gly Ile Gly Gly Gly Gly	280	285	290	
cgc tac gac ggt ctg atg gca cag ctt gcc gga cag gat ctg tct gcc	1027			
Arg Tyr Asp Gly Leu Met Ala Gln Leu Gly Gly Gln Asp Leu Ser Gly	295	300	305	
atc gcc tat gcc ctg ggt gtg gat cgc acc atg ttg gct ctg gaa gct	1075			
Ile Gly Tyr Gly Leu Gly Val Asp Arg Thr Met Leu Ala Leu Glu Ala	310	315	320	325
gaa ggt gtg act gtt ggt gct gag cgt cgc gtt gat gtg tac gcc gtt	1123			
Glu Gly Val Thr Val Gly Ala Glu Arg Val Asp Val Tyr Gly Val	330	335	340	
cca ctg gcc aag gat gct aag aag gct ctt gct gga atc gtg aac acg	1171			
Pro Leu Gly Lys Asp Ala Lys Lys Ala Leu Ala Gly Ile Val Asn Thr	345	350	355	
ctg cgc gct gcg ggt att tcc acc gat atg tct tac gcc gac cgt gcc	1219			
Leu Arg Ala Ala Gly Ile Ser Thr Asp Met Ser Tyr Gly Asp Arg Gly	360	365	370	
ctg aag ggt gcc atg aag gcc gct gac cgc tcc aac gcg ttg tac acc	1267			
Leu Lys Gly Ala Met Lys Gly Ala Asp Arg Ser Asn Ala Leu Tyr Thr	375	380	385	
ttg gtg ctg gcc gag cag gag ctg gag aac aac acc atc gcg gtg aag	1315			
Leu Val Leu Gly Glu Gln Glu Leu Glu Asn Asn Thr Ile Ala Val Lys	390	395	400	405
gat atg cgt gcg cat gag cag cac gat gtc gca ttg gac gag gtt gtg	1363			
Asp Met Arg Ala His Glu Gln His Asp Val Ala Leu Asp Glu Val Val				

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410

415

420

gcc ttt ttg cag ggg aaa ctt att taaataattc ataagtaaaa aac
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 425

1410

<210> 298

<211> 429

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 298

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 20 25 30

Ala Val Arg Asp Ala Phe Val Asn Gln Ala His Lys Ala Gly Phe Glu
 35 40 45

His Ile Glu Leu Pro Ile Phe Glu Asp Thr Gly Leu Phe Ala Arg Gly
 50 55 60

Val Gly Glu Ser Thr Asp Val Val Ser Lys Glu Met Tyr Thr Phe Ala
 65 70 75 80

Asp Arg Gly Glu Arg Ser Val Thr Leu Arg Pro Glu Gly Thr Ala Gly
 85 90 95

Val Met Arg Ala Val Ile Glu His Ser Leu Asp Arg Gly Gln Leu Pro
 100 105 110

Val Lys Leu Asn Tyr Ala Gly Pro Phe Phe Arg Tyr Glu Arg Pro Gln
 115 120 125

Ala Gly Arg Tyr Arg Gln Leu Gln Gln Val Gly Val Glu Ala Ile Gly
 130 135 140

Val Asp Asp Pro Ala Leu Asp Ala Glu Ile Ile Ala Leu Ala Asp Arg
 145 150 155 160

Ser Tyr Arg Ser Leu Gly Leu Gln Asp Phe Arg Leu Glu Leu Thr Ser
 165 170 175

Leu Gly Asp Arg His Cys Arg Pro Glu Tyr Arg Gln Lys Leu Gln Asp
 180 185 190

Phe Leu Phe Ala Leu Pro Leu Asp Glu Thr Arg Lys Arg Ala Glu
 195 200 205

Ile Asn Pro Leu Arg Val Leu Asp Asp Lys Arg Pro Glu Val Gln Glu
 210 215 220

Met Thr Ala Asp Ala Pro Leu Met Leu Asp His Leu Asp Ala Glu Cys
 225 230 235 240

Arg Glu His Phe Glu Thr Val Thr Gly Leu Leu Asp Asp Met Gly Val
 245 250 255

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Pro Tyr Val Ile Asn Pro Arg Met Val Arg Gly Leu Asp Tyr Tyr Thr
 260 265 270
 Lys Thr Cys Phe Glu Phe Val His Asp Gly Leu Gly Ala Gln Ser Gly
 275 280 285
 Ile Gly Gly Gly Gly Arg Tyr Asp Gly Leu Met Ala Gln Leu Gly Gly
 290 295 300
 Gln Asp Leu Ser Gly Ile Gly Tyr Gly Leu Gly Val Asp Arg Thr Met
 305 310 315 320
 Leu Ala Leu Glu Ala Glu Gly Val Thr Val Gly Ala Glu Arg Arg Val
 325 330 335
 Asp Val Tyr Gly Val Pro Leu Gly Lys Asp Ala Lys Lys Ala Leu Ala
 340 345 350
 Gly Ile Val Asn Thr Leu Arg Ala Ala Gly Ile Ser Thr Asp Met Ser
 355 360 365
 Tyr Gly Asp Arg Gly Leu Lys Gly Ala Met Lys Gly Ala Asp Arg Ser
 370 375 380
 Asn Ala Leu Tyr Thr Leu Val Leu Gly Glu Gln Glu Leu Glu Asn Asn
 385 390 395 400
 Thr Ile Ala Val Lys Asp Met Arg Ala His Glu Gln His Asp Val Ala
 405 410 415
 Leu Asp Glu Val Val Ala Phe Leu Gln Gly Lys Leu Ile
 420 425

<210> 299
 <211> 3057
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(3034)
 <223> RXA02726

<400> 299
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 Leu Phe Leu Ala Thr
 1 5
 aga cca tgc cgt ggg tac cgc gtt cct cgt gtc ttc agt tgg gat acc 163
 Arg Pro Cys Arg Gly Tyr Arg Val Pro Arg Val Phe Ser Trp Asp Thr
 10 15 20
 cac ggc ttg cca gct gaa ctt gag gct gaa aag cag ctc ggc atc aag 211
 His Gly Leu Pro Ala Glu Leu Glu Ala Glu Lys Gln Leu Gly Ile Lys
 25 30 35
 gag aag ggc gag atc gag gcc atg ggt ctt gcc aag ttc aac gag tac 259
 Asp Lys Gly Glu Ile Glu Ala Met Gly Leu Ala Lys Phe Asn Glu Tyr

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tgt gca acc tcc gtg ttg cag tac acc aag gaa tgg gaa gag tac gtc Cys Ala Thr Ser Val Leu Gln Tyr Thr Lys Glu Trp Glu Glu Tyr Val	307		
55	60	65	
acc cgc cag gct cgt tgg gtg gac ttt gaa aac ggc tac aag acc atg Thr Arg Gln Ala Arg Trp Val Asp Phe Glu Asn Gly Tyr Lys Thr Met	355		
70	75	80	85
gac ctt tct ttc atg gag tcc gtg atc tgg gcg ttc aag gaa ctc tac Asp Leu Ser Phe Met Glu Ser Val Ile Trp Ala Phe Lys Glu Leu Tyr	403		
90	95	100	
gac aag ggc ctg atc tac cag ggt ttc cgc gtt ctt cct tac tcc tgg Asp Lys Gly Leu Ile Tyr Gln Gly Phe Arg Val Leu Pro Tyr Ser Trp	451		
105	110	115	
gca gag cac acc cca ctg tcc aac cag gaa acc cga ctg gat gac tcc Ala Glu His Thr Pro Leu Ser Asn Gln Glu Thr Arg Leu Asp Asp Ser	499		
120	125	130	
tac aag ctg cgc cag gat cca acc ctg acc gtc acg ttc cca gtc acc Tyr Lys Leu Arg Gln Asp Pro Thr Leu Thr Val Thr Phe Pro Val Thr	547		
135	140	145	
ggc gtc gtc gaa ggt tct tct gca aac gct ggc ctg gtg gga gcg ttg Gly Val Val Glu Gly Ser Ser Ala Asn Ala Gly Leu Val Gly Ala Leu	595		
150	155	160	165
gct ctt gcg tgg acg act acc ccg tgg acc ctt cca tcc aac ctt gcg Ala Leu Ala Trp Thr Thr Thr Pro Trp Thr Leu Pro Ser Asn Leu Ala	643		
170	175	180	
ttg gct gtg aac cca gcg gtg acc tac gca ttg gtt gag gtt gct gaa Leu Ala Val Asn Pro Ala Val Thr Tyr Ala Leu Val Glu Val Ala Glu	691		
185	190	195	
gac ggt gag gca gaa ttc gtc ggc aag cgt gtg ctt ttg gct aag gac Asp Gly Glu Ala Glu Phe Val Gly Lys Arg Val Leu Leu Ala Lys Asp	739		
200	205	210	
ctc gtt ggt tcc tac gcc aag gaa ctc ggt gct gag gct gtt atc gtt Leu Val Gly Ser Tyr Ala Lys Glu Leu Gly Ala Glu Ala Val Ile Val	787		
215	220	225	
tct gag cac cca ggc tct gaa ctg gtc gga ctg acc tac gag cca atc Ser Glu His Pro Gly Ser Glu Leu Val Gly Leu Thr Tyr Glu Pro Ile	835		
230	235	240	245
ttt gga tat ttc cgc gat cac gcg aac gga ttc cag atc ctc ggt gca Phe Gly Tyr Phe Arg Asp His Ala Asn Gly Phe Gln Ile Leu Gly Ala	883		
250	255	260	
gag tac gtc acc acc gaa gac ggc acc ggt atc gtc cac cag gca cca Glu Tyr Val Thr Thr Glu Asp Gly Thr Gly Ile Val His Gln Ala Pro	931		
265	270	275	
gct ttc ggt gaa gac gat atg aac acc tgt aac gct gcc ggc att gag Ala Phe Gly Glu Asp Asp Met Asn Thr Cys Asn Ala Ala Gly Ile Glu	979		
280	285	290	

002290*6620960

cca	gtc	atc	cca	gag	gac	atc	gac	ggc	aag	ttc	acc	ggt	ttg	gtt	cct	1027
Pro	Glu	Ile	Pro	Val	Asp	Ile	Asp	Gly	Lys	Phe	Thr	Gly	Leu	Val	Pro	
295300																
gaa	tac	caa	ggt	cag	ctt	gtt	ttc	gat	gcc	aac	aag	gac	atc	atc	aag	1075
Glu	Tyr	Gln	Gly	Gln	Leu	Val	Phe	Asp	Ala	Asn	Lys	Asp	Ile	Ile	Lys	
310315																
gac	ttg	aag	gct	gca	ggt	cgc	gtg	gtt	cgc	cac	cag	acc	atc	gaa	cac	1123
Asp	Leu	Lys	Ala	Ala	Gly	Arg	Val	Val	Arg	His	Gln	Thr	Ile	Glu	His	
330335																
tcc	tac	cca	cac	tct	tgg	cgt	tcc	ggt	gag	cca	ctg	atc	tac	atg	gct	1171
Ser	Tyr	Pro	His	Ser	Trp	Arg	Ser	Gly	Glu	Pro	Leu	Ile	Tyr	Met	Ala	
345350																
ctg	cca	tct	tgg	ttt	gtg	aat	gtc	acc	gaa	atc	cgc	gac	cgc	atg	gtt	1219
Leu	Pro	Trp	Trp	Phe	Val	Asn	Val	Thr	Glu	Ile	Arg	Asp	Arg	Met	Val	
360365																
gag	gtc	aac	cag	gac	atc	gag	tgg	atg	cca	gcg	cac	atc	cgc	gac	ggc	1267
Glu	Val	Asn	Gln	Asp	Ile	Glu	Trp	Met	Pro	Ala	His	Ile	Arg	Asp	Gly	
375380																
cag	ttc	ggc	aag	tgg	cta	gaa	ggt	gcc	cgc	gac	tgg	aac	atc	tcc	cgt	1315
Gln	Phe	Gly	Lys	Trp	Leu	Glu	Gly	Ala	Arg	Asp	Trp	Asn	Ile	Ser	Arg	
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His	Ala	Pro	Ala	Asp	Phe	Ile	Val	Glu	Tyr	Ile	Gly	Gln	Thr	Arg	Gly	
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Trp	Phe	Tyr	Leu	Leu	His	Val	Leu	Ser	Thr	Ala	Leu	Phe	Asp	Arg	Pro	
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Asn Thr Leu Tyr Thr Val Leu Glu Thr Leu Thr Arg Val Ala Ala Pro
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Arg Ser Val His Leu Thr Asp Phe Pro Ser Ala Glu Ser Phe Pro Ala
730 735 740

gat gct gat ttg gtt cgc acc atg gat gag atc cgt ggc gtg tgc tct 2371
Asp Ala Asp Leu Val Arg Thr Met Asp Glu Ile Arg Gly Val Cys Ser
745 750 755

gcg gct tcc tct gtt cgt aag gct cac aag ctg cgt aac cgt ctg cca 2419
Ala Ala Ser Ser Val Arg Lys Ala His Lys Leu Arg Asn Arg Leu Pro
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Thr Ser Asp Val Asp Ser Val Gly Thr Phe Glu Val Val Val Asn Ala
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Trp Glu Glu Tyr 65	Val Thr Arg Gln	Ala Arg Trp Val	Asp Phe Glu Asn 80
Gly Tyr Lys Thr 85	Met Asp Leu Ser	Phe Met Glu Ser	Val Ile Trp Ala 95
Phe Lys Glu Leu 100	Tyr Asp Lys Gly	Leu Ile Tyr Gln	Gly Phe Arg Val 110
Leu Pro Tyr Ser 115	Trp Ala Glu His	Thr Pro Leu Ser	Asn Gln Glu Thr 125
Arg Leu Asp Asp 130	Ser Tyr Lys Leu	Arg Gln Asp Pro	Thr Leu Thr Val 140
Thr Phe Pro Val 145	Thr Gly Val Val	Glu Gly Ser Ser	Ala Asn Ala Gly 160
Leu Val Gly Ala 165	Leu Ala Leu Ala	Trp Thr Thr Thr	Pro Trp Thr Leu 175
Pro Ser Asn Leu 180	Ala Leu Ala Val	Asn Pro Ala Val	Thr Tyr Ala Leu 190
Val Glu Val Ala 195	Glu Asp Gly Glu	Ala Glu Phe Val	Gly Lys Arg Val 205
Leu Leu Ala Lys 210	Asp Leu Val Gly	Ser Tyr Ala Lys	Glu Leu Gly Ala 220
Glu Ala Val Ile 225	Val Ser Glu His	Pro Gly Ser Glu	Leu Val Gly Leu 240
Thr Tyr Glu Pro 245	Ile Phe Gly Tyr	Phe Arg Asp His	Ala Asn Gly Phe 255
Gln Ile Leu Gly 260	Ala Glu Tyr Val	Thr Thr Glu Asp	Gly Thr Gly Ile 270
Val His Gln Ala 275	Pro Ala Phe Gly	Glu Asp Asp Met	Asn Thr Cys Asn 285
Ala Ala Gly Ile 290	Glu Pro Val Ile	Pro Val Asp Ile	Asp Gly Lys Phe 300
Thr Gly Leu Val 305	Pro Glu Tyr Gln	Gly Gln Leu Val	Phe Asp Ala Asn 320
Lys Asp Ile Ile 325	Lys Asp Leu Lys	Ala Ala Gly Arg	Val Val Arg His 335

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Gln Thr Ile Glu His Ser Tyr Pro His Ser Trp Arg Ser Gly Glu Pro
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 His Ile Arg Asp Gly Gln Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp
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 Trp Asn Ile Ser Arg Ser Arg Tyr Trp Gly Ser Pro Ile Pro Ala Trp
 405 410 415
 Val Ser Asp Asn Asp Glu Tyr Pro Arg Val Asp Val Tyr Gly Ser Leu
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 Asp Glu Leu Glu Ala Asp Phe Gly Val Arg Pro Lys Ser Leu His Arg
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 Pro Asp Ile Asp Glu Leu Thr Arg Pro Asn Pro Asp Asp Pro Thr Gly
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 Lys Ser Thr Met Arg Arg Val Thr Asp Val Leu Asp Val Trp Phe Asp
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 Ser Gly Ser Met Pro Phe Ala Gln Val His Tyr Pro Phe Glu Asn Lys
 485 490 495
 Glu Trp Phe Asp Thr His Ala Pro Ala Asp Phe Ile Val Glu Tyr Ile
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 Gly Gln Thr Arg Gly Trp Phe Tyr Leu Leu His Val Leu Ser Thr Ala
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 Asn Ala Tyr Ser Phe Leu Gln Leu Tyr Thr Ser Lys Asn Ala Thr Trp
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 His Asp Leu Val Ala Glu Thr Gln Ala Ala Leu Asp Gly Thr Asp Ile
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 770 775 780
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 Val Val Val Asn Ala Lys Val Ala Gly Pro Arg Leu Gly Lys Asp Val
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 Glu Arg Leu Val Ala Ala Asn Pro Asp Ser Thr Ala Gln Ile Asp Gly
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 915 920 925
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Ala Asp Gly Lys Ala Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met
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Phe Pro Tyr Pro Ser Gly Ala Gly Leu His Val Gly His Pro Leu Gly
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Asn Val Leu His Thr Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu
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Gln Tyr Ala Ile Gln Thr Gly Thr His Pro Arg Thr Thr Met Ala
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Asp Ser Arg Arg Ala Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp
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Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro Ala Asp Gly Lys Ala
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Gln Tyr Ala Ile Gln Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala
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006290 062300

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 Val Ala Pro Asp Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg
 115 120 125

gtt tac gag atg gcc atg gga cct ttg gac acc tcc cgt cca tgg gca 432
 Val Tyr Glu Met Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala
 130 135 140

acc aag gac gtc gtc ggt gcg cag cgc ttc ctc agc gtc 471
 Thr Lys Asp Val Val Gly Ala Gln Arg Phe Leu Ser Val
 145 150 155

<210> 308

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 308

Asn Glu Arg Tyr Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn
 1 5 10 15

Asp Pro Gly Gly Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val
 20 25 30

Leu His Leu Leu Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu
 35 40 45

Gly His Val Ser Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly
 50 55 60

Tyr Ile Gln Ala Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro
 65 70 75 80

Ala Asp Asp Val Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu
 85 90 95

Glu Val Asn Gln Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala
 100 105 110

Val Ala Pro Asp Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg
 115 120 125

Val Tyr Glu Met Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala
 130 135 140

Thr Lys Asp Val Val Gly Ala Gln Arg Phe Leu Ser Val
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<210> 309

<211> 505

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (75)..(482)

<223> FRXA01061

<400> 309

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 Leu Arg Val Asn Thr Val Val Ala Lys Leu Ile Glu
 1 5 10
 tac gtc aac tac ctg acc aaa aca tac cca gac acc atc cca gct ggc 158
 Tyr Val Asn Tyr Leu Thr Lys Thr Tyr Pro Asp Thr Ile Pro Ala Gly
 15 20 25
 gca gtc ctg cca ctg atc gtc atg gtc tcc cct atc gca cca cac atc 206
 Ala Val Leu Pro Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile
 30 35 40
 gcg gag gaa etc tgg aag aag etc ggc cac gac gac acc gtc acc tac 254
 Ala Glu Glu Leu Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr
 45 50 55 60
 gaa cca ttc ccc acc ttt gag gaa aaa tgg etc acc gac gat gaa atc 302
 Glu Pro Phe Pro Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile
 65 70 75
 gaa ctg cca gtc cag gtc aac ggc aag gtc cgc ggt cgc atc acc gtt 350
 Glu Leu Pro Val Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val
 80 85 90
 gca gcc gac gcc agc cag gag cag gtc atc gag gca gcg ctt gcc gac 398
 Ala Ala Asp Ala Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp
 95 100 105
 gag aag gtg cag gag caa atc tcc ggc aag aac ctg atc aag cag atc 446
 Glu Lys Val Gln Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile
 110 115 120
 gtt gtt cca gga cgc atg gtt aac ctt gtg gtg aag taatccccct 492
 Val Val Pro Gly Arg Met Val Asn Leu Val Val Lys
 125 130 135
 cgggttagat tcc 505

<210> 310
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 310
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 Leu Thr Lys Thr Tyr Pro Asp Thr Ile Pro Ala Gly Ala Val Leu Pro
 20 25 30
 Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile Ala Glu Glu Leu
 35 40 45
 Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr Glu Pro Phe Pro
 50 55 60
 Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile Glu Leu Pro Val
 65 70 75 80

002290.0620960

Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val Ala Ala Asp Ala
85 90 95

Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp Glu Lys Val Gln
100 105 110

Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile Val Val Pro Gly
115 120 125

Arg Met Val Asn Leu Val Val Lys
130 135

<210> 311

<211> 1002

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {1}..(1002)

<223> RXA00968

<400> 311

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atg cag cgt aac tgg att ggc cgt tcc cgc ggc gct gaa gtt gat ttc 96
Met Gln Arg Asn Trp Ile Gly Arg Ser Arg Gly Ala Glu Val Asp Phe
20 25 30

agt gca gag ggc gaa acc gtc acc gtg ttt acc acc cgc cca gat act 144
Ser Ala Glu Gly Glu Thr Val Thr Val Phe Thr Thr Arg Pro Asp Thr
35 40 45

ctg ttc ggc gcg acc tac atg gtt ctt gca cct gag cat gag ctg gtc 192
Leu Phe Gly Ala Thr Tyr Met Val Leu Ala Pro Glu His Glu Leu Val
50 55 60

gac gtg ctg ctg gag aag gct ggt tcc tac gag ggc gtt gat gcc cgt 240
Asp Val Leu Leu Glu Lys Ala Gly Ser Tyr Glu Gly Val Asp Ala Arg
65 70 75 80

tgg acc aat ggc cag gcg agc cct gcg gaa gct gtc gct gca tac cgc 288
Trp Thr Asn Gly Gln Ala Ser Pro Ala Glu Ala Val Ala Ala Tyr Arg
85 90 95

gcc tcc atc gcc gcg aag tcc gac ctg gag cgt cag gaa aac aag gaa 336
Ala Ser Ile Ala Ala Lys Ser Asp Leu Glu Arg Gln Glu Asn Lys Glu
100 105 110

aag acc ggc gtc ttc ctg ggc gtt tac gcg acc aac cca gtc aac ggc 384
Lys Thr Gly Val Phe Leu Gly Val Tyr Ala Thr Asn Pro Val Asn Gly
115 120 125

gat cag atc aca gtg ttc atc gct gac tac gtt ctg acc ggc tac ggc 432
Asp Gln Ile Thr Val Phe Ile Ala Asp Tyr Val Leu Thr Gly Tyr Gly
130 135 140

00602630, 0662300

acc ggc gcc atc atg gcg gtt cct gct cac gac gag cgc gac tac gaa Thr Gly Ala Ile Met Ala Val Pro Ala His Asp Glu Arg Asp Tyr Glu	145	150	155		480
ttc gcc acc gtt ttg ggt ctg cct atc aag gaa gtt gtc gca ggt gcc Phe Ala Thr Val Leu Gly Leu Pro Ile Lys Glu Val Val Ala Gly Gly	165	170	175		528
aac atc gaa gag gct gct ttc acc gaa tct ggc gaa gca gtc aac tct Asn Ile Glu Glu Ala Ala Phe Thr Glu Ser Gly Glu Ala Val Asn Ser	180	185	190		576
gcg aac gac aac gcg ctg gat atc aac ggc ctt gcc aag gat gag gct Ala Asn Asp Asn Gly Leu Asp Ile Asn Gly Leu Ala Lys Asp Glu Ala	195	200	205		624
att gcc aag acc atc gaa tgg ttg gaa gaa aag gaa ctt gcc cgc gcc Ile Ala Lys Thr Ile Glu Trp Leu Glu Glu Lys Glu Leu Gly Arg Gly	210	215	220		672
acc atc cag tac aag ctg cgc gac tgg ctg ttc gct cgc cag cgt tac Thr Ile Gln Tyr Lys Leu Arg Asp Trp Leu Phe Ala Arg Gln Arg Tyr	225	230	235		720
tgg gcc gag cct ttc cca atc gtc tac gac gaa aac ggc caa gca cat Trp Gly Glu Pro Phe Pro Ile Val Tyr Asp Glu Asn Gly Gln Ala His	245	250	255		768
gct ctg cca gac tcc atg ctt cca gtc gag ctg cca gag gta gag gac Ala Leu Pro Asp Ser Met Leu Pro Val Glu Leu Pro Glu Val Glu Asp	260	265	270		816
tac aag cct gtc tcc ttc gac cct gaa gac gca gac tcc gag cct tcc Tyr Lys Pro Val Ser Phe Asp Pro Glu Asp Ala Asp Ser Glu Pro Ser	275	280	285		864
cca cca ctg gct aag gcc cgc gaa tgg gtt gag gtg gaa ctc gat ctc Pro Pro Leu Ala Lys Ala Arg Glu Trp Val Glu Val Glu Leu Asp Leu	290	295	300		912
ggc gat gcc aag aag aag tac acc cgc gac acc aac gtc atg cca cag Gly Asp Gly Lys Lys Lys Tyr Thr Arg Asp Thr Asn Val Met Pro Gln	305	310	315		960
tgg gca ggt tcc tcc tgg tac cag ctg cgc tac gtc gat cca Trp Ala Gly Ser Ser Trp Tyr Gln Leu Arg Tyr Val Asp Pro	325	330			1002
<210> 312					
<211> 334					
<212> PRT					
<213> <i>Corynebacterium glutamicum</i>					
<400> 312					
Leu Ile Asp Asp Leu Glu Leu Leu Asp Trp Thr Glu Lys Val Lys Ser	1	5	10	15	
Met Gln Arg Asn Trp Ile Gly Arg Ser Arg Gly Ala Glu Val Asp Phe	20	25	30		

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<212>	DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1678)

<223> RXA01522

<400> 313

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tttaccocagt tcgcatacct ttgcactacc ctaggaaatc gtg act aat tcc aat 115
 Val Thr Asn Ser Asn
 1 5

ccc act tcc aag aac aat tcc gcc gat ttg cct gag cag ctg cga att 163
 Pro Thr Ser Lys Asn Asn Ser Ala Asp Leu Pro Glu Gln Leu Arg Ile
 10 15 20

cgt cgc gaa aag cgc gag cgc att ctg gac agt gga ttg gac gcc tac 211
 Arg Arg Glu Lys Arg Glu Arg Ile Leu Asp Ser Gly Leu Asp Ala Tyr
 25 30 35

cca gtc gag gtt gat cgc acc atc tca atc tct gac ctg cgc tcc caa 259
 Pro Val Glu Val Asp Arg Thr Ile Ser Ile Ser Asp Leu Arg Ser Gln
 40 45 50

ttt gtt gtc att aca gaa gac ctc caa gag cgc gaa gaa ggc gta acc 307
 Phe Val Val Ile Thr Glu Asp Leu Gln Glu Arg Glu Glu Gly Val Thr
 55 60 65

tac ctc gaa gta ggc gaa gaa acc gac gtt gag gtc gca atc gct ggc 355
 Tyr Leu Glu Val Gly Glu Glu Thr Asp Val Glu Val Ala Ile Ala Gly
 70 75 80 85

cgc gtc atg ttc gtt cgc aac acc ggc aag ctc tgc ttc gca tcc atc 403
 Arg Val Met Phe Val Arg Asn Thr Gly Lys Leu Cys Phe Ala Ser Ile
 90 95 100

caa gaa gga aac ggc acc acc gtc caa gca atg ctg tcc ctg gca gca 451
 Gln Glu Gly Asn Gly Thr Thr Val Gln Ala Met Leu Ser Leu Ala Ala
 105 110 115

gtc ggt gaa gaa tcc ctc aag gcc tgg aaa gcc gat gtg gac atg ggt 499
 Val Gly Glu Glu Ser Leu Lys Ala Trp Lys Ala Asp Val Asp Met Gly
 120 125 130

gac atc gtt tcc gtc cgc ggc aaa gta atc tcc tcc aag cgt ggc gaa 547
 Asp Ile Val Ser Val Arg Gly Lys Val Ile Ser Ser Lys Arg Gly Glu
 135 140 145

ctc tcc gtg atg gct gac tcc tgg cac atg gcc tcc aag tcc ctg cgc 595
 Leu Ser Val Met Ala Asp Ser Trp His Met Ala Ser Lys Ser Leu Arg
 150 155 160 165

cca ctg cca gtc gca ttc ggc gac ctc agc gaa gac acc cgc gtc cgc 643
 Pro Leu Pro Val Ala Phe Ala Asp Leu Ser Glu Asp Thr Arg Val Arg
 170 175 180

cac cgc tac acc gac ctc atc atg cgc gaa caa gcc cgc acc aac ggc 691
 His Arg Tyr Thr Asp Leu Ile Met Arg Glu Gln Ala Arg Thr Asn Ala
 185 190 195

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ctc acc cgc atc aag gtc atg cgt gca ctc cgc cac tac ctc gaa gac 739
 Leu Thr Arg Ile Lys Val Met Arg Ala Leu Arg His Tyr Leu Glu Asp
 200 205 210

caa gac ttc ctt gag gta gaa acc ccc atg ctg caa acc ctc cac ggt 787
 Gln Asp Phe Leu Glu Val Glu Thr Pro Met Leu Gln Thr Leu His Gly
 215 220 225

ggc gca gca gca cga cca ttc gaa acc cac tcc aac gcc ctc gac att 835
 Gly Ala Ala Ala Arg Pro Phe Glu Thr His Ser Asn Ala Leu Asp Ile
 230 235 240 245

gac ctc tac ctg cgc atc gca cca gag ctt tac ctc aag cgc tgc gtt 883
 Asp Leu Tyr Leu Arg Ile Ala Pro Glu Leu Tyr Leu Lys Arg Cys Val
 250 255 260

gtc ggc ggc atc gag cgc gtc ttc gaa gtc aac cgc aac ttc cgc aac 931
 Val Gly Gly Ile Glu Arg Val Phe Glu Val Asn Arg Asn Phe Arg Asn
 265 270 275

gaa ggc gtc gac tcc tcc cac tcc cca gaa ttc gcc atg ctc gaa acc 979
 Glu Gly Val Asp Ser Ser His Ser Pro Glu Phe Ala Met Leu Glu Thr
 280 285 290

tac gaa gcc tgg gga acc tac gaa acc gcc gcg aaa ctg atc aag ggt 1027
 Tyr Glu Ala Trp Gly Thr Tyr Glu Thr Gly Ala Lys Leu Ile Lys Gly
 295 300 305

ctc gtc caa tcc gtc gcc caa gaa gtc ttc gga acc acc ctg gtc acc 1075
 Leu Val Gln Ser Val Ala Gln Glu Val Phe Gly Thr Thr Leu Val Thr
 310 315 320 325

ctc gca gac ggc acc gaa tac gac ctc ggc ggc gag tgg aaa gtc atc 1123
 Leu Ala Asp Gly Thr Glu Tyr Asp Leu Gly Gly Glu Trp Lys Val Ile
 330 335 340

gag atg tac cct tcc ctc aac gaa gcc ctc gca cgc aaa ttc cca gga 1171
 Glu Met Tyr Pro Ser Leu Asn Glu Ala Leu Ala Arg Lys Phe Pro Gly
 345 350 355

caa cca gaa gta acc atc gac tcc acc gtc gaa gaa ctc cgc gaa atc 1219
 Gln Pro Glu Val Thr Ile Asp Ser Thr Val Glu Glu Leu Arg Glu Ile
 360 365 370

gcc aag gta atc ggc ctc tcc gtc ccc gaa aac ggc ggc tgg gga cac 1267
 Ala Lys Val Ile Gly Leu Ser Val Pro Glu Asn Gly Gly Trp Gly His
 375 380 385

ggc aaa ctc gtc gaa gaa atc tgg gaa ctc ctc tgc gaa gac caa ctc 1315
 Gly Lys Leu Val Glu Glu Ile Trp Glu Leu Leu Cys Glu Asp Gln Leu
 390 395 400 405

tac gga cca atc ttt gtc aaa gac ttc cca gta gaa acc ttc cca ctc 1363
 Tyr Gly Pro Ile Phe Val Lys Asp Phe Pro Val Glu Thr Phe Pro Leu
 410 415 420

aca cgc caa cac cgc acc aag cca ggc gtc acc gaa aag tgg gac ctc 1411
 Thr Arg Gln His Arg Thr Lys Pro Gly Val Thr Glu Lys Trp Asp Leu
 425 430 435

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 Tyr Val Arg Gly Phe Glu Leu Ala Thr Gly Tyr Ser Glu Leu Ile Asp
 440 445 450

cca gtc att caa cgc gaa cgc ttc gaa ggc caa gcc cgc ctc gcc gcc 1507
 Pro Val Ile Gln Arg Glu Arg Phe Glu Gly Gln Ala Arg Leu Ala Ala
 455 460 465

gac gga gac gac gaa gcc atg gtc ctc gac gaa gac ttc ctc acc gca 1555
 Asp Gly Asp Asp Glu Ala Met Val Leu Asp Glu Asp Phe Leu Thr Ala
 470 475 480 485

atg gaa caa ggc atg cca cca acc tcc ggc aac ggc atg gga atc gac 1603
 Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn Gly Met Gly Ile Asp
 490 495 500

cgc ctc ctc atg gcc ctc acc ggc ctc gga atc cgc gaa acc gta ctc 1651
 Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile Arg Glu Thr Val Leu
 505 510 515

ttc cca atg gtg aaa cca gaa caa aag taggtttttg ctctttgtgc 1698
 Phe Pro Met Val Lys Pro Glu Gln Lys
 520 525

ttg 1701

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 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Gly Leu Asp Ala Tyr Pro Val Glu Val Asp Arg Thr Ile Ser Ile Ser
 35 40 45
 Asp Leu Arg Ser Gln Phe Val Val Ile Thr Glu Asp Leu Gln Glu Arg
 50 55 60
 Glu Glu Gly Val Thr Tyr Leu Glu Val Gly Glu Glu Thr Asp Val Glu
 65 70 75 80
 Val Ala Ile Ala Gly Arg Val Met Phe Val Arg Asn Thr Gly Lys Leu
 85 90 95
 Cys Phe Ala Ser Ile Gln Glu Gly Asn Gly Thr Thr Val Gln Ala Met
 100 105 110
 Leu Ser Leu Ala Ala Val Gly Glu Glu Ser Leu Lys Ala Trp Lys Ala
 115 120 125
 Asp Val Asp Met Gly Asp Ile Val Ser Val Arg Gly Lys Val Ile Ser
 130 135 140
 Ser Lys Arg Gly Glu Leu Ser Val Met Ala Asp Ser Trp His Met Ala

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145 150 155 160
 Ser Lys Ser Leu Arg Pro Leu Pro Val Ala Phe Ala Asp Leu Ser Glu
 165 170 175
 Asp Thr Arg Val Arg His Arg Tyr Thr Asp Leu Ile Met Arg Glu Gln
 180 185 190
 Ala Arg Thr Asn Ala Leu Thr Arg Ile Lys Val Met Arg Ala Leu Arg
 195 200 205
 His Tyr Leu Glu Asp Gln Asp Phe Leu Glu Val Glu Thr Pro Met Leu
 210 215 220
 Gln Thr Leu His Gly Gly Ala Ala Ala Arg Pro Phe Glu Thr His Ser
 225 230 235 240
 Asn Ala Leu Asp Ile Asp Leu Tyr Leu Arg Ile Ala Pro Glu Leu Tyr
 245 250 255
 Leu Lys Arg Cys Val Val Gly Gly Ile Glu Arg Val Phe Glu Val Asn
 260 265 270
 Arg Asn Phe Arg Asn Glu Gly Val Asp Ser Ser His Ser Pro Glu Phe
 275 280 285
 Ala Met Leu Glu Thr Tyr Glu Ala Trp Gly Thr Tyr Glu Thr Gly Ala
 290 295 300
 Lys Leu Ile Lys Gly Leu Val Gln Ser Val Ala Gln Glu Val Phe Gly
 305 310 315 320
 Thr Thr Leu Val Thr Leu Ala Asp Gly Thr Glu Tyr Asp Leu Gly Gly
 325 330 335
 Glu Trp Lys Val Ile Glu Met Tyr Pro Ser Leu Asn Glu Ala Leu Ala
 340 345 350
 Arg Lys Phe Pro Gly Gln Pro Glu Val Thr Ile Asp Ser Thr Val Glu
 355 360 365
 Glu Leu Arg Glu Ile Ala Lys Val Ile Gly Leu Ser Val Pro Glu Asn
 370 375 380
 Gly Gly Trp Gly His Gly Lys Leu Val Glu Glu Ile Trp Glu Leu Leu
 385 390 395 400
 Cys Glu Asp Gln Leu Tyr Gly Pro Ile Phe Val Lys Asp Phe Pro Val
 405 410 415
 Glu Thr Phe Pro Leu Thr Arg Gln His Arg Thr Lys Pro Gly Val Thr
 420 425 430
 Glu Lys Trp Asp Leu Tyr Val Arg Gly Phe Glu Leu Ala Thr Gly Tyr
 435 440 445
 Ser Glu Leu Ile Asp Pro Val Ile Gln Arg Glu Arg Phe Glu Gly Gln
 450 455 460
 Ala Arg Leu Ala Ala Asp Gly Asp Asp Glu Ala Met Val Leu Asp Glu
 465 470 475 480

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Asp Phe Leu Thr Ala Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn
485 490 495

Gly Met Gly Ile Asp Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile
500 505 510

Arg Glu Thr Val Leu Phe Pro Met Val Lys Pro Glu Gln Lys
515 520 525

<210> 315

<211> 619

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(619)

<223> RXA02015

<400> 315

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aaccgagtggtg ctgaaggagc gcgaagactg gcgtccaaac gtg ttg aag ttc tgc 115
Val Leu Lys Phe Ser
1 5

ctc aac ctg ctg gac gat atc cgc cca cgc gca atg tgc cgc gat atc 163
Leu Asn Leu Leu Asp Ile Arg Pro Arg Ala Met Ser Arg Asp Ile
10 15 20

gac tgg ggc atc cca atc cca gtt gaa gga tgg caa gac aac aac gcc 211
Asp Trp Gly Ile Pro Ile Pro Val Glu Gly Trp Gln Asp Asn Asn Ala
25 30 35

aag aag ctc tac gtc tgg ttc gac gct gtc gtg ggc tac ttg tcc gca 259
Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val Gly Tyr Leu Ser Ala
40 45 50

tcc atc gaa tgg gcc tac cgc tcc ggc gac cca gaa gca tgg cgc acc 307
Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro Glu Ala Trp Arg Thr
55 60 65

ttc tgg aat gat cca gaa acc aag tcc tac tac ttc atg ggc aaa gac 355
Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Phe Met Gly Lys Asp
70 75 80 85

aac atc acc ttc cac tcc cag atc tgg cca gcg gag ctt ctc ggc tac 403
Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala Glu Leu Leu Gly Tyr
90 95 100

gca ggc aag ggc tcc cgc ggt gga gaa atc ggt gac ctg ggt gtt ctg 451
Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly Asp Leu Gly Val Leu
105 110 115

aac ctg cct act gag gtt gtt tcc tct gag ttc ctg act atg tct gga 499
Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe Leu Thr Met Ser Gly
120 125 130

tcc aag ttc tcc tca tcc aag ggc gtt gtc atc tac gtg aag gac ttc 547

00220.652300

Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile Tyr Val Lys Asp Phe
 135 140 145

ctc aag gag ttc ggc cca gat gcg ctg cga tac ttc atc gct gcg agg 595
 Leu Lys Glu Phe Gly Pro Asp Ala Leu Arg Tyr Phe Ile Ala Ala Arg
 150 155 160 165

ccc aga aac aac gac acc gac ttc 619
 Pro Arg Asn Asn Asp Thr Asp Phe
 170

<210> 316
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 <212> PRT
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<400> 316
 Val Leu Lys Phe Ser Leu Asn Leu Leu Asp Asp Ile Arg Pro Arg Ala
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Met Ser Arg Asp Ile Asp Trp Gly Ile Pro Ile Pro Val Glu Gly Trp
 20 25 30

Gln Asp Asn Asn Ala Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val
 35 40 45

Gly Tyr Leu Ser Ala Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro
 50 55 60

Glu Ala Trp Arg Thr Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Tyr
 65 70 75 80

Phe Met Gly Lys Asp Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala
 85 90 95

Glu Leu Leu Gly Tyr Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly
 100 105 110

Asp Leu Gly Val Leu Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe
 115 120 125

Leu Thr Met Ser Gly Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile
 130 135 140

Tyr Val Lys Asp Phe Leu Lys Glu Phe Gly Pro Asp Ala Leu Arg Tyr
 145 150 155 160

Phe Ile Ala Ala Arg Pro Arg Asn Asn Asp Thr Asp Phe
 165 170

<210> 317
 <211> 1212
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1189)
 <223> RXA01582

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<400> 317
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tcgcccgtga gtaaacccca attcatgcccc agcgggtatg atg gcg ggg tta gtt 115
Met Ala Gly Leu Val
1 5

gac tta aca ata aac atg agg gaa ggg ctg gac tac acg gtg tcc gaa 163
Asp Leu Thr Ile Asn Met Arg Glu Gly Leu Asp Tyr Thr Val Ser Glu
10 15 20

att cag ttg acc gaa gcc agt ttg aac gag gcg gcc gac gcc gcg atc 211
Ile Gln Leu Thr Glu Ala Ser Leu Asn Glu Ala Ala Asp Ala Ala Ile
25 30 35

aag gct ttc gac ggt gca caa aac cta gat gaa ctc gca gca cta cgc 259
Lys Ala Phe Asp Gly Ala Gln Asn Leu Asp Glu Leu Ala Ala Leu Arg
40 45 50

cgc gat cac ttg ggt gat gcc gca cct att ccg cag gca cga cgc tca 307
Arg Asp His Leu Gly Asp Ala Ala Pro Ile Pro Gln Ala Arg Arg Ser
55 60 65

ttg gga act att cct aaa gat cag cgc aag gat gcg ggc cgc ttt gtc 355
Leu Gly Thr Ile Pro Lys Asp Gln Arg Lys Asp Ala Gly Arg Phe Val
70 75 80 85

aac atg gca ctt ggt cgc gca gaa aag cac ttt gct cag gtc aag gtt 403
Asn Met Ala Leu Gly Arg Ala Glu Lys His Phe Ala Gln Val Lys Val
90 95 100

gtt ttg gaa gaa aag gcg aac gca gaa gtc cta gag ctt gag cgc gtt 451
Val Leu Glu Glu Lys Arg Asn Ala Glu Val Leu Glu Leu Glu Arg Val
105 110 115

gac gtc acc gtt cca acc acc cgc gag cag gtt ggt gcg ctg cac ccc 499
Asp Val Thr Val Pro Thr Thr Arg Glu Gln Val Gly Ala Leu His Pro
120 125 130

atc acg atc ctc aac gag cag atc gca gac atc ttc gtg ggc atg ggc 547
Ile Thr Ile Leu Asn Glu Gln Ile Ala Asp Ile Phe Val Gly Met Gly
135 140 145

tgg gaa atc gcc gag ggc cca gag gtg gaa gca gaa tac ttc aac ttc 595
Trp Glu Ile Ala Glu Gly Pro Glu Val Glu Ala Glu Tyr Phe Asn Phe
150 155 160 165

gac gca ctg aac ttc ctg cct gat cac cca gct cgt aca ctg cag gac 643
Asp Ala Leu Asn Phe Leu Pro Asp His Pro Ala Arg Thr Leu Gln Asp
170 175 180

acc ttc cac att gcg ccg gaa ggc tcc cgc cag gtg ctg cgt acc cac 691
Thr Phe His Ile Ala Pro Glu Gly Ser Arg Gln Val Leu Arg Thr His
185 190 195

acc tca cca gtt cag gtg cgc acc atg ctc aac cgt gaa gtt ccg atc 739
Thr Ser Pro Val Gln Val Arg Thr Met Leu Asn Arg Glu Val Pro Ile
200 205 210

tac atc gca tgc cct ggc cgt gtg ttc cgt acc gac gaa ctc gat gca 787

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Tyr Ile Ala Cys Pro Gly Arg Val Phe Arg Thr Asp Glu Leu Asp Ala
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 aca cac acc cct gtg ttc cac cag atc gaa ggc ctt gca gtt gat aag 835
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 Gly Leu Thr Met Ala His Leu Arg Gly Thr Leu Asp His Leu Ala Lys
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 Glu Leu Phe Gly Pro Glu Thr Lys Thr Arg Met Arg Ser Asn Tyr Phe
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Ala Gly Arg Phe Val Asn Met Ala Leu Gly Arg Ala Glu Lys His Phe
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 Gly Ala Leu His Pro Ile Thr Ile Leu Asn Glu Gln Ile Ala Asp Ile
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 Phe Val Gly Met Gly Trp Glu Ile Ala Glu Gly Pro Glu Val Glu Ala
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 Arg Thr Leu Gln Asp Thr Phe His Ile Ala Pro Glu Gly Ser Arg Gln
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 Val Leu Arg Thr His Thr Ser Pro Val Gln Val Arg Thr Met Leu Asn
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 225 230 235 240
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 Asp His Leu Ala Lys Glu Leu Phe Gly Pro Glu Thr Lys Thr Arg Met
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 Arg Ser Asn Tyr Phe Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Val
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 Trp Phe Pro Asn Lys Lys Gly Gly Ala Gly Trp Ile Glu Trp Gly Gly
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 Cys Gly Met Val Asn Pro Asn Val Leu Arg Ala Val Gly Val Asp Pro
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 Glu Glu Tyr Thr Gly Phe Ala Phe Gly Met Gly Ile Glu Arg Thr Leu
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Glu Leu Thr Glu Phe Lys Lys Pro Ile Arg His Cys His Val Asn Val	10 15 20	
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Gly Asp Ala Asn Gly Thr Gly Glu Leu Gln Ser Ile Val Cys Gly Ala	25 30 35	
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Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu Ser Ala Arg Gly Leu	120 125 130	
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Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr Phe Thr Asp Pro Ala	135 140 145	
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Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys Val Pro Ala Val Glu	150 155 160 165	
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Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu Thr Lys Ala Ile Arg	170 175 180	
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Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro Ala Ala Glu Ser Pro	185 190 195	
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acc ctc aat gag gaa gac gtt gtg atc acc gat gac aac ggc att cag Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp Asp Asn Gly Ile Gln 265 270 275			931
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 Tyr Ala Glu Ile Ile Pro Ser Pro Phe Met Asp Pro Glu Val Phe Asp
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gta tgg gga ctc gca gca gac gac gag cgc cgc aag acc gtt tcc gtt 1603
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ctc aac oca ctt gag gca gaa cgc aac gtc ctg agc acc tcc ttg ctg 1651
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 Pro Ser Met Leu Asp Ala Val Lys Arg Asn Val Ala Arg Gly His Asn
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gat ttc tcc ctg ttc gcc ctg cag cag gtc gcc ttc gag cac gga tcc 1747
 Asp Phe Ser Leu Phe Gly Leu Gln Gln Val Ala Phe Glu His Gly Ser
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 Gly Val Ser Pro Met Pro Ser Val Ala Ser Arg Pro Glu Glu Ser Val
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gtg gca gaa ctg gtg gat tca ctg cca aac cag cca ctg cat gtc gca 1843
 Val Ala Glu Leu Val Asp Ser Leu Pro Asn Gln Pro Leu His Val Ala
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 Pro Ala Arg Thr Cys Ala Met Glu Leu Asp Leu Ser Ala Leu Pro Leu
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745 750 755

gag gaa gcc aac gaa gca cga ctt cag gca gca gag cta gca aag gag 2419
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<213> *Corynebacterium glutamicum*

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Ser Tyr Gly Glu Pro Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu
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Asp Thr Val Phe Asp Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu
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Ser Ala Arg Gly Leu Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr
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Phe Thr Asp Pro Ala Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys
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 Gln Arg Pro Val Asn Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu
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 Leu Leu Gly Gln Pro Met His Ala Phe Asp Ala Ala Lys Val Thr Gly
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 Asp His Val Lys Arg Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp
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<213> Corynebacterium glutamicum

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<223> FRXA01583

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Val Glu Thr Ile Glu
1 5

gag ctc acc gag ttc aag aag ccc atc cgc cac tgc cac gtc aat gtt 163

Glu Leu Thr Glu Phe Lys Lys Pro Ile Arg His Cys His Val Asn Val
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Gly Asp Ala Asn Gly Thr Gly Glu Leu Gln Ser Ile Val Cys Gly Ala
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cgc aac ttc aag gaa ggc gac acc gtt gtc gtg tcc ctt cct ggc gct 259

Arg Asn Phe Lys Glu Gly Asp Thr Val Val Val Ser Leu Pro Gly Ala
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gtg ctg cct ggc gat ttc gcg atc tct gct cgt gaa act tac gga cgc 307

Val Leu Pro Gly Asp Phe Ala Ile Ser Ala Arg Glu Thr Tyr Gly Arg
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Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu Ser Ala Arg Gly Leu
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Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr Phe Thr Asp Pro Ala
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Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys Val Pro Ala Val Glu
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Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu Asp His Val Lys Arg	
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Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp Asp Asn Gly Ile Gln	
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Phe Glu Arg Gly Val Asp Pro Ala Ile Val Glu Ile Ala Leu Asp Ile	
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Val Thr Arg Pro Ser Glu Leu Ala Gly Val Asp Tyr Ser Ala Glu Thr	
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Gln Arg Pro Val Asn Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu 210 215 220		
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Asp His Val Lys Arg Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp 260 265 270		
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Pro Ile Thr Met Lys Val Thr Arg Pro Ser Glu Leu Ala Gly Val Asp 370 375 380		
Tyr Ser Ala Glu Thr Val Ile Ala Arg Leu Glu Glu Val Gly Cys Thr 385 390 395 400		
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 465 470 475 480
 Pro Glu Val Phe Asp Val Trp Gly Leu Ala Asp Asp Glu Arg Arg
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 Lys Thr Val Ser Val Leu Asn Pro Leu Glu Ala Glu Arg Asn Val Leu
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 Ser Thr Ser Leu Leu Pro Ser Met Leu Asp Ala Val Lys Arg Asn Val
 515 520 525
 Ala Arg Gly His Asn Asp Phe Ser Leu Phe Gly Leu Gln Gln Val Ala
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 Ile Pro Ala Glu Asp Val Arg Ala Val Val Lys Ala Gly Ala Gly Glu
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 Leu Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg
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 Gly Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala
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 ggc cgc acc ctc acc gat gag gaa gcc aac gaa gca cga ctt cag gca 240
 Gly Arg Thr Leu Thr Asp Glu Glu Ala Asn Glu Ala Arg Leu Gln Ala
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Met Ile Thr Arg Leu
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tcc acg ctg ttt ttg cgc acc ctg cgc gaa gac cct gca gat gca gaa 163
Ser Thr Leu Phe Leu Arg Thr Leu Arg Glu Asp Pro Ala Asp Ala Glu
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gtt cca agc cac aag ctg ctt gtc cgt gca gga tat atc cgc cga gtt 211
Val Pro Ser His Lys Leu Leu Val Arg Ala Gly Tyr Ile Arg Arg Val
25 30 35

gcc cca ggt atc tac tcc tgg ttg cca ctg ggt ttg cgc gca gtg cgc 259
Ala Pro Gly Ile Tyr Ser Trp Leu Pro Leu Gly Leu Arg Ala Val Arg
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aac att gaa gct gtc gta cgc gag gaa atg gat gcg atc gga gga cag 307

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Asn Ile Glu Ala Val Val Arg Glu Glu Met Asp Ala Ile Gly Gly Gln
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 Glu Leu Leu Phe Pro Thr Leu Leu Pro Arg Glu Pro Tyr Glu Thr Thr
 70 75 80 85
 cag cgt tgg aca gaa tac ggc gat tgc ctg ttc cgt ctg aag gac cgc 403
 Gln Arg Trp Thr Thr Tyr Gly Asp Ser Leu Phe Arg Leu Lys Asp Arg
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 aag ggt gcc gac tac ctg ctc gga cca acc cac gag gaa atg ttc gcc 451
 Lys Gly Ala Asp Tyr Leu Leu Gly Pro Thr His Glu Glu Met Phe Ala
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 gcc acg gtg aag gat ctg tac aac tcc tac aag gac ttc cca gtc acc 499
 Ala Thr Val Lys Asp Leu Tyr Asn Ser Tyr Lys Asp Phe Pro Val Thr
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 ttg tac cag atc cag acc aag tac cgc gat gag gaa cgc cca cgc gca 547
 Leu Tyr Gln Ile Gln Thr Lys Tyr Arg Asp Glu Glu Arg Pro Arg Ala
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 Gly Val Leu Arg Gly Arg Glu Phe Val Met Lys Asp Ser Tyr Ser Phe
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 Asp Ile Ser Asp Ala Gly Leu Asp Glu Ser Tyr Ala Lys His Arg Ala
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 Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr Ala Ile Cys
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 Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu Glu Phe Leu
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 Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val Arg Ser Thr Ser Gly
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 aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca gcc gtt gag 835
 Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro Gly Val Glu
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 cgt gac atc gaa ggc ctg cca gaa cca gtc acc tac gaa act cct gtt 883
 Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu Thr Pro Val
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 tct gaa acc atc gat gct ttg gtt gat tgg gct aac tcc atc gac gtg 931
 Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser Ile Asp Val
 265 270 275
 cag atc gag gcc cgc gag gtc acc gca gat gac acc ctc aag tgc att 979
 Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp Thr Lys Cys Ile
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 gtg gtg aag gtc cgc gag cca ggt gcc gaa gaa gca gaa ctc act gga 1027
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Asp	Asn	Pro	Phe	Leu	Val	Lys	Gly	Tyr	Val	Gly	Pro	Val	Gly	Leu	Ala	
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Lys	Asn	Gly	Val	Lys	Val	Leu	Ala	Asp	Pro	Arg	Val	Val	Thr	Gly	Thr	
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tcc	tgg	atc	acc	ggc	gcc	gat	gaa	aag	gaa	cgc	cac	gtc	gta	ggc	ctc	1267
Ser	Trp	Ile	Thr	Gly	Ala	Asp	Glu	Lys	Glu	Arg	His	Val	Val	Gly	Leu	
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gtc	gcc	gga	cgc	gat	ttc	acc	cca	gac	ggc	ttc	atc	gaa	gct	gca	gaa	1315
Val	Ala	Gly	Arg	Asp	Phe	Thr	Pro	Asp	Gly	Phe	Ile	Glu	Ala	Ala	Glu	
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Ile	Lys	Glu	Gly	Asp	Pro	Ala	Pro	Ala	Gly	Glu	Gly	Thr	Leu	Thr	Leu	
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gct	cgc	ggc	atc	gaa	att	ggc	ata	tct	tcc	agc	tcg	gcc	gca	agt	aca	1411
Ala	Arg	Gly	Ile	Glu	Ile	Gly	Ile	Ser	Ser	Ser	Ser	Ala	Ala	Ser	Thr	
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ccg	aag	cct	tcg	acg	tcc	aaa	tcc	tgg	acg	aaa	acg	gca	agc	gcg	cca	1459
Pro	Lys	Pro	Ser	Thr	Ser	Lys	Ser	Trp	Thr	Lys	Thr	Ala	Ser	Ala	Pro	
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Ser	Gln	Pro	Trp	Ala	Leu	Arg	Ala	Arg	Cys	His	Pro	Pro	Ala	Arg	Arg	
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cct	ggc	aga	aca	gcg	cca	cga	tgacgctggc	ctcaactggt	ccg							1551
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 Pro Tyr Glu Thr Thr Gln Arg Trp Thr Glu Tyr Gly Asp Ser Leu Phe
 85 90 95
 Arg Leu Lys Asp Arg Lys Gly Ala Asp Tyr Leu Leu Gly Pro Thr His
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 Glu Glu Met Phe Ala Ala Thr Val Lys Asp Leu Tyr Asn Ser Tyr Lys
 115 120 125
 Asp Phe Pro Val Thr Leu Tyr Gln Ile Gln Thr Lys Tyr Arg Asp Glu
 130 135 140
 Glu Arg Pro Arg Ala Gly Val Leu Arg Gly Arg Glu Phe Val Met Lys
 145 150 155 160
 Asp Ser Tyr Ser Phe Asp Ile Ser Asp Ala Gly Leu Asp Glu Ser Tyr
 165 170 175
 Ala Lys His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu
 180 185 190
 Glu Tyr Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala
 195 200 205
 Ser Glu Glu Phe Leu Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val
 210 215 220
 Arg Ser Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr
 225 230 235 240
 Gln Pro Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr
 245 250 255
 Tyr Glu Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala
 260 265 270
 Asn Ser Ile Asp Val Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp
 275 280 285
 Thr Leu Lys Cys Ile Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu
 290 295 300
 Ala Glu Leu Thr Gly Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met
 305 310 315 320
 Lys Arg Leu Glu Ala Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val
 325 330 335
 Glu Ser Asp Phe Ala Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly
 340 345 350
 Pro Val Gly Leu Ala Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg
 355 360 365

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Val Val Thr Gly Thr Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg
 370 375 380

His Val Val Gly Leu Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe
 385 390 395 400

Ile Glu Ala Ala Glu Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu
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Gly Thr Leu Thr Leu Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser Ser
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Ser Ala Ala Ser Thr Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys
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 Leu Asp Glu Ser Tyr Ala Lys
 1 5

cac cgc gca gcg tat cag cgc atc ttt gac cgc ctt ggc ttg gaa tac 162
 His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr
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gcc atc tgc cag gca acc tct ggt gcc atg gcc gga tcc gct tcc gag 210
 Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu
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gaa ttc ctt gca gta tct gaa aac gcc gaa gat acc ttc gtg cgc tct 258
 Glu Phe Leu Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val Arg Ser
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acc tcc gcc aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca 306
 Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro
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ggc gtt gag cgt gac atc gaa gcc ctg cca gaa cca gtc acc tac gaa 354
 Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu
 75 80 85

act cct gtt tct gaa acc atc gat gct ttg gtt gat tgg gct aac tcc 402
 Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser

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120 125 130 135																
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185 190 195																
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235 240 245																
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250 255 260																
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265 270 275																
agc Ser	gcg Ala	cca Pro	tcc Ser	caa Gln	cca Pro	tgg Trp	gct Ala	cga Leu	cgg Arg	gct Ala	cgg Arg	tgt Cys	cac His	cgc Pro	cct Pro	978
280 285 290 295																
gct Ala	cgc Arg	cgt Arg	cct Pro	ggc Gly	aga Arg	aca Thr	cgc Ala	cca Pro	cga Arg	tgacgctggc	ctcaactggt					1028
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Met Gly Gly Ser Ala Ser Glu Glu Phe Leu Ala Val Ser Glu Asn Gly
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Glu Asp Thr Phe Val Arg Ser Thr Ser Gly Asn Tyr Ala Ala Asn Val
50 55 60

Glu Ala Val Val Thr Gln Pro Gly Val Glu Arg Asp Ile Glu Gly Leu
65 70 75 80

Pro Glu Pro Val Thr Tyr Glu Thr Pro Val Ser Glu Thr Ile Asp Ala
85 90 95

Leu Val Asp Trp Ala Asn Ser Ile Asp Val Gln Ile Glu Gly Arg Glu
100 105 110

Val Thr Ala Asp Asp Thr Leu Lys Cys Ile Val Val Lys Val Arg Glu
115 120 125

Pro Gly Ala Glu Glu Ala Glu Leu Thr Gly Ile Leu Leu Pro Gly Asp
130 135 140

Arg Glu Val Asp Met Lys Arg Leu Glu Ala Ser Leu Glu Pro Ala Glu
145 150 155 160

Val Glu Leu Ala Val Glu Ser Asp Phe Ala Asp Asn Pro Phe Leu Val
165 170 175

Lys Gly Tyr Val Gly Pro Val Gly Leu Ala Lys Asn Gly Val Lys Val
180 185 190

Leu Ala Asp Pro Arg Val Val Thr Gly Thr Ser Trp Ile Thr Gly Ala
195 200 205

Asp Glu Lys Glu Arg His Val Val Gly Leu Val Ala Gly Arg Asp Phe
210 215 220

Thr Pro Asp Gly Phe Ile Glu Ala Ala Glu Ile Lys Glu Gly Asp Pro
225 230 235 240

Ala Pro Ala Gly Glu Gly Thr Leu Thr Leu Ala Arg Gly Ile Glu Ile
245 250 255

Gly Ile Ser Ser Ser Ser Ala Ala Ser Thr Pro Lys Pro Ser Thr Ser
260 265 270

Lys Ser Trp Thr Lys Thr Ala Ser Ala Pro Ser Gln Pro Trp Ala Leu
275 280 285

Arg Ala Arg Cys His Pro Pro Ala Arg Arg Pro Gly Arg Thr Ala Pro
290 295 300

Arg
305

170										175										180										
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Arg	Glu	Ala	Gly	Phe	Ser	Met	Met	Ile	Pro	Pro	Val	Leu	Val	Arg	Pro															
185																														
gaa	atc	atg	gcg	ggc	act	gga	ttc	ttg	ggt	gat	cac	tcc	gag	gag	atc	739														
Glu	Ile	Met	Ala	Gly	Thr	Gly	Phe	Leu	Gly	Asp	His	Ser	Glu	Glu	Ile															
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Tyr	Tyr	Leu	Glu	Arg	Asp	Asp	Met	Tyr	Leu	Val	Gly	Thr	Ser	Glu	Val															
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Lys	Val	Glu	Met	Phe	Val	Tyr	Cys	Lys	Pro	Glu	Asp	Ala	Glu	Asp	Val															
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His	Gln	Gln	Leu	Leu	Gly	Met	Glu	Lys	Glu	Met	Leu	Ala	Ala	Ile	Glu															
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Ala	Ala	Arg	Lys	Phe	Asp	Thr	Glu	Ala	Trp	Val	Pro	Thr	Gln	Asp	Thr															
330																														
tac	cgt	gaa	ctc	acc	tgc	acc	tct	aac	tgc	acc	act	ttc	cag	gct	cgt	1171														
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360																														
gca	acc	ctg	aac	ggt	acg	ttg	gct	acc	act	cgt	tgg	ctt	gtc	gcg	atc	1267														
Ala	Thr	Leu	Asn	Gly	Thr	Leu	Ala	Thr	Thr	Arg	Trp	Leu	Val	Ala	Ile															
375																														
ctg	gag	aac	aac	cag	cag	gcc	gat	ggc	tct	ggt	ggt	ggt	oct	gag	gcg	1315														
Leu	Glu	Asn	Asn	Gln	Gln	Ala	Asp	Gly	Ser	Val	Val	Val	Pro	Glu	Ala															
390																														
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Leu	Arg	Pro	Phe	Val	Gly	Lys	Asp	Val	Leu	Lys	Pro	Val	Lys	Gln	Ala															
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Gly

1389

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35 40 45
Arg Ala Glu Gln Lys Ala Phe Gly Lys Lys Ile Gly Gln Ala Ser Pro
50 55 60
Glu Asp Arg Pro Ala Leu Leu Glu Gly Ser Asn Glu Leu Lys Ala Lys
65 70 75 80
Val Lys Asp Ala Glu Ala Ala Gln Glu Ala Ala Glu Ala Lys Val Asn
85 90 95
Glu Leu Gln Met Lys Leu Ser Asn Val Val Ser Gly Ala Pro Ala Gly
100 105 110
Gly Glu Asp Asp Phe Val Val Leu Glu Thr Ile Gly Glu Pro Arg Thr
115 120 125
Phe Asp Phe Glu Pro Lys Asp His Leu Glu Leu Gly Glu Ser Leu Gly
130 135 140
Leu Ile Asp Met Lys Arg Gly Thr Lys Val Ser Gly Ala Arg Phe Tyr
145 150 155 160
Tyr Leu Thr Gly Asp Gly Ala Met Leu Gln Leu Gly Met Leu Met Leu
165 170 175
Ala Ala Gln Lys Ala Arg Glu Ala Gly Phe Ser Met Met Ile Pro Pro
180 185 190
Val Leu Val Arg Pro Glu Ile Met Ala Gly Thr Gly Phe Leu Gly Asp
195 200 205
His Ser Glu Glu Ile Tyr Tyr Leu Glu Arg Asp Asp Met Tyr Leu Val
210 215 220
Gly Thr Ser Glu Val Ala Leu Ala Gly Tyr His Lys Asp Glu Ile Ile
225 230 235 240
Asp Leu Asn Glu Gly Pro Val Lys Tyr Ala Gly Trp Ser Ser Cys Phe
245 250 255
Arg Arg Glu Ala Gly Ser Tyr Gly Lys Asp Thr Arg Gly Ile Leu Arg

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	275						280					285				
Asp	Ala	Glu	Asp	Val	His	Gln	Gln	Leu	Leu	Gly	Met	Glu	Lys	Glu	Met	
	290					295					300					
Leu	Ala	Ala	Ile	Glu	Val	Pro	Tyr	Arg	Val	Ile	Asp	Val	Ala	Gly	Gly	
	305				310					315					320	
Asp	Leu	Gly	Ala	Ser	Ala	Ala	Arg	Lys	Phe	Asp	Thr	Glu	Ala	Trp	Val	
			325						330					335		
Pro	Thr	Gln	Asp	Thr	Tyr	Arg	Glu	Leu	Thr	Ser	Thr	Ser	Asn	Cys	Thr	
			340					345					350			
Thr	Phe	Gln	Ala	Arg	Leu	Gln	Thr	Arg	Tyr	Arg	Asp	Glu	Asn	Gly		
	355					360					365					
Lys	Pro	Gln	Ile	Ala	Ala	Thr	Leu	Asn	Gly	Thr	Leu	Ala	Thr	Thr	Arg	
	370					375					380					
Trp	Leu	Val	Ala	Ile	Leu	Glu	Asn	Asn	Gln	Gln	Ala	Asp	Gly	Ser	Val	
	385				390					395					400	
Val	Val	Pro	Glu	Ala	Leu	Arg	Pro	Phe	Val	Gly	Lys	Asp	Val	Leu	Lys	
			405						410					415		
Pro	Val	Lys	Gln	Ala	Gly											
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ccccaacaac tagaagtaca tcaaggacat ttttaaacac atg aac atc att gac 115																
Met Asn Ile Ile Asp 5																
gaa ctc tcc tgg cgc gga ctc atc aac cag tcc acc gac ctt gag gcc 163																
Glu Leu Ser Trp Arg Gly Leu Ile Asn Gln Ser Thr Asp Leu Glu Ala 20																
ctt cgc gag gaa gct tca acc ccc atc acc ttg tac tgc gga ttc gac 211																
Leu Arg Glu Glu Ala Ser Thr Pro Ile Thr Leu Tyr Cys Gly Phe Asp 35																
cca acc ggt cca tcc ctc cac gca gga cac ctc gtt cca ctg ctc atg 259																
Pro Thr Gly Pro Ser Leu His Ala Gly His Leu Val Pro Leu Leu Met 40 45 50																

ctg cgc cgt ttc cag caa gca gga cac aac cca atc gtg ctc gca ggt 307
 Leu Arg Arg Phe Gln Gln Ala Gly His Asn Pro Ile Val Leu Ala Gly
 55 60 65

ggc gca acc ggc atg atc ggc gac ccc cgc gat gtc ggc gag cgc acc 355
 Gly Ala Thr Gly Met Ile Gly Asp Pro Arg Asp Val Gly Glu Arg Thr
 70 75 80 85

atg aac tcc gca gac acc gtc tct gat tgg gca gaa cgc atc tcc ggt 403
 Met Asn Ser Ala Asp Thr Val Ser Asp Trp Ala Glu Arg Ile Ser Gly
 90 95 100

cag ctc agc cgc ttc gtt gat ttc gac ggc gag cac gca gcc cgt ctg 451
 Gln Leu Ser Arg Phe Val Asp Phe Asp Gly Glu His Ala Arg Leu
 105 110 115

gtc aac aac gcc gag tgg acc aac gaa atg tcc gta gtg acc ttc ctc 499
 Val Asn Asn Ala Glu Trp Thr Asn Glu Met Ser Val Val Thr Phe Leu
 120 125 130

cgt gat gta gga aag cac ttc tcc ctc aac acc atg ctc gcc cgc gac 547
 Arg Asp Val Gly Lys His Phe Ser Leu Asn Thr Met Leu Ala Arg Asp
 135 140 145

acc gtc aag cgt cgc ctc gag tcc gac ggc att tcc tac acc gag ttc 595
 Thr Val Lys Arg Arg Leu Glu Ser Asp Gly Ile Ser Tyr Thr Glu Phe
 150 155 160 165

tcc tac atg ctg cta cag gcc aac gac tac gtt gaa ctg aac aag cgc 643
 Ser Tyr Met Leu Leu Gln Ala Asn Asp Tyr Val Glu Leu Asn Lys Arg
 170 175 180

ttc ggc tgc acc ctg cag gta ggt ggc ggt gac cag tgg ggc aac atc 691
 Phe Gly Cys Thr Leu Gln Val Gly Gly Gly Asp Gln Trp Gly Asn Ile
 185 190 195

gtt tct ggc gtt gac ctc aac cgt cgc gtc aac ggc acc tct gtc cac 739
 Val Ser Gly Val Asp Leu Asn Arg Arg Val Asn Gly Thr Ser Val His
 200 205 210

gca gtg acc gta cct ttg gtt acc gat tcc gac ggc aag aag ttc ggc 787
 Ala Val Thr Val Pro Leu Val Thr Asp Ser Asp Gly Lys Lys Phe Gly
 215 220 225

aag tcc acc ggc ggc gga agc ctc tgg ttg gat cgc gaa atg acc agc 835
 Lys Ser Thr Gly Gly Gly Ser Leu Trp Leu Asp Pro Glu Met Thr Ser
 230 235 240 245

cca tac gct tgg tac cag tac ttc atc aac gca tcc gac gct gac gtg 883
 Pro Tyr Ala Trp Tyr Gln Tyr Phe Ile Asn Ala Ser Asp Ala Asp Val
 250 255 260

atc cgt tac ctc cgc tgg ttc acc ttc ctc acc cag gaa gaa ctt gct 931
 Ile Arg Tyr Leu Arg Trp Phe Thr Phe Leu Thr Gln Glu Glu Leu Ala
 265 270 275

gag ttg gaa gtt gaa gtt gca gag cgc cca ttc aag cgc gaa gca cag 979
 Glu Leu Glu Val Glu Val Ala Glu Arg Pro Phe Lys Arg Glu Ala Gln
 280 285 290

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cgt cgt ctt gca cgc gaa atg acc aac ttg gtt cac gga acc gaa gca 1027
 Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val His Gly Thr Glu Ala
 295 300 305

acc gaa gca gtc gag ctt gct gct caa gca ctg ttc ggc cgc gca gaa 1075
 Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu Phe Gly Arg Ala Glu
 310 315 320 325

ctc cgc gac cta gac gaa aaa act ctc gct gca tcc gtt tct gaa act 1123
 Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala Ser Val Ser Glu Thr
 330 335 340

gca gtt gca gaa atc aag gca ggg gag cca cgc acc atc ata gat ctg 1171
 Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg Thr Ile Ile Asp Leu
 345 350 355

ctc gtg gcc agc gga ctt gct gat tcc aag ggc gca gca aag cgt gca 1219
 Leu Val Ala Glu Ser Gly Leu Ala Asp Ser Lys Gly Ala Ala Lys Arg Ala
 360 365 370

gtc aag gaa ggc ggt gcg tac gta aac aac gaa cgc atc gaa tcg gat 1267
 Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu Arg Ile Glu Ser Asp
 375 380 385

gat tgg gag cct ttc gct gaa gat ctt ctt cac ggt tca tgg cta gta 1315
 Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His Gly Ser Trp Leu Val
 390 395 400 405

ctg cgc cgt ggc aag aag aac ttc gca gga gtt cag atc ctc ggc 1360
 Leu Arg Arg Gly Lys Lys Asn Phe Ala Gly Val Gln Ile Leu Gly
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taataatcgc tgaatgatt ggc 1383

<210> 332

<211> 420

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 332

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Thr Asp Leu Glu Ala Leu Arg Glu Glu Ala Ser Thr Pro Ile Thr Leu
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Tyr Cys Gly Phe Asp Pro Thr Gly Pro Ser Leu His Ala Gly His Leu
 35 40 45

Val Pro Leu Leu Met Leu Arg Arg Phe Gln Gln Ala Gly His Asn Pro
 50 55 60

Ile Val Leu Ala Gly Gly Ala Thr Gly Met Ile Gly Asp Pro Arg Asp
 65 70 75 80

Val Gly Glu Arg Thr Met Asn Ser Ala Asp Thr Val Ser Asp Trp Ala
 85 90 95

Glu Arg Ile Ser Gly Gln Leu Ser Arg Phe Val Asp Phe Asp Gly Glu
 100 105 110

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His Ala Ala Arg Leu Val Asn Asn Ala Glu Trp Thr Asn Glu Met Ser
 115 120 125
 Val Val Thr Phe Leu Arg Asp Val Gly Lys His Phe Ser Leu Asn Thr
 130 135 140
 Met Leu Ala Arg Asp Thr Val Lys Arg Arg Leu Glu Ser Asp Gly Ile
 145 150 155 160
 Ser Tyr Thr Glu Phe Ser Tyr Met Leu Leu Gln Ala Asn Asp Tyr Val
 165 170 175
 Glu Leu Asn Lys Arg Phe Gly Cys Thr Leu Gln Val Gly Gly Asp
 180 185 190
 Gln Trp Gly Asn Ile Val Ser Gly Val Asp Leu Asn Arg Arg Val Asn
 195 200 205
 Gly Thr Ser Val His Ala Val Thr Val Pro Leu Val Thr Asp Ser Asp
 210 215 220
 Gly Lys Lys Phe Gly Lys Ser Thr Gly Gly Gly Ser Leu Trp Leu Asp
 225 230 235 240
 Pro Glu Met Thr Ser Pro Tyr Ala Trp Tyr Gln Tyr Phe Ile Asn Ala
 245 250 255
 Ser Asp Ala Asp Val Ile Arg Tyr Leu Arg Trp Phe Thr Phe Leu Thr
 260 265 270
 Gln Glu Glu Leu Ala Glu Leu Glu Val Glu Val Ala Glu Arg Pro Phe
 275 280 285
 Lys Arg Glu Ala Gln Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val
 290 295 300
 His Gly Thr Glu Ala Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu
 305 310 315 320
 Phe Gly Arg Ala Glu Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala
 325 330 335
 Ser Val Ser Glu Thr Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg
 340 345 350
 Thr Ile Ile Asp Leu Leu Val Ala Ser Gly Leu Ala Asp Ser Lys Gly
 355 360 365
 Ala Ala Lys Arg Ala Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu
 370 375 380
 Arg Ile Glu Ser Asp Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His
 385 390 395 400
 Gly Ser Trp Leu Val Leu Arg Arg Gly Lys Lys Asn Phe Ala Gly Val
 405 410 415
 Gln Ile Leu Gly
 420

00602033 0062300

<210> 333
 <211> 1994
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(1971)
 <223> RXA02509

<400> 333
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 Asp Leu Pro Asn Lys Gly Pro Glu Ala Ile Val Cys Ala Lys Asp Ala
 1 5 10 15
 gaa ggc caa cta aag gat ctt tca cac gtc cca gaa acc act act acg 96
 Glu Gly Gln Leu Lys Asp Leu Ser His Val Pro Glu Thr Thr Ala Thr
 20 25 30
 ttc acc gct gta cct gca aat act gat gac ggc cgc gca gta atc cgc 144
 Phe Thr Ala Val Pro Ala Asn Thr Asp Asp Gly Arg Ala Val Ile Arg
 35 40 45
 cac tcg tgc gct cac gtg ctg gca cag gct gtc cag gca gaa ttc cca 192
 His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro
 50 55 60
 gga acc aag ttg ggc atc ggc cca gcc att gaa aat ggt ttc tac tac 240
 Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr
 65 70 75 80
 gac ttc gat gcg gct gag cct ttc act ccg gaa gat ctc aag acc att 288
 Asp Phe Asp Ala Ala Glu Pro Phe Thr Pro Glu Asp Leu Lys Thr Ile
 85 90 95
 gaa aag cgg atg aag aag atc atc aag acc ggc cag aag ttt gag cgc 336
 Glu Lys Arg Met Lys Lys Ile Ile Lys Thr Gly Gln Lys Phe Glu Arg
 100 105 110
 cgc gtc tat gaa tcc gct gaa gct gca gcg gaa gag ttg aag aac gag 384
 Arg Val Tyr Glu Ser Ala Glu Ala Ala Ala Glu Glu Lys Lys Asn Glu
 115 120 125
 cct tac aag ctg gaa ctt atc cag gac aag ggc aac gtt gat ccc aac 432
 Pro Tyr Lys Leu Glu Leu Ile Gln Asp Lys Gly Asn Val Asp Pro Asn
 130 135 140
 tct gat gaa gcc acc gaa gtg ggc gca gcc gaa ctg acc gcg tat gac 480
 Ser Asp Glu Ala Thr Glu Val Gly Ala Gly Glu Leu Thr Ala Tyr Asp
 145 150 155 160
 aac gtc aac cct cgc acc agt gag gtg gag tgg tct gat ctt tgc cgt 528
 Asn Val Asn Pro Arg Thr Ser Glu Val Glu Trp Ser Asp Leu Cys Arg
 165 170 175
 gga cca cac atc cca acc acc cgc tac att cca gca ttc gca ttg acc 576
 Gly Pro His Ile Pro Thr Thr Arg Tyr Ile Pro Ala Phe Ala Leu Thr
 180 185 190
 cga tca tcc gct gct tat tgg cgt ggc gat cag gat aat gct ggc ctg 624

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Arg Ser Ser Ala Ala Tyr Trp Arg Gly Asp Gln Asp Asn Ala Gly Leu
 195 205
 cag cgc atc tac ggt acc gcg tgg gag gat aag gaa tcc ctc gat gct 672
 Gln Arg Ile Tyr Gly Thr Ala Trp Glu Asp Lys Glu Ser Leu Asp Ala
 210 215 220
 tac cag acc atg ctc gct gag gca gaa aag cgc gat cac cgc cgt cta 720
 Tyr Gln Thr Met Leu Ala Glu Ala Glu Lys Arg Asp His Arg Arg Leu
 225 230 235 240
 ggc act gaa ctt gat ttg ttc tcc ttc cca gat gat ctg ggc tct ggt 768
 Gly Thr Glu Leu Asp Leu Phe Ser Phe Pro Asp Asp Leu Gly Ser Gly
 245 250 255
 ctg cca gta ttc cat ccc aac ggt ggc atc gtg cgc aat gag atg gaa 816
 Leu Pro Val Phe His Pro Asn Gly Gly Ile Val Arg Asn Glu Met Glu
 260 265 270
 gat cac tcc cgt cgc cgc cac atc gca gcg ggc tac tcc ttt gtg aac 864
 Asp His Ser Arg Arg Arg His Ile Ala Ala Gly Tyr Ser Phe Val Asn
 275 280 285
 acc ccg cac atc acc aag cag gat ctc ttt gag cgt tcc ggt cac ctt 912
 Thr Pro His Ile Thr Lys Gln Asp Leu Phe Glu Arg Ser Gly His Leu
 290 295 300
 ggt ttc tac aag gat ggc atg ttc cct cca atg cag gtg gat gcg gag 960
 Gly Phe Tyr Lys Asp Gly Met Phe Pro Pro Met Gln Val Asp Ala Glu
 305 310 315 320
 ttc gac gaa gac ggc aat gtg acc aag ccg ggc caa gag tac tac ctc 1008
 Phe Asp Glu Asp Gly Asn Val Thr Lys Pro Gly Gln Glu Tyr Tyr Leu
 325 330 335
 aag ccc atg aac tgc cca atg cac aac ctc atc ttc gat tct cgt gga 1056
 Lys Pro Met Asn Cys Pro Met His Asn Leu Ile Phe Asp Ser Arg Gly
 340 345 350
 cgt tct tac cgt gag ctt cca ctg cgt ctt ttt gag ttc ggc aac gtc 1104
 Arg Ser Tyr Arg Glu Leu Pro Leu Arg Leu Phe Glu Phe Gly Asn Val
 355 360 365
 tac cgc tac gaa aag tcc ggt gtg atc cac ggc ctg acc cgt gcc cgt 1152
 Tyr Arg Tyr Glu Lys Ser Gly Val Ile His Gly Leu Thr Arg Ala Arg
 370 375 380
 ggc ttc acc cag gac gat gct cac atc tac tgc acc gag gat cag ctg 1200
 Gly Phe Thr Gln Asp Asp Ala His Ile Tyr Cys Thr Glu Asp Gln Leu
 385 390 395 400
 gaa gca gag ctc acc tct gtg ctg gac ttc atc ctg tgc ctg ctg cgc 1248
 Glu Ala Glu Leu Thr Ser Val Leu Asp Phe Ile Leu Ser Leu Leu Arg
 405 410 415
 gat tac ggt ttg gat gat ttc tac ctg gag ctc tcc acc cgc gat cct 1296
 Asp Tyr Gly Leu Asp Asp Phe Tyr Leu Glu Leu Ser Thr Arg Asp Pro
 420 425 430
 aag aag tca gtc ggt tct gat gag atc tgg gag cgt tcc act gaa atc 1344
 Lys Lys Ser Val Gly Ser Asp Glu Ile Trp Glu Arg Ser Thr Glu Ile

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$\langle 210 \rangle$	334
$\langle 211 \rangle$	657

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 334

Asp Leu Pro Asn Lys Gly Pro Glu Ala Ile Val Cys Ala Lys Asp Ala
1 5 10 15

Glu Gly Gln Leu Lys Asp Leu Ser His Val Pro Glu Thr Thr Ala Thr
20 25 30

Phe Thr Ala Val Pro Ala Asn Thr Asp Asp Gly Arg Ala Val Ile Arg
35 40 45

His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro
50 55 60

Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr
65 70 75 80

Asp Phe Asp Ala Ala Glu Pro Phe Thr Pro Glu Asp Leu Lys Thr Ile
85 90 95

Glu Lys Arg Met Lys Lys Ile Ile Lys Thr Gly Gln Lys Phe Glu Arg
100 105 110

Arg Val Tyr Glu Ser Ala Glu Ala Ala Ala Glu Glu Leu Lys Asn Glu
115 120 125

Pro Tyr Lys Leu Glu Leu Ile Gln Asp Lys Gly Asn Val Asp Pro Asn
130 135 140

Ser Asp Glu Ala Thr Glu Val Gly Ala Gly Glu Leu Thr Ala Tyr Asp
145 150 155 160

Asn Val Asn Pro Arg Thr Ser Glu Val Glu Trp Ser Asp Leu Cys Arg
165 170 175

Gly Pro His Ile Pro Thr Thr Arg Tyr Ile Pro Ala Phe Ala Leu Thr
180 185 190

Arg Ser Ser Ala Ala Tyr Trp Arg Gly Asp Gln Asp Asn Ala Gly Leu
195 200 205

Gln Arg Ile Tyr Gly Thr Ala Trp Glu Asp Lys Glu Ser Leu Asp Ala
210 215 220

Tyr Gln Thr Met Leu Ala Glu Ala Glu Lys Arg Asp His Arg Arg Leu
225 230 235 240

Gly Thr Glu Leu Asp Leu Phe Ser Phe Pro Asp Asp Leu Gly Ser Gly
245 250 255

Leu Pro Val Phe His Pro Asn Gly Gly Ile Val Arg Asn Glu Met Glu
260 265 270

Asp His Ser Arg Arg Arg His Ile Ala Ala Gly Tyr Ser Phe Val Asn
275 280 285

Thr Pro His Ile Thr Lys Gln Asp Leu Phe Glu Arg Ser Gly His Leu
290 295 300

[illegible]

Gly Phe Tyr Lys Asp Gly Met Phe Pro Pro Met Gln Val Asp Ala Glu
 305 310 315 320
 Phe Asp Glu Asp Gly Asn Val Thr Lys Pro Gly Gln Glu Tyr Tyr Leu
 325 330 335
 Lys Pro Met Asn Cys Pro Met His Asn Leu Ile Phe Asp Ser Arg Gly
 340 345 350
 Arg Ser Tyr Arg Glu Leu Pro Leu Arg Leu Phe Glu Phe Gly Asn Val
 355 360 365
 Tyr Arg Tyr Glu Lys Ser Gly Val Ile His Gly Leu Thr Arg Ala Arg
 370 375 380
 Gly Phe Thr Gln Asp Asp Ala His Ile Tyr Cys Thr Glu Asp Gln Leu
 385 390 395 400
 Glu Ala Glu Leu Thr Ser Val Leu Asp Phe Ile Leu Ser Leu Leu Arg
 405 410 415
 Asp Tyr Gly Leu Asp Asp Phe Tyr Leu Glu Leu Ser Thr Arg Asp Pro
 420 425 430
 Lys Lys Ser Val Gly Ser Asp Glu Ile Trp Glu Arg Ser Thr Glu Ile
 435 440 445
 Leu Asn Arg Val Ala Thr Asn Ser Gly Leu Glu Leu Val Pro Asp Pro
 450 455 460
 Glu Gly Ala Ala Phe Tyr Gly Pro Lys Ile Ser Val Gln Ala Arg Asp
 465 470 475 480
 Ala Ile Gly Arg Thr Trp Gln Met Ser Thr Val Gln Leu Asp Phe Asn
 485 490 495
 Met Pro Glu Arg Phe Asn Leu Glu Tyr Thr Ser Ser Asp Gly Ser Lys
 500 505 510
 Gln Gln Pro Ile Met Ile His Arg Ala Leu Phe Gly Ser Ile Glu Arg
 515 520 525
 Phe Phe Gly Val Leu Leu Glu His Tyr Ala Gly Ala Phe Pro Ala Trp
 530 535 540
 Leu Ala Pro His Gln Val Met Gly Ile Pro Val Ala Asp Asp Cys Ile
 545 550 555 560
 Pro His Leu Glu Thr Ile Thr Ala Gln Leu Arg Glu Lys Gly Ile Arg
 565 570 575
 Ala Asp Val Asp Thr Ser Asp Asp Arg Met Gln Lys Lys Ile Arg Asn
 580 585 590
 His Thr Thr Gly Lys Val Pro Phe Met Leu Leu Ala Gly Ala Arg Asp
 595 600 605
 Val Glu Ala Asn Ala Val Ser Phe Arg Phe Leu Asp Gly Thr Gln Val
 610 615 620
 Asn Gly Val Pro Val Asp Glu Ala Ile Ala Val Ile Ser Ser Trp Ile

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625 630 635 640

Gly Asp Arg Ile Asn Asp Gln Pro Ser Glu Asp Ser Ile Ala Ala Arg
645 650 655

Arg

<210> 335
<211> 461
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(438)
<223> RXN03169

<400> 335
gat ctg cag aac ccc acc gcc aag atg tcc aag tcc ggc gac aac ccg 48
Asp Leu Gln Asn Pro Thr Ala Lys Met Ser Lys Ser Gly Asp Asn Pro
1 5 10 15

aag ggc atc atc aac ctg ctt gat gat cca aag gtg tcc acc aag cgc 96
Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg
20 25 30

atc aag tcc gca gtc acc gac aac gac ggc gtc atc gcc tac gat cca 144
Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
35 40 45

gaa aac aag cct ggc gtg tcc aac ttg ctg gtc atc cag tct gcg ctg 192
Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
50 55 60

acg ggt acc tcc atc gat tcg ctt gtc gac ggc tac cag ggc gct ggc 240
Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
65 70 75 80

tac ggt gcg ttg aag ggt gac acc gcc gac gcg ctt gag gct ttc acc 288
Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr
85 90 95

act cct ttg aag gca aag tac gac gag tac atg aat gac cgc ggc gag 336
Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu
100 105 110

ctc gaa cga gtc ttg gct atc ggt gct gag cgc gcc acc gaa gtt gcc 384
Leu Glu Arg Val Leu Ala Ile Gly Ala Glu Arg Ala Thr Glu Val Ala
115 120 125

aac gaa acc ttg gct gat gtg tac gac aag att ggt ttc ttg gcg tct 432
Asn Glu Thr Leu Ala Asp Val Tyr Asp Lys Ile Gly Phe Leu Ala Ser
130 135 140

cgt cgc taacaactag accctcgatt att 461
Arg Arg
145

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<210> 336
 <211> 146
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 336
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 Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg
 20 25 30
 Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
 35 40 45
 Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
 50 55 60
 Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
 65 70 75 80
 Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr
 85 90 95
 Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu
 100 105 110
 Leu Glu Arg Val Leu Ala Ile Gly Ala Glu Arg Ala Thr Glu Val Ala
 115 120 125
 Asn Glu Thr Leu Ala Asp Val Tyr Asp Lys Ile Gly Phe Leu Ala Ser
 130 135 140
 Arg Arg
 145

<210> 337
 <211> 461
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(438)
 <223> FRXA02860

<400> 337
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 1 5 10 15
 aag ggc atc atc aac ctg ctt gat gat cca aag gtg tcc acc aag cgc 96
 Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg
 20 25 30
 atc aag tcc gca gtc acc gac aac gac ggc gtc atc gcc tac gat cca 144
 Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
 35 40 45
 gaa aac aag cct ggc gtg tcc aac ttg ctg gtc atc cag tct gcg ctg 192

002290.53325900

145

<211> 580

<213> *Corynebacterium glutamicum*

<221> CDS

<222> {101} .. {580}

<223> RXN03078

<400> 339

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accggaag gtcgtccaa ggtgactaca ctgatacagc atg acg acg cag gat 115
Met Thr Thr Gln Asp
1 5

aaa gat ctc acc gca caa acc gct tcc aga gtc ctt tct gga att cag 163
Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val Leu Ser Gly Ile Gln
10 15 20

ccc acc gcc gat tcc tat cac ctg ggc aat tac ttg gga gca gtc aag 211
Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr Leu Gly Ala Val Lys
25 30 35

cag tgg att gac ctg caa gat tcc tac gat gcc ttc tac ttc att cca 259
Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala Phe Tyr Phe Ile Pro
40 45 50

gat ctc cac gcg att acc gtc gat cag gaa cca gaa gag ctg cgc aac 307
Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro Glu Glu Leu Arg Asn
55 60 65

Ggc acc att tcc ggc gcc gca cag ctg ctg gcc ctg gcc att gat cca 355
Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala Leu Gly Ile Asp Pro
70 75 80 85

gaa cgc tcc acc ttg ttt gtg cag tgc cat gtt ccc gca cat gca gaa 403
Glu Arg Ser Thr Leu Phe Val Gln Ser His Val Pro Ala His Ala Glu
90 95 100

ctg tca tgg gtt ctg acc tgc ctg acc ggt ttc ggc gag gca tcc cgc 451
Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe Gly Glu Ala Ser Arg
105 110 115

atg acc cag ttc aag gac aag tcc tcc aag cgt ggc gcc gac cgt acc 499
Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg Gly Ala Asp Arg Thr
120 125 130

tca gct ggt ctg ttc acc tac ccg atg ctg atg gca gca gat att ttg 547
Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met Ala Ala Asp Ile Leu
135 140 145

ctg tac cgc cca cat ctt gtc cca gtc ggt gaa 580
Leu Tyr Arg Pro His Leu Val Pro Val Gly Glu
150 155 160

<210> 340
 <211> 160
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 340
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 Leu Ser Gly Ile Gln Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr
 20 25 30
 Leu Gly Ala Val Lys Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala
 35 40 45
 Phe Tyr Phe Ile Pro Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro
 50 55 60
 Glu Glu Leu Arg Asn Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala
 65 70 75 80
 Leu Gly Ile Asp Pro Glu Arg Ser Thr Leu Phe Val Gln Ser His Val
 85 90 95
 Pro Ala His Ala Glu Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe
 100 105 110
 Gly Glu Ala Ser Arg Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg
 115 120 125
 Gly Ala Asp Arg Thr Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met
 130 135 140
 Ala Ala Asp Ile Leu Leu Tyr Arg Pro His Leu Val Pro Val Gly Glu
 145 150 155 160

<210> 341
 <211> 580
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(580)
 <223> FRXA02866

<400> 341
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 accggaaaaag gtctgtccaa ggtgactaca ctgatacagc atg acg acg cag gat 115
 Met Thr Thr Gln Asp
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 aaa gat ctc acc gca caa acc gct tcc aga gtc ctt tct gga att cag 163
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Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr Leu Gly Ala Val Lys
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Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala Phe Tyr Phe Ile Pro
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Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro Glu Glu Leu Arg Asn
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Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala Leu Gly Ile Asp Pro
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Glu Arg Ser Thr Leu Phe Val Gln Ser His Val Pro Ala His Ala Glu
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Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe Gly Glu Ala Ser Arg
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Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met Ala Ala Asp Ile Leu
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Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala Ser Asp Lys Pro Gly
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Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr Gly Gln Leu His Met
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Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro Gly Met Asp His Ala
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Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr
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Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala
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Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe
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Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val
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Thr	Ile	His	Pro	Lys	Ser	Leu	Glu	Pro	Arg	Tyr	Phe	Asp	Trp	Val	Asp
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Ile	Pro	Ile	Trp	Tyr	Gly	Pro	Asn	Asp	Glu	Ile	Ile	Cys	Val	Gly	Pro
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Thr	Trp	Phe	Ser	Ser	Ala	Leu	Trp	Pro	Phe	Ser	Thr	Met	Gly	Trp	Pro
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Val Ala Val Asp Ala Asp Ala Ala Arg Arg Ile Gly Asp Val Glu Lys
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 Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Glu Gln Val Arg Leu
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gag ctc tac cac ttt gcg tgg aac gag ttc tgt gac tgg tac ctg gaa 2131
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<212> PRT

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 35 40 45

Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr
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Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala
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Leu Ala Arg Arg Lys Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro
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Gly Met Asp His Ala Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met
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Leu Lys Glu Thr Glu Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu
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Phe Ile Ala Lys Val Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile
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Gly Glu Gln Met Arg Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu
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Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe
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Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val
 180 185 190

Asn Trp Ser Pro Val Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile
 195 200 205

Tyr Lys Asp Val Glu Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu
 210 215 220

Asn Asp Asp Glu Pro His Val Ile Val Ala Thr Thr Arg Val Glu Thr
 225 230 235 240

Met Leu Gly Asp Val Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr
 245 250 255

Lys Asp Leu Val Gly Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu
 260 265 270

Ser Leu Lys Val Val Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser
 275 280 285

Gly Ala Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu
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Gly Leu Arg His Asn Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly

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 Arg Ile Ala Asp Thr Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu
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 Ala Arg Ile Lys Val Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val
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 Lys Glu Ile Arg Pro Tyr Val His Ser Val Gly His Ser Glu Arg Ser
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 Gly Glu Ala Ile Glu Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val
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 Glu Glu Leu Ala Lys Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr
 385 390 395 400
 Thr Ile His Pro Lys Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp
 405 410 415
 Asn Met His Asp Trp Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg
 420 425 430
 Ile Pro Ile Trp Tyr Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro
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 Asp Glu Gln Ala Pro Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp
 450 455 460
 Thr Trp Phe Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro
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 Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val
 485 490 495
 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Met Phe
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 Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys
 515 520 525
 Asp Gly Arg Pro Gln Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu
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 Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly
 545 550 555 560
 Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg
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 Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly
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 Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn
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 Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro
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 Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu
 625 630 635 640

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 <223> RXN00454

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 Met Gly Gly Glu Ala
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ggc tgc acg tta gac ttg gca cct atg tca gat ctt tca ttc acc ctc 163
 Gly Cys Thr Leu Asp Leu Ala Pro Met Ser Asp Leu Ser Phe Thr Leu
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aac aac aag ctt gcc gat gac gcc ccc ggc aag cat ggt cgt aca ggt 211
 Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys His Gly Arg Thr Gly
 25 30 35

gta atc cac aca cct cac ggt gat att gcc acc cct gct ttc att cct 259
 Val Ile His Thr Pro His Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro
 40 45 50

gtg gct acc aaa gcc acg gtg aaa acc ctt acc cct gag cag att cgg 307
 Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr Pro Glu Gln Ile Arg
 55 60 65

gag acc ggc gca cag gct att ttg tcc aac gcc tac cac ctg tat ctg 355
 Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu
 70 75 80 85

cag cct ggc ccc gac atc gtg gac gag gct ggc ggt gtg tct gcc ttt 403
 Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly Gly Val Ser Ala Phe
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 Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val
 105 110 115

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 Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu Ala Met Asp Thr Thr
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aac ttg acg cgc aac gat atc aag gcg gct aaa aaa gag cgc atg gcg 547

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RESEARCH

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cgt gcc agc atc gat gat	ggc acg tac tac	gaa ttc aag gaa gaa ttc	1363
Arg Ala Ser Ile Asp Asp	Gly Thr Tyr Tyr	Glu Phe Lys Glu Glu Phe	
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tta ggc cgg tac tac gcg	tcg aag gtt tca	taacottcgc ggcgtttcac	1413
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Pro Ala Phe Ile	Pro Val Ala Thr Lys Ala	Thr Val Lys Thr Leu Thr	
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Pro Glu Gln Ile	Arg Glu Thr Gly Ala Gln	Ala Ile Leu Ser Asn Ala	
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Tyr His Leu Tyr	Leu Gln Pro Gly Pro Asp	Ile Val Asp Glu Ala Gly	
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Gly Val Ser Ala	Phe Glu Asn Trp His Gly	Pro Thr Tyr Thr Asp Ser	
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Lys Glu Arg Met	Ala Leu Val Asp Glu Asp	Gly Val Asp Phe Lys Ser	
	145	150 155	160
Val Ile Asp Gly	Ser Lys His Arg Phe Thr	Pro Glu Val Ser Met Gln	
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Ile Gln His Gln	Leu Gly Ala Asp Ile Ile	Phe Ala Phe Asp Glu Leu	
	180	185 190	
Thr Thr Leu Val	Asp Thr Tyr Asp	Tyr Gln Val Glu Ser Val Glu Arg	
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Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu His Glu Arg Leu Thr
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Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu Trp Gly Val Val Gln
225 230 235 240

Gly Ala Gln Phe Glu Asp Leu Arg Arg Gln Ala Val Lys Gly Leu Leu
245 250 255

Asp Leu Asp Arg Gln Ala Ala Asp Glu Gly Arg Arg Gly Phe Gly Gly
260 265 270

Phe Gly Ile Gly Gly Ala Leu Glu Lys Glu Asn Leu Gly Thr Ile Val
275 280 285

Gly Trp Val Cys Asp Glu Leu Pro Glu Asp Lys Pro Arg His Leu Leu
290 295 300

Gly Ile Ser Glu Pro Asp Asp Leu Phe Val Ala Val Glu Ala Gly Ala
305 310 315 320

Asp Thr Phe Asp Cys Val Ala Pro Thr Arg Leu Gly Arg Arg Gly Gly
325 330 335

Val Tyr Thr Leu Asp Gly Arg Met Asn Leu Thr Gly Ala Arg Phe Lys
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Arg Asp Phe Lys Gly Ile Asp Glu Glu Val Gly Gly Tyr Ala Ser Glu
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Asn Tyr Ser Arg Ala Tyr Ile His His Leu Leu Lys Ala Lys Glu Phe
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Leu Ala Gly Thr Leu Cys Thr Met His Asn Leu His Phe Met Ile Thr
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<223> FRXA00454

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Val Lys Thr Leu Thr Pro Glu Gln Ile Arg Glu Thr Gly Ala Gln Ala

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		35						40					45																
gtg	gac	gag	gct	ggc	ggt	gtg	tct	gcc	ttt	gag	aac	tgg	cac	ggc	ccc														192
Val	Asp	Glu	Ala	Gly	Gly	Val	Ser	Ala	Phe	Glu	Asn	Trp	His	Gly	Pro														
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acc	tac	acc	gac	tcc	ggc	gga	ttc	cag	gtc	atg	agc	ctg	ggc	tcc	ggc														240
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Phe	Lys	Lys	Val	Leu	Ala	Met	Asp	Thr	Thr	Asn	Leu	Thr	Arg	Asn	Asp														
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Ile	Lys	Ala	Ala	Lys	Lys	Glu	Arg	Met	Ala	Leu	Val	Asp	Glu	Asp	Gly														
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Glu	Val	Ser	Met	Gln	Ile	Gln	His	Gln	Leu	Gly	Ala	Asp	Ile	Ile	Phe														
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Ala	Phe	Asp	Glu	Leu	Thr	Thr	Leu	Val	Asp	Thr	Tyr	Asp	Tyr	Gln	Val														
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Glu	Ser	Val	Glu	Arg	Thr	Arg	Arg	Trp	Ala	Gln	Arg	Cys	Leu	Leu	Glu														
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His	Glu	Arg	Leu	Thr	Gln	Glu	Arg	Val	Asp	Lys	Pro	Leu	Gln	Ser	Leu														
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tgg	gga	gtg	gtg	cag	ggg	gcg	cag	ttc	gag	gat	ttg	cgt	cga	caa	gca														624
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gta	aaa	ggc	ctg	ttg	gac	ctg	gat	cgc	cag	gcc	gcc	gac	gaa	ggc	cgt														672
Val	Lys	Gly	Leu	Leu	Asp	Leu	Asp	Arg	Gln	Ala	Ala	Asp	Glu	Gly	Arg														
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Leu	Gly	Thr	Ile	Val	Gly	Trp	Val	Cys	Asp	Glu	Leu	Pro	Glu	Asp	Lys														
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35 40 45

Val Asp Glu Ala Gly Gly Val Ser Ala Phe Glu Asn Trp His Gly Pro
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Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly
65 70 75 80

Phe Lys Lys Val Leu Ala Met Asp Thr Thr Asn Leu Thr Arg Asn Asp
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Ile Lys Ala Ala Lys Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly
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Val Asp Phe Lys Ser Val Ile Asp Gly Ser Lys His Arg Phe Thr Pro
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Glu Val Ser Met Gln Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe
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Ala Phe Asp Glu Leu Thr Thr Leu Val Asp Thr Tyr Asp Tyr Gln Val
145 150 155 160

Glu Ser Val Glu Arg Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu
165 170 175

His Glu Arg Leu Thr Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu
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Trp Gly Val Val Gln Gly Ala Gln Phe Glu Asp Leu Arg Arg Gln Ala
195 200 205

Val Lys Gly Leu Leu Asp Leu Asp Arg Gln Ala Ala Asp Glu Gly Arg
210 215 220

Arg Gly Phe Gly Gly Phe Gly Ile Gly Gly Ala Leu Glu Lys Glu Asn
225 230 235 240

Leu Gly Thr Ile Val Gly Trp Val Cys Asp Glu Leu Pro Glu Asp Lys
245 250 255

Pro Arg His Leu Leu Gly Ile Ser Glu Pro Asp Asp Leu Phe Val Ala

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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 Met Asn Ala Pro Ala
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cct aaa cct gga ctc gtg atc gtc gac aag ccc gcc gga atg aca tcc 163
 Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro Ala Gly Met Thr Ser
 10 15 20

cat gac gtg gtg tcc aaa ttg cgc cgc gca ttt tcc acc cgc aaa gta 211
 His Asp Val Val Ser Lys Leu Arg Arg Ala Phe Ser Thr Arg Lys Val
 25 30 35

ggc cac gca ggc acc ctc gac ccc atg gca acc ggc gtg tta gtc gtc 259
 Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr Gly Val Leu Val Val
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gga att gag cgc gga acc cgc ttc ctg gca cac atg gtg gcc tcc acc 307
 Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His Met Val Ala Ser Thr
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 Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala Ala Thr Ser Thr Asp
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gat gca gaa ggc gag gtt atc tcc aca aca gac gca tcc ggc ctc gac 403
 Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp Ala Ser Gly Leu Asp
 90 95 100

cac agc acc atc ctt gct gaa atc gtc aac ctc acc ggc gac atc atg 451
 His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu Thr Gly Asp Ile Met
 105 110 115

caa aaa ccc acc aaa gtc tcc gcc atc aaa atc gac ggc aaa cgc gcc 499
 Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile Asp Gly Lys Arg Ala
 120 125 130

cac gaa cgc gtc cgc gac ggc gaa gaa gta gac att ccc gca cgt ccc 547
 His Glu Arg Val Arg Asp Gly Glu Glu Val Asp Ile Pro Ala Arg Pro
 135 140 145

00602039 062700

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 Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr His Val Asp Gly Glu
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 Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser Ser Gly Thr Tyr Ile
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 Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu Gln Val Gly Gly His
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 ctg acc gcg ctt agg cgc aca gag gtc gcc cct ttt acg ctt aac gac 739
 Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro Phe Thr Leu Asn Asp
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 gcg acc ccc ctc tcc aaa ctc caa gag aat cca gaa ctc tcc ctc aac 787
 Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro Glu Leu Ser Leu Asn
 215 220 225
 ctc gac cag gca ctc acc cgc agt tac cca gtc ctt gac atc acc gaa 835
 Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val Leu Asp Ile Thr Glu
 230 235 240 245
 gac gaa gcc gtt gac ctg tcc atg gcc aaa tgg ttg gaa cct cgc gga 883
 Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp Leu Glu Pro Arg Gly
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<211> 297

<212> PRT

<213> Corynebacterium glutamicum

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Ser Thr Arg Lys Val Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr
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Gly Val Leu Val Val Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His
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Met Val Ala Ser Thr Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala

0002290 6320350

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Ala Ser Gly Leu Asp His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu	100	105	110
Thr Gly Asp Ile Met Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile	115	120	125
Asp Gly Lys Arg Ala His Glu Arg Val Arg Asp Gly Glu Glu Val Asp	130	135	140
Ile Pro Ala Arg Pro Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr	145	150	155
His Val Asp Gly Glu Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser	165	170	175
Ser Gly Thr Tyr Ile Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu	180	185	190
Gln Val Gly Gly His Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro	195	200	205
Phe Thr Leu Asn Asp Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro	210	215	220
Glu Leu Ser Leu Asn Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val	225	230	235
Leu Asp Ile Thr Glu Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp	245	250	255
Leu Glu Pro Arg Gly Leu Lys Gly Val His Ala Ala Val Thr Pro Ser	260	265	270
Gly Lys Ala Val Ala Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr	275	280	285
Val Phe Val Ala His Pro Asn Thr Leu	290	295	

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 Met Asn Ala Pro Ala
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Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro Ala Gly Met Thr Ser	
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cat gac gtg gtg tcc aaa ttg cgc cgc gca ttt tcc acc cgc aaa gta	211
His Asp Val Val Ser Lys Leu Arg Arg Ala Phe Ser Thr Arg Lys Val	
25 30 35	
ggc cac gca ggc acc ctc gac ccc atg gca acc ggc gtg tta gtc gtc	259
Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr Gly Val Leu Val Val	
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Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His Met Val Ala Ser Thr	
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aaa gcc tac gac gcc acc att cga ctc ggc gcc gcc acc agc acc gat	355
Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala Ala Thr Ser Thr Asp	
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Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp Ala Ser Gly Leu Asp	
90 95 100	
cac agc acc atc ctt gct gaa atc gtc aac ctc acc ggc gac atc atg	451
His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu Thr Gly Asp Ile Met	
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Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile Asp Gly Lys Arg Ala	
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cac gaa cgc gtc cgc gac ggc gaa gaa gta gac att ccc gca cgt ccc	547
His Glu Arg Val Arg Asp Gly Glu Glu Val Asp Ile Pro Ala Arg Pro	
135 140 145	
gtc acc gtc agc gtc ttt gac gtg ctc gac tac cac gtc gac ggt gaa	595
Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr His Val Asp Gly Glu	
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ttt tat gac tta gat gtg cgc gtc cac tgc tcc tcc ggc acc tac atc	643
Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser Ser Gly Thr Tyr Ile	
170 175 180	
cgc gcg ctc gcc cgc gac ctc ggc aac gct ttg cag gtc ggc ggc cac	691
Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu Gln Val Gly Gly His	
185 190 195	
ctg acc gcg ctt agg cgc aca gag gtc ggc cct ttt acg ctt aac gac	739
Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro Phe Thr Leu Asn Asp	
200 205 210	
gcg acc ccc ctc tcc aaa ctc caa gag aat cca gaa ctc tcc ctc aac	787
Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro Glu Leu Ser Leu Asn	
215 220 225	
ctc gac cag gca ctc acc cgc agt tac cca gtc ctt gac atc acc gaa	835
Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val Leu Asp Ile Thr Glu	
230 235 240 245	

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Gly Asp Val Gly Gln Leu Val Phe Leu His Met Arg Phe His Gly Phe
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 360 365 370
 gcg ggt gaa ttg ctg cca cgt ttg cac aag tta gtg cgt gct gat tgc 1267
 Ala Gly Glu Leu Leu Pro Arg Leu His Lys Leu Val Arg Ala Asp Cys
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 390 395 400 405
 cat ttg gaa gag cgc atc gcg gag atc gcc gca aag gaa gat ctt gcc 1363
 His Leu Glu Glu Arg Ile Ala Glu Ile Ala Lys Glu Asp Leu Ala
 410 415 420
 agg gtg cgc cca gat ttg gat ggc aat gag atc atg gag att ctg aac 1411
 Arg Val Arg Pro Asp Leu Asp Gly Asn Glu Ile Met Glu Ile Leu Asn
 425 430 435
 atc caa gcc gga cct gaa gtg ggt aag gcg tgg gcg ttt ttg aag gag 1459
 Ile Gln Ala Gly Pro Glu Val Gly Lys Ala Trp Ala Phe Leu Lys Glu
 440 445 450
 ctt cgt ttg gag cgc ggt cct ttg gat cgt gaa gtt gcc atc gca gag 1507
 Leu Arg Leu Glu Arg Gly Pro Leu Asp Arg Glu Val Ala Ile Ala Glu
 455 460 465
 ctg aag agc tgg tgg gaa gga gaa aac aat gag tgatttttat gccgacaggt 1560
 Leu Lys Ser Trp Trp Glu Gly Glu Asn Asn Glu
 470 475 480
 tgt 1563

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Ala Ile Gly Glu Leu Ser Asp Ile Leu Val Pro Leu Ala Ala Ala Phe
 20 25 30
 Ser Ser Lys Gly His Ser Leu Tyr Leu Val Gly Gly Ser Val Arg Asp
 35 40 45
 Ala Phe Leu Gly Glu Leu Gly His Asp Leu Asp Phe Thr Thr Ser Ala
 50 55 60
 Arg Pro Glu Glu Thr Lys Ala Ile Leu Asp Asp Tyr Ala Asp Val Val
 65 70 75 80
 Trp Asp Thr Gly Ile Ala Phe Gly Thr Leu Ser Ala Glu Lys His Gly
 85 90 95

00220 00220 00220

Gln Gln Ile Glu Ile Thr Thr Phe Arg Ser Asp Leu Tyr Asp Gly Asn
 100 105
 Ser Arg Asn Pro Glu Val Thr Phe Gly Asp Thr Leu Glu Gly Asp Leu
 115 120 125
 Ile Arg Arg Asp Phe Lys Val Asn Ala Met Ala Val Glu Ile Gln Ala
 130 135 140
 Asp Gly Glu Leu Thr Phe His Asp Pro Val Gly Gly Leu Glu Asp Leu
 145 150 155 160
 Leu Thr His Thr Leu Asp Thr Pro Ala Thr Pro Glu Gln Ser Phe Asn
 165 170 175
 Asp Asp Pro Leu Arg Met Leu Arg Ala Ala Arg Phe Val Ser Gln Leu
 180 185 190
 Asn Phe Thr Leu Ala Pro Arg Val Ile Thr Ala Met Thr Glu Met Ala
 195 200 205
 Gln Gln Ile Thr Arg Ile Thr Val Glu Arg Met Gln Val Glu Leu Asp
 210 215 220
 Lys Met Ile Leu Gly Lys Asn Pro Glu Ala Gly Ile Asp Leu Met Val
 225 230 235 240
 Glu Ser Gly Ile Ala Gln Ile Ile Tyr Pro Glu Ile Pro Ala Met Gln
 245 250 255
 Met Thr Gln Asp Glu His Met Gln His Lys Asp Val Tyr Ala His Ser
 260 265 270
 Leu Gln Val Met Arg Gln Ala Ile Asp Gln Glu Glu Asp Gly Pro Asp
 275 280 285
 Leu Val Leu Arg Trp Ala Ala Leu Leu His Asp Cys Gly Lys Pro Asp
 290 295 300
 Thr Arg Asp Phe Asn Glu Glu Gly Arg Val Ser Phe His Gln His Glu
 305 310 315 320
 Val Val Gly Ala Lys Leu Val Arg Arg Arg Met Arg Lys Leu Lys Tyr
 325 330 335
 Ser Lys Gln Met Val Gly Asp Val Gly Gln Leu Val Phe Leu His Met
 340 345 350
 Arg Phe His Gly Phe Ser Glu Gly Gln Trp Thr Asp Ser Ala Val Arg
 355 360 365
 Arg Tyr Ala Ala Asp Ala Gly Glu Leu Leu Pro Arg Leu His Lys Leu
 370 375 380
 Val Arg Ala Asp Cys Thr Thr Arg Asn Lys Arg Lys Ala Ala Arg Leu
 385 390 395 400
 Gln Ala Thr Tyr Asp His Leu Glu Glu Arg Ile Ala Glu Ile Ala Ala
 405 410 415

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Lys Glu Asp Leu Ala Arg Val Arg Pro Asp Leu Asp Gly Asn Glu Ile
420 425 430

Met Glu Ile Leu Asn Ile Gln Ala Gly Pro Glu Val Gly Lys Ala Trp
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Ala Phe Leu Lys Glu Leu Arg Leu Glu Arg Gly Pro Leu Asp Arg Glu
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<220>
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<223> RXN01704

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Ala Asp Arg Val Asp Ser Arg Cys Pro Ala Ala Ala Ala Gly Ala Gly
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tgc tgt gac tat gca gaa ctc aac cca act gtg gag ctt gag atc aag 144
Cys Cys Asp Tyr Ala Glu Leu Asn Pro Thr Val Glu Leu Glu Ile Lys
35 40 45

tcc cgc gtg ctt cgt gat cag ttg gag cgc atc ggt gga atc gat gag 192
Ser Arg Val Leu Arg Asp Gln Leu Glu Arg Ile Gly Gly Ile Asp Glu
50 55 60

ctt cct gaa ttt gag ctt caa gat ctg gag cca aca gct ggt tgg cgt 240
Leu Pro Glu Phe Glu Leu Gln Asp Leu Glu Pro Thr Ala Gly Trp Arg
65 70 75 80

acc cgc gtt cgc ctc ggc gtt gat gcg tct ggt cgt gcc ggg ttc cgc 288
Thr Arg Val Arg Leu Gly Val Asp Ala Ser Gly Arg Ala Gly Phe Arg
85 90 95

aag ctg aag tcc aat gag ttg gtt act gag gtt gcg tgt tct cag gtt 336
Lys Leu Lys Ser Asn Glu Leu Val Thr Glu Val Ala Cys Ser Gln Val
100 105 110

gtg cca gag ctt ctt gag ggc ctt gtg ggt gag ggc gct cgt cgt ttc 384
Val Pro Glu Leu Leu Glu Gly Leu Val Gly Glu Gly Ala Arg Arg Phe
115 120 125

acc cct ggc gtg gag atc att gca gct att gat gat gcg ggt cag cgc 432
Thr Pro Gly Val Glu Ile Ile Ala Ala Ile Asp Asp Ala Gly Gln Arg

002290.06300

130	135	140	
cac gtt gtg gaa tcc cgt aag gct cct cgt ggt cgt cgt act gaa act			480
His Val Val Glu Ser Arg Lys Ala Pro Arg Gly Arg Arg Thr Glu Thr			
145	150	155	160
gtg ttg aag gtg ctg gaa ggc act ggc gag gtg gag cag aag gta ggc			528
Val Leu Lys Val Leu Glu Gly Thr Gly Val Glu Gln Lys Val Gly			
	165	170	175
gat tac acc tgg aag ttc cca gtt tct tcc ttc tgg cag gcg cac acc			576
Asp Tyr Thr Trp Lys Phe Pro Val Ser Ser Phe Trp Gln Ala His Thr			
	180	185	190
aag gcc cct gcg gcg tat tca gag ttc atc gcc gaa gcg tta acc gga			624
Lys Ala Pro Ala Ala Tyr Ser Glu Phe Ile Ala Glu Ala Leu Thr Gly			
	195	200	205
ttg gaa ctg gtt gac gtc gat aag cgt ggc cct gtt gcg tgg gac ctt			672
Leu Glu Leu Val Asp Val Asp Lys Arg Gly Pro Val Ala Trp Asp Leu			
	210	215	220
tat ggc ggc gtc ggc ctg ttc gcg ccg att atc acc agc aag ctg cag			720
Tyr Gly Gly Val Gly Leu Phe Ala Pro Ile Ile Thr Ser Lys Leu Gln			
	225	230	240
gca gct gtc cac tct gtg gag ctg tcc cca ggt tca gcg gag gct ggc			768
Ala Ala Val His Ser Val Glu Leu Ser Pro Gly Ser Ala Glu Ala Gly			
	245	250	255
gaa gag gcg ttg gct ggt ttg cct gtc act ttc cac act ggt cgg gta			816
Glu Glu Ala Leu Ala Gly Leu Pro Val Thr Phe His Thr Gly Arg Val			
	260	265	270
gag ggc atg gcg tcc cag ctg cct tcg cca aac gtg gtt gtt ttg gat			864
Glu Gly Met Ala Ser Gln Leu Pro Ser Pro Asn Val Val Val Leu Asp			
	275	280	285
cct cct cgc acc ggt gca ggc agt gac gtg ttg aag agc atc gcg gag			912
Pro Pro Arg Thr Gly Ala Gly Ser Asp Val Leu Lys Ser Ile Ala Glu			
	290	295	300
gct aag cct cag ctg gtt atc cac att ggt tgt gac ccg gcg act ttc			960
Ala Lys Pro Gln Leu Val Ile His Ile Gly Cys Asp Pro Ala Thr Phe			
	305	310	315
gct cgc gac gtt gcc gat tgg aag ctc aac ggc tac gaa atg gat caa			1008
Ala Arg Asp Val Ala Asp Trp Lys Leu Asn Gly Tyr Glu Met Asp Gln			
	325	330	335
ttg gct gtt ttt aac gcg ttc cct gga act cac cac ttt gag acg att			1056
Leu Ala Val Phe Asn Ala Phe Pro Gly Thr His His Phe Glu Thr Ile			
	340	345	350
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Gly Val Phe Val Arg Val Ser			
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<213> Corynebacterium glutamicum

<400> 360

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Cys Cys Asp Tyr Ala Glu Leu Asn Pro Thr Val Glu Leu Glu Ile Lys
35 40 45

Ser Arg Val Leu Arg Asp Gln Leu Glu Arg Ile Gly Gly Ile Asp Glu
50 55 60

Leu Pro Glu Phe Glu Leu Gln Asp Leu Glu Pro Thr Ala Gly Trp Arg
65 70 75 80

Thr Arg Val Arg Leu Gly Val Asp Ala Ser Gly Arg Ala Gly Phe Arg
85 90 95

Lys Leu Lys Ser Asn Glu Leu Val Thr Glu Val Ala Cys Ser Gln Val
100 105 110

Val Pro Glu Leu Leu Glu Gly Leu Val Gly Glu Gly Ala Arg Arg Phe
115 120 125

Thr Pro Gly Val Glu Ile Ile Ala Ala Ile Asp Asp Ala Gly Gln Arg
130 135 140

His Val Val Glu Ser Arg Lys Ala Pro Arg Gly Arg Arg Thr Glu Thr
145 150 155 160

Val Leu Lys Val Leu Glu Gly Thr Gly Glu Val Glu Gln Lys Val Gly
165 170 175

Asp Tyr Thr Trp Lys Phe Pro Val Ser Ser Phe Trp Gln Ala His Thr
180 185 190

Lys Ala Pro Ala Ala Tyr Ser Glu Phe Ile Ala Glu Ala Leu Thr Gly
195 200 205

Leu Glu Leu Val Asp Val Asp Lys Arg Gly Pro Val Ala Trp Asp Leu
210 215 220

Tyr Gly Gly Val Gly Leu Phe Ala Pro Ile Ile Thr Ser Lys Leu Gln
225 230 235 240

Ala Ala Val His Ser Val Glu Leu Ser Pro Gly Ser Ala Glu Ala Gly
245 250 255

Glu Glu Ala Leu Ala Gly Leu Pro Val Thr Phe His Thr Gly Arg Val
260 265 270

Glu Gly Met Ala Ser Gln Leu Pro Ser Pro Asn Val Val Val Leu Asp
275 280 285

Pro Pro Arg Thr Gly Ala Gly Ser Asp Val Leu Lys Ser Ile Ala Glu
290 295 300

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gcg ccg att atc acc agc aag ctg caq qca gct gtc cac tct gtg gag 480

Figure 6

Glu Phe Ile Ala Glu Ala Leu Thr Gly Leu Glu Leu Val Asp Val Asp
 115 120 125
 Lys Arg Gly Pro Val Ala Trp Asp Leu Tyr Gly Gly Val Gly Leu Phe
 130 135 140
 Ala Pro Ile Ile Thr Ser Lys Leu Gln Ala Ala Val His Ser Val Glu
 145 150 155 160
 Leu Ser Pro Gly Ser Ala Glu Ala Gly Glu Glu Ala Leu Ala Gly Leu
 165 170 175
 Pro Val Thr Phe His Thr Gly Arg Val Glu Gly Met Ala Ser Gln Leu
 180 185 190
 Pro Ser Pro Asn Val Val Val Leu Asp Pro Pro Arg Thr Gly Ala Gly
 195 200 205
 Ser Asp Val Leu Lys Ser Ile Ala Glu Ala Lys Pro Gln Leu Val Ile
 210 215 220
 His Ile Gly Cys Asp Pro Ala Thr Phe Ala Arg Asp Val Ala Asp Trp
 225 230 235 240
 Lys Leu Asn Gly Tyr Glu Met Asp Gln Leu Ala Val Phe Asn Ala Phe
 245 250 255
 Pro Gly Thr His His Phe Glu Thr Ile Gly Val Phe Val Arg Val Ser
 260 265 270

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 <212> DNA
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 <222> (101)..(919)
 <223> RXA02523

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 ctccgaaaaat cttgattccc accgtctgcg gcttgatgtc gtg acc att ttc ccc 115
 Val Thr Ile Phe Pro
 1 5
 gaa tac ctg gat cct ctg cgc cat gcc ctg ctg ggt aag gcg att gag 163
 Glu Tyr Leu Asp Pro Leu Arg His Ala Leu Leu Gly Lys Ala Ile Glu
 10 15 20
 gat ggc att ttg gaa gtc ggt gtt cat gat ctt cgg aat tgg gcg acc 211
 Asp Gly Ile Leu Glu Val Gly Val His Asp Leu Arg Asn Trp Ala Thr
 25 30 35
 ggc gga cac aag gcc gtc gac gat acc ccg tat ggc ggt ggc ccg gcc 259
 Gly Gly His Lys Ala Val Asp Asp Thr Pro Tyr Gly Gly Gly Pro Gly

002250 6E820960

40	45	50	
atg gtg atg aag cca gag gtc tgg ggg cca gcg ctt gat gat gtc gcc Met Val Met Lys Pro Glu Val Trp Gly Pro Ala Leu Asp Asp Val Ala 55 60 65			307
gca ggc cgg gtg agc ggt gcg gaa ctc gat tgc gcc tgc ctg cac ctg Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser Ala Ser Leu His Leu 70 75 80 85			355
aaa aat gtg cgc cat gat gag ctg ggt ggc gtc gaa aag cgt gct tat Lys Asn Val Arg His Asp Glu Leu Gly Gly Val Glu Lys Arg Ala Tyr 90 95 100			403
gtc gtg gaa gaa gac cgc gac ctg cgc ctg ttg ctg gtg ccc acc cgc Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu Leu Val Pro Thr Pro 105 110 115			451
gct ggc aag cgc ttc acg cag gcg gat gcg cag gcg tgg tcc aac gag Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln Ala Trp Ser Asn Glu 120 125 130			499
gag cac att gtg ttc gcg tgc ggg cgc tac gag ggc att gac cag cgc Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu Gly Ile Asp Gln Arg 135 140 145			547
gtt att gat gat gcc gcc aac cgc tac cgc gtg cgc gag gta tgc atc Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val Arg Glu Val Ser Ile 150 155 160 165			595
ggc gat tat gtg ctg atc ggc ggg gaa gtg gca gtc ctg gtc atc gcg Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala Val Leu Val Ile Ala 170 175 180			643
gaa gcc gtc gtg cgc ctg atc cct ggc gtg ctc gga aac cgt agc agc Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu Gly Asn Arg Arg Ser 185 190 195			691
cac gaa gaa gac agc ttc tcc gat ggc ctg ctc gaa ggc cgc tgc tac His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu Glu Gly Pro Ser Tyr 200 205 210			739
aca aag cgc cgc acc tgg cgc gga ctt gac gtc ccc gaa gta cta ttc Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val Pro Glu Val Leu Phe 215 220 225			787
tgc ggc aac cac gcc aag gtc gat cgc tgg cga cgc gat cag gcg ctc Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg Arg Asp Gln Ala Leu 230 235 240 245			835
cta cgc acc cag gca att agg cct gag ctt atc gac gca tcc ctc ctc Leu Arg Thr Gln Ala Ile Arg Pro Glu Leu Ile Asp Ala Ser Leu Leu 250 255 260			883
gat tcc acc gac ctc aaa gta ttg gga ctg gac aaa tgacagagac Asp Ser Thr Asp Leu Lys Val Leu Gly Leu Asp Lys 265 270			929
cacacctcaa ccc			942

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Val Thr Ile Phe Pro Glu Tyr Leu Asp Pro Leu Arg His Ala Leu Leu
1 5 10 15

Gly Lys Ala Ile Glu Asp Gly Ile Leu Glu Val Gly Val His Asp Leu
20 25 30

Arg Asn Trp Ala Thr Gly Gly His Lys Ala Val Asp Asp Thr Pro Tyr
35 40 45

Gly Gly Gly Pro Gly Met Val Met Lys Pro Glu Val Trp Gly Pro Ala
50 55 60

Leu Asp Asp Val Ala Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser
65 70 75 80

Ala Ser Leu His Leu Lys Asn Val Arg His Asp Glu Leu Gly Gly Val
85 90 95

Glu Lys Arg Ala Tyr Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu
100 105 110

Leu Val Pro Thr Pro Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln
115 120 125

Ala Trp Ser Asn Glu Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu
130 135 140

Gly Ile Asp Gln Arg Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val
145 150 155 160

Arg Glu Val Ser Ile Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala
165 170 175

Val Leu Val Ile Ala Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu
180 185 190

Gly Asn Arg Arg Ser His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu
195 200 205

Glu Gly Pro Ser Tyr Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val
210 215 220

Pro Glu Val Leu Phe Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg
225 230 235 240

Arg Asp Gln Ala Leu Leu Arg Thr Gln Ala Ile Arg Pro Glu Leu Ile
245 250 255

Asp Ala Ser Leu Leu Asp Ser Thr Asp Leu Lys Val Leu Gly Leu Asp
260 265 270

Lys

gcg gat gat ctt ctt act cgc ctg gcg tat tca ggc ggt gac ctg ctg 643
Ala Asp Asp Leu Leu Thr Arg Leu Ala Tyr Ser Gly Gly Asp Leu Leu
170 175 180

ORGANIZATIONAL

gtt gag acc atg act ggc ctg gag cag ggc aca atc acc ccg cgc gcc 691
 Val Glu Thr Met Thr Gly Leu Glu Gln Gly Thr Ile Thr Pro Arg Ala
 185 190 195

cag gaa ggc gag gcc acg tac gcc tca aaa atc acc acc cag gac gcg 739
 Gln Glu Gly Glu Ala Thr Tyr Ala Ser Lys Ile Thr Thr Gln Asp Ala
 200 205 210

cag att gat tgg tgc aag ccc gcc gag gtc atc gac cgc cac atc agg 787
 Gln Ile Asp Trp Ser Lys Pro Ala Glu Val Ile Asp Arg His Ile Arg
 215 220 225

gca cat acc cca gga cct ggc gca tgg acc acg ctt gtc gac gcc cgc 835
 Ala His Thr Pro Gly Pro Gly Ala Trp Thr Thr Leu Val Asp Ala Arg
 230 235 240 245

ctc aag gtc ggg ccc atc agc cac tca ggc gag gtc gaa gta gca gcg 883
 Leu Lys Val Gly Pro Ile Ser His Ser Gly Glu Val Glu Val Ala Ala
 250 255 260

gac ttg gcg cct ggc gcc atc ctg gcg caa aag aac tcc gtg gtg gtc 931
 Asp Leu Ala Pro Gly Ala Ile Leu Ala Gln Lys Asn Ser Val Val Val
 265 270 275

gga acg ggc acc aca cca att gtt ctg ggc aat atc caa ccc ccg gga 979
 Gly Thr Gly Thr Thr Pro Ile Val Leu Gly Asn Ile Gln Pro Pro Gly
 280 285 290

aag aaa atg atg aat gca gca gac tgg gcg cgt ggt gtc caa ctt gat 1027
 Lys Lys Met Met Asn Ala Ala Asp Trp Ala Arg Gly Val Gln Leu Asp
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 Gln Glu Ala Lys Phe Gln
 310 315

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 <213> Corynebacterium glutamicum

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Gln Lys Leu Ile Asp Ser Asp His Glu Val Val Ala Val Leu Thr Gln
 20 25 30

Pro Asp Ala Arg Arg Gly Arg Gly Arg Thr Leu His Pro Ser Ala Val
 35 40 45

Ala Glu Leu Ala Gln Gln His Gly Ile Glu Val Leu Lys Pro Thr Ser
 50 55 60

Leu Lys Ala Asp Thr Glu Asp Gly Gln Ala Ile Arg Gln Arg Leu Ala
 65 70 75 80

Glu Leu Ala Pro Asp Cys Leu Pro Val Val Ala Tyr Gly Gln Leu Ile
 85 90 95

00000000.052000

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Ala Ala Gly His Glu Val Val Gly Val His Leu Ala Leu Ser Gln Asp
25 30 35

ccg caa acg gtg cgt gag tct tgc cgc ggt tgc tgc tct ctg gaa gat 259
Pro Gln Thr Val Arg Glu Ser Ser Arg Gly Cys Cys Ser Leu Glu Asp
40 45 50

tcc gct gat gct cgt cgc gtg tgt gac aag ttg ggt atc ccg ttt tat 307
Ser Ala Asp Ala Arg Arg Val Cys Asp Lys Leu Gly Ile Pro Phe Tyr
55 60 65

gtc tgg gat ttc tgc gat cgt ttc aag gaa gat gtg atc gac aac ttc 355
Val Trp Asp Phe Ser Asp Arg Phe Lys Glu Asp Val Ile Asp Asn Phe
70 75 80 85

att gat tct tac gcg atc ggt gag act cca aac cct tgc ctg cgt tgt 403
Ile Asp Ser Tyr Ala Ile Gly Glu Thr Pro Asn Pro Cys Leu Arg Cys
90 95 100

aat gag aaa atc aag ttt gcc gcc ttg ctt gag cgt gcc atc gcg ctt 451
Asn Glu Lys Ile Lys Phe Ala Ala Leu Leu Glu Arg Gly Ile Ala Leu
105 110 115

ggt ttc gat gca gtg gtt acc gcc cac tac gcg cgc ttg acc cag cct 499
Gly Phe Asp Ala Val Val Thr Gly His Tyr Ala Arg Leu Thr Gln Pro
120 125 130

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Ala Asp Gly Gly Asp Gly Tyr Leu Arg Arg Gly Val Asp Pro Asn Lys
135 140 145

gat cag tct tac gtg ctt ggt gtg ctt gcc gct cat gag atc gag cac 595
Asp Gln Ser Tyr Val Leu Gly Val Leu Gly Ala His Glu Ile Glu His
150 155 160 165

tgc atg ttc cca gtc gcc gat acc atc aag cct gaa atc cgt gaa gaa 643
Cys Met Phe Pro Val Gly Asp Thr Ile Lys Pro Glu Ile Arg Glu Glu
170 175 180

gcc agt gct gca ggt ttc tct gtg gca aag aag cca gac tcc tac gac 691
Ala Ser Ala Ala Gly Phe Ser Val Ala Lys Lys Pro Asp Ser Tyr Asp
185 190 195

att tgc ttc att ccg gat gcc aac acc cag gcg ttc ttg gcc aag cac 739
Ile Cys Phe Ile Pro Asp Gly Asn Thr Gln Ala Phe Leu Gly Lys His
200 205 210

atc ggt atg cgt ccg gcc atg atc gtg gat cag gaa gcc acg cat ctc 787
Ile Gly Met Arg Pro Gly Met Ile Val Asp Gln Glu Gly Thr His Leu
215 220 225

cgt gag cac gct ggt gtc cat gaa ttc acc att ggt cag cgc aag gcc 835
Arg Glu His Ala Gly Val His Glu Phe Thr Ile Gly Gln Arg Lys Gly
230 235 240 245

ctt gac att aag gct cca gca gcc gat ggt cgt cca cgt tac gtc acc 883
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5

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 Met Thr Asn Lys Tyr
 1 5
 ctg gtt gaa ggc tct gaa aac gag ctg acc aca aag acc gca gca gag 163
 Leu Val Glu Gly Ser Glu Asn Glu Leu Thr Thr Lys Thr Ala Ala Glu
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 ctg gca ggt ctt att cat tcc cgc gag gta act tcc cgc gag gtt act 211
 Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr Ser Arg Glu Val Thr
 25 30 35
 caa cgc cac cta gat cgc att gct gcg gtt gac gcc gat att cat gca 259
 Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp Gly Asp Ile His Ala
 40 45 50
 ttt ctc cac gtt ggc cag gag gag gcc ctg aac gcg gcg gat gac gtc 307
 Phe Leu His Val Gly Gln Glu Ala Leu Asn Ala Ala Asp Asp Val
 55 60 65
 gat aag cgt cta gac gct gga gag gca cct gcc tcg gct ttg gct gcc 355
 Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala Ser Ala Leu Ala Gly
 70 75 80 85
 gtg cgc ctt gcg ctg aag gat gtc ttt acc acc act gat gcg ccg acc 403
 Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr Asp Ala Pro Thr
 90 95 100
 acg gcg gca tcg aag atg ctt gag gcc tac atg agc cct tat gac gcg 451
 Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met Ser Pro Tyr Asp Ala
 105 110 115
 act gtg acc cgc aag atc cgt gag gct gcc atc cca att ttg ggt aag 499
 Thr Val Thr Arg Lys Ile Arg Glu Ala Gly Ile Pro Ile Leu Gly Lys
 120 125 130
 acc aac atg gat gag ttt gcg atg ggt tcc tcc act gag aac tcc gca 547
 Thr Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala
 135 140 145
 tac gcc cca acc cac aat ccg tgg gat ctg gag cgc acc gca ggt ggt 595

0002290-0002090

09502373

390 395 400 405

gac ttc gcc aag gct tac gag cag gtc gac atc ttg gtg tcc cca acc 1363
 Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile Leu Val Ser Pro Thr
 410 415 420

act cca acc acc gcg ttc aag ctg ggg gag aag gtc acc gat ccg ctg 1411
 Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys Val Thr Asp Pro Leu
 425 430 435

gag atg tac aac ttc gac ttg tgc acc ctg cca ctg aac ctg gct ggt 1459
 Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro Leu Asn Leu Ala Gly
 440 445 450

ctc gcg ggc atg tcc ctg cct tcc ggc ttg gca tca gat act ggt ctg 1507
 Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala Ser Asp Thr Gly Leu
 455 460 465

cct gtt ggt ttg cag ctg atg gct cct gct ttc cag gac gat cgt ctc 1555
 Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe Gln Asp Asn Leu Leu
 470 475 480 485

tac cgc gtc ggc gct gct ttt gaa gct gga cgc aag taggttctaa 1601
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 490 495

acctttttta aga 1614

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Lys Thr Ala Ala Glu Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr
 20 25 30
 Ser Arg Glu Val Thr Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp
 35 40 45
 Gly Asp Ile His Ala Phe Leu His Val Gly Gln Glu Ala Leu Asn
 50 55 60
 Ala Ala Asp Asp Val Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala
 65 70 75 80
 Ser Ala Leu Ala Gly Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr
 85 90 95
 Thr Asp Ala Pro Thr Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met
 100 105 110
 Ser Pro Tyr Asp Ala Thr Val Thr Arg Lys Ile Arg Glu Ala Gly Ile
 115 120 125
 Pro Ile Leu Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Ser Ser
 130 135 140

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Thr Glu Asn Ser Ala Tyr Gly Pro Thr His Asn Pro Trp Asp Leu Glu
 145 150 155 160
 Arg Thr Ala Gly Gly Ser Gly Gly Gly Ser Ser Ala Ala Leu Ala Ala
 165 170 175
 Gly Gln Ala Pro Leu Ala Ile Gly Thr Asp Thr Gly Gly Ser Ile Arg
 180 185 190
 Gln Pro Ala Ala Leu Thr Asn Thr Val Gly Val Lys Pro Thr Tyr Gly
 195 200 205
 Thr Val Ser Arg Tyr Gly Leu Ile Ala Cys Ala Ser Ser Leu Asp Gln
 210 215 220
 Gly Gly Pro Thr Ala Arg Thr Val Leu Asp Thr Ala Leu Leu His Glu
 225 230 235 240
 Val Ile Ala Gly His Asp Ala Phe Asp Ala Thr Ser Val Asn Arg Pro
 245 250 255
 Val Ala Pro Val Val Gln Ala Ala Arg Glu Gly Ala Asn Gly Asp Leu
 260 265 270
 Lys Gly Val Lys Val Gly Val Val Lys Gln Phe Asp Arg Asp Gly Tyr
 275 280 285
 Gln Pro Gly Val Leu Glu Ala Phe His Ala Ser Val Glu Gln Met Arg
 290 295 300
 Ser Gln Gly Ala Glu Ile Val Glu Val Asp Cys Pro His Phe Asp Asp
 305 310 315 320
 Ala Leu Gly Ala Tyr Tyr Leu Ile Leu Pro Cys Glu Val Ser Ser Asn
 325 330 335
 Leu Ala Arg Phe Asp Gly Met Arg Tyr Gly Leu Arg Ala Gly Asp Asp
 340 345 350
 Gly Thr Arg Ser Ala Asp Glu Val Met Ala Tyr Thr Arg Ala Gln Gly
 355 360 365
 Phe Gly Pro Glu Val Lys Arg Arg Ile Ile Leu Gly Thr Tyr Ala Leu
 370 375 380
 Ser Val Gly Tyr Tyr Asp Ala Tyr Tyr Leu Gln Ala Gln Arg Val Arg
 385 390 395 400
 Thr Leu Ile Ala Gln Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile
 405 410 415
 Leu Val Ser Pro Thr Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys
 420 425 430
 Val Thr Asp Pro Leu Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro
 435 440 445
 Leu Asn Leu Ala Gly Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala
 450 455 460

00602600 602600

Ser Asp Thr Gly Leu Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe
465 470 475 480

Gln Asp Asp Arg Leu Tyr Arg Val Gly Ala Ala Phe Glu Ala Gly Arg
485 490 495

Lys

<210> 375

<211> 420

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(397)

<223> RXA00210

<400> 375

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cttgtaccac ttgtgactag cgaagaggat cagaaaccaa gtg cct gag att tcg 115
Val Pro Glu Ile Ser
1 5

cgc gac cag gtc gct cac ctt gcc aaa ctt tcc aga ctg gcg ctc act 163
Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser Arg Leu Ala Leu Thr
10 15 20

gag gaa gaa ctc gag cag ttt gct gga cag atc gat gac att gtc gga 211
Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile Asp Asp Ile Val Gly
25 30 35

tat gtt tcc gca gtt caa aac gtc gac gcc gca ggt gtt gag cct atg 259
Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala Gly Val Glu Pro Met
40 45 50

agc cac ccg cac agc atc gcc acc acc atg cgt gaa gat gtc gtg cac 307
Ser His Pro His Ser Ile Ala Thr Thr Met Arg Glu Asp Val Val His
55 60 65

aag acc ctc gat gct gcg gct gcg ttg gac caa gcg ccc gct gtc gag 355
Lys Thr Leu Asp Ala Ala Ala Leu Asp Gln Ala Pro Ala Val Glu
70 75 80 85

gat gga cgt ttt atg gtt ccg cag att ctg ggt gag gcc gac 397
Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly Glu Gly Asp
90 95

taataattat gaccaacaag tac 420

<210> 376

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Val Pro Glu Ile Ser Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser

002290.5332960

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Arg Leu Ala Leu Thr Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile	20	25	30
Asp Asp Ile Val Gly Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala	35	40	45
Gly Val Glu Pro Met Ser His Pro His Ser Ile Ala Thr Thr Met Arg	50	55	60
Glu Asp Val Val His Lys Thr Leu Asp Ala Ala Ala Leu Asp Gln	65	70	75
Ala Pro Ala Val Glu Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly	85	90	95
Glu Gly Asp			

<210> 377

<211> 1260

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1237)

<223> RXA02686

<400> 377

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tggttacaca gcttaaccgc ccgaactaag gtgggtgtcc atg tct gtt gct caa	115
Met Ser Val Ala Gln	
1 5	

tta gcg aac cgc ttg gcc caa ctc tcc ccc gcc gag cat ggt ttt gca	163
Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala Glu His Gly Phe Ala	
10 15 20	

tgg ttc gac cct gaa atc acc gct ggc cat ggc gtt ggc cgg ttg cat	211
Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly Val Gly Pro Leu His	
25 30 35	

ggc atg gtg att cca gcc aag gac ctc aac gat gtc gca ggc atg ccc	259
Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp Val Ala Gly Met Pro	
40 45 50	

acc gcg ttc gga aat gca tct cgg cga aag gta gca aca gat acc gat	307
Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val Ala Thr Asp Thr Asp	
55 60 65	

ccg ttc atc caa aat ctc atc gac cgc ggc gcg atc atc gct ggc aaa	355
Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala Ile Ile Ala Gly Lys	
70 75 80 85	

acc caa acc agc gag ctc ggc atg acg gcg tat tgc gaa ccc atc gac	403
Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr Cys Glu Pro Ile Asp	
90 95 100	

00602686.062300

ggt ggt gca gcc atc agc gtg cct gtt gaa ggt gtc ggc att cat ett 1171
 Gly Gly Ala Ala Ile Ser Val Pro Val Glu Gly Val Gly Ile His Leu
 345 350 355

ggt ggg ata cgc gta cga gat gaa gac ctc tta gga tta gca gca ttt 1219
 Gly Gly Ile Arg Val Arg Asp Glu Asp Leu Leu Gly Leu Ala Ala Phe
 360 365 370

gtg gaa aga gct gtg gca tgagtagttc agtaaatgtca ccg 1260
 Val Glu Arg Ala Val Ala
 375

<210> 378

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 378

Met Ser Val Ala Gln Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala
 1 5 10 15

Glu His Gly Phe Ala Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly
 20 25 30

Val Gly Pro Leu His Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp
 35 40 45

Val Ala Gly Met Pro Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val
 50 55 60

Ala Thr Asp Thr Asp Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala
 65 70 75 80

Ile Ile Ala Gly Lys Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr
 85 90 95

Cys Glu Pro Ile Asp Met Asp Ala Pro Ser Asn Pro Val Leu Pro Gly
 100 105 110

His Thr Pro Gly Gly Ser Ser Gly Gly Ala Ala Val Ala Val Ala Arg
 115 120 125

Ser Leu Val Asp Ala Ala His Ala Ser Asp Gly Gly Gly Ser Ile Arg
 130 135 140

Val Pro Ala Ala Ala Cys Gly Leu Val Gly Phe Lys Pro Ala His Asp
 145 150 155 160

Ser Ser Gly Gly Asn Pro Ser Thr Gln Gly Phe Ile Thr Arg Asp Val
 165 170 175

Ala Thr Gln Val Arg Leu His Ala Leu Gln Pro Arg Thr Arg Arg Leu
 180 185 190

Arg Ile Gly Val Leu Ala Glu Pro Ile His Ala Asn Ser Leu Val Asp
 195 200 205

Ala Pro Phe Leu Ser Ile Leu Glu Ser Thr Ala His Leu Leu Glu Lys
 210 215 220

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Ala Gly His Glu Ile Val Ser Val Pro Leu Pro Tyr Gly Ala Trp Ala
225 230 235 240

Phe Asp Ala Tyr Thr Glu Val Phe Met Met Lys Ser Ala Gly Leu Thr
245 250 255

Asn Leu Gly Ser Pro Ile Thr Arg Trp Leu Ser Glu Gln Gly Arg Ser
260 265 270

Leu Ser Pro Ser Asp Arg Gln Ser Ser Val Lys Ala Phe Asp Ser Val
275 280 285

Ala Glu Thr Val His Gly Ala Trp Asp Ile Asp Val Leu Leu Thr Pro
290 295 300

Thr Leu Ala Tyr Ala Pro Pro Lys Ile Gly Tyr Phe Ser Ser Met Pro
305 310 315 320

Pro Glu Glu Asp Phe Leu Ala Gln Thr Lys Trp Thr Pro Trp Ala Thr
325 330 335

Leu Phe Asn Met Thr Gly Gly Ala Ala Ile Ser Val Pro Val Glu Gly
340 345 350

Val Gly Ile His Leu Gly Gly Ile Arg Val Arg Asp Glu Asp Leu Leu
355 360 365

Gly Leu Ala Ala Phe Val Glu Arg Ala Val Ala
370 375

<210> 379

<211> 886

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> RXA02625

<400> 379

ctcaattaag cagcaatccg agccggggga gcgctgtcag aaatggaccg tgccacccca 60

tgacaacatg cttgcacaat gatgactaga ataatgaccc atg act gca gcc ttt 115
Met Thr Ala Ala Phe
1 5

tat gat ctg atg gac ttc gat gaa gtt cta gag aaa tat gac cgg gtg 163
Tyr Asp Leu Met Asp Phe Asp Glu Val Leu Glu Lys Tyr Asp Pro Val
10 15 20

atg gga ctt gag gtc cac gtc gaa ctg ggc act gag acc aag atg ttc 211
Met Gly Leu Glu Val His Val Glu Leu Gly Thr Glu Thr Lys Met Phe
25 30 35

tct gca tct tct gca cac ttt ggc gct gaa ccc aat agc aat gtt gac 259
Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro Asn Ser Asn Val Asp
40 45 50

cca gtt tct ttg ggt ctc cca ggc gca ctt cct gtg gtt aac gcc aag 307

00602039 002300

Pro Val Ser Leu Gly Leu	Pro Gly Ala Leu	Pro Val Val Asn Ala Lys	
55	60	65	
ggc gtg gag tgg gca att aag att gga ctg gcg ctg aac tgc agc atc			355
Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala Leu Asn Cys Ser Ile			
70	75	80	85
gct gag tcc tca cgc ttt gca cgt aag aac tac ttc tac ccg gat cag			403
Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Gln			
	90	95	100
cct aag aac tac cag atc tcc cag tat gac gag cca atc gca tac gac			451
Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu Pro Ile Ala Tyr Asp			
	105	110	115
ggc tac ctg gat gtt gtt ctg gag gac gcc acc gag tgg cgt gtg gaa			499
Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr Glu Trp Arg Val Glu			
	120	125	130
atc gaa cgc gct cac atg gag gaa gac acc gga aag ctc acc cac ctg			547
Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly Lys Leu Thr His Leu			
	135	140	145
ggt ggt act tct ggt cgt att cac gcc gca acc gct tct ttg gtg gac			595
Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr Ala Ser Leu Val Asp			
	150	155	160
tgc aac cgt gca gcc gtc cct ttg att gag gtt gtc acc aag cca atc			643
Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val Val Thr Lys Pro Ile			
	170	175	180
gaa gcc gct gcc gct cgc gct cca gag atc gct aag gct tat gtc tcc			691
Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala Lys Ala Tyr Val Ser			
	185	190	195
gca ctg cgc gat ctg gtt aag gcg ctc ggt gtg tcc gac gcc cgc ttg			739
Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val Ser Asp Gly Arg Leu			
	200	205	210
gat cag ggt tct atg cgt gtc gac gcc aac ctg tcc ctg cgc ccg atc			787
Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu Ser Leu Arg Pro Ile			
	215	220	225
ggc cag gag gaa ttc gcc acc cgt acc gaa acc aag aac atc aac tcc			835
Gly Gln Glu Glu Phe Gly Thr Arg Thr Glu Thr Lys Asn Ile Asn Ser			
	230	235	240
ctg aag tcc gtt gag cag gcc agc acc ttt gag atg cag cgc cag gct			883
Leu Lys Ser Val Glu Gln Ala Ser Thr Phe Glu Met Gln Arg Gln Ala			
	250	255	260
cag			886
Gln			

<210> 380

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

00602879 062300

<400> 380

Met Thr Ala Ala Phe Tyr Asp Leu Met Asp Phe Asp Glu Val Leu Glu
 1 5 10 15

Lys Tyr Asp Pro Val Met Gly Leu Glu Val His Val Glu Leu Gly Thr
 20 25 30

Glu Thr Lys Met Phe Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro
 35 40 45

Asn Ser Asn Val Asp Pro Val Ser Leu Gly Leu Pro Gly Ala Leu Pro
 50 55 60

Val Val Asn Ala Lys Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala
 65 70 75 80

Leu Asn Cys Ser Ile Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr
 85 90 95

Phe Tyr Pro Asp Gln Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu
 100 105 110

Pro Ile Ala Tyr Asp Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr
 115 120 125

Glu Trp Arg Val Glu Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly
 130 135 140

Lys Leu Thr His Leu Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr
 145 150 155 160

Ala Ser Leu Val Asp Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val
 165 170 175

Val Thr Lys Pro Ile Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala
 180 185 190

Lys Ala Tyr Val Ser Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val
 195 200 205

Ser Asp Gly Arg Leu Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu
 210 215 220

Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Arg Thr Glu Thr
 225 230 235 240

Lys Asn Ile Asn Ser Leu Lys Ser Val Glu Gln Ala Ser Thr Phe Glu
 245 250 255

Met Gln Arg Gln Ala Gln
 260

<210> 381

<211> 659

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(636)

002290* 6362960

<223> RXA01398

<400> 381

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Lys Glu Thr Ala Glu Asp Tyr Arg Tyr Phe Asn Asp Pro Asp Leu Pro	
1 5 10 15	
cca gtg att gcg cct cgt gag tgg gtg gaa gaa atc cgc gca act ctt	96
Pro Val Ile Ala Pro Arg Glu Trp Val Glu Glu Ile Arg Ala Thr Leu	
20 25 30	
cca gag ctg cct tgg gtt cgc cgt gca cgt atc cag gaa gag tgg aag	144
Pro Glu Leu Pro Trp Val Arg Arg Ala Arg Ile Gln Glu Glu Trp Lys	
35 40 45	
ctt tcc gac gcc gag atg cgc gac ctc atc aac gcc aac gcg ctc gac	192
Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp	
50 55 60	
ctc atc atc gag acc gtg gaa gcg ggt acc act cct gat gaa gct cgt	240
Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg	
65 70 75 80	
gct tgg tgg gtt tct tac atc tct cag aag gct aac gag tct ggt gtc	288
Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val	
85 90 95	
gag ctc gat gct ctc ggt gtt gcg cca gct cac gtt gct cgc gtc gtt	336
Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val	
100 105 110	
gcg ctt gtt tct gaa gcc aag ctg acc aat aag ctg gca cgt cag gct	384
Ala Leu Val Ser Glu Gly Lys Leu Thr Asn Lys Leu Ala Arg Gln Ala	
115 120 125	
atc gac gcc gtt att gct gcc gaa gcc gat gtg gac gcg gtt gtt gct	432
Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala	
130 135 140	
gct cgt gga ctg gaa gtt gtt cgc gat gac gcc gca att gaa aag gct	480
Ala Arg Gly Leu Glu Val Val Arg Asp Asp Gly Ala Ile Glu Lys Ala	
145 150 155 160	
gtc gat gat gcc ttg gct gca aac cca gac atc gtg gag aag tac cgc	528
Val Asp Asp Ala Leu Ala Ala Asn Pro Asp Ile Val Glu Lys Tyr Arg	
165 170 175	
gct gcc aac acc aag gtc acc gcc atc gtt ggt gct gtc atg aag	576
Ala Gly Asn Thr Lys Val Thr Gly Ala Ile Val Gly Ala Val Met Lys	
180 185 190	
gcg acc cgc ggt aag gct gac cca gct cag gtg aac cag ctg atc gca	624
Ala Thr Arg Gly Lys Ala Asp Pro Ala Gln Val Asn Gln Leu Ile Ala	
195 200 205	
aag aag ttg gct taagcttttt gccgttgagc tgc	659
Lys Lys Leu Ala	
210	

<210> 382

006290.68820960

<211> 212
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 382

Lys Glu Thr Ala Glu Asp Tyr Arg Tyr Phe Asn Asp Pro Asp Leu Pro
 1 5 10 15
 Pro Val Ile Ala Pro Arg Glu Trp Val Glu Glu Ile Arg Ala Thr Leu
 20 25 30
 Pro Glu Leu Pro Trp Val Arg Arg Ala Arg Ile Gln Glu Glu Trp Lys
 35 40 45
 Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp
 50 55 60
 Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg
 65 70 75 80
 Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val
 85 90 95
 Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val
 100 105 110
 Ala Leu Val Ser Glu Gly Lys Leu Thr Asn Lys Leu Ala Arg Gln Ala
 115 120 125
 Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala
 130 135 140
 Ala Arg Gly Leu Glu Val Val Arg Asp Asp Gly Ala Ile Glu Lys Ala
 145 150 155 160
 Val Asp Asp Ala Leu Ala Ala Asn Pro Asp Ile Val Glu Lys Tyr Arg
 165 170 175
 Ala Gly Asn Thr Lys Val Thr Gly Ala Ile Val Gly Ala Val Met Lys
 180 185 190
 Ala Thr Arg Gly Lys Ala Asp Pro Ala Gln Val Asn Gln Leu Ile Ala
 195 200 205
 Lys Lys Leu Ala
 210

<210> 383
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..{1003}

<223> RXA02228

<400> 383

acagaagcgt caactgctca acttctcgac agcgacgaca cacacggcgt gggacgtac 60

00000000 00000000

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				Val	Val	Thr	Pro	Ile	5							
				1												
gca	gtg	gtt	gga	ccc	act	gca	tct	gga	aaa	tca	gct	ttg	gga	att	gct	163
Ala	Val	Val	Gly	Pro	Thr	Ala	Ser	Gly	Lys	Ser	Ala	Leu	Gly	Ile	Ala	20
				10					15							
cta	gcc	cac	aag	ctt	gac	ggt	gaa	gta	gtc	aat	gtg	gat	tcc	atg	cag	211
Leu	Ala	His	Lys	Leu	Asp	Gly	Glu	Val	Val	Asn	Val	Asp	Ser	Met	Gln	35
			25					30								
ctg	tac	aaa	ggc	atg	gac	atc	ggc	acg	gca	aag	ctg	act	gtc	gaa	gaa	259
Leu	Tyr	Lys	Gly	Met	Asp	Ile	Gly	Thr	Ala	Lys	Leu	Thr	Val	Glu	Glu	50
		40					45									
cgc	gaa	ggc	att	gcg	cat	cat	cag	ctc	gat	gtc	tgg	gac	gtt	acc	gaa	307
Arg	Glu	Gly	Ile	Ala	His	His	Gln	Leu	Asp	Val	Trp	Asp	Val	Thr	Glu	60
	55										65					
act	gcg	tca	gtg	gcg	agg	ttt	caa	tcc	gac	gcc	gtt	gcc	gat	gtg	gaa	355
Thr	Ala	Ser	Val	Ala	Arg	Phe	Gln	Ser	Asp	Ala	Val	Ala	Asp	Val	Glu	70
					75					80					85	
gat	att	atg	tcc	cgt	ggc	aaa	acc	ccc	atc	ttg	gtt	ggc	ggc	tcc	atg	403
Asp	Ile	Met	Ser	Arg	Gly	Lys	Thr	Pro	Ile	Leu	Val	Gly	Gly	Ser	Met	90
									95					100		
ttg	tac	gtc	caa	tct	ttg	gtc	gat	gat	tgg	caa	ttc	cca	cct	acc	gac	451
Leu	Tyr	Val	Gln	Ser	Leu	Val	Asp	Asp	Trp	Gln	Phe	Pro	Pro	Thr	Asp	105
								110					115			
agc	gct	gtt	cgc	gca	cgc	ttt	gag	gcc	cgc	ttg	gca	gac	atc	ggt	gtc	499
Ser	Ala	Val	Arg	Ala	Arg	Phe	Glu	Ala	Arg	Leu	Ala	Asp	Ile	Gly	Val	120
								125					130			
gaa	gca	cta	cac	gct	gaa	ctt	act	cag	ctt	gac	cca	gaa	gca	gca	gcc	547
Glu	Ala	Leu	His	Ala	Glu	Leu	Thr	Gln	Leu	Asp	Pro	Glu	Ala	Ala	Ala	135
																140
gtc	atc	gaa	agc	aat	gat	ccc	cga	cgc	acc	gtc	cga	gca	tta	gaa	gtc	595
Val	Ile	Glu	Ser	Asn	Asp	Pro	Arg	Arg	Thr	Val	Arg	Ala	Leu	Glu	Val	150
					155					160					165	
att	gaa	cta	acc	ggc	cag	ccc	ttc	caa	gca	agc	caa	ccg	ccc	aaa	gac	643
Ile	Glu	Leu	Thr	Gly	Gln	Pro	Phe	Gln	Ala	Ser	Gln	Pro	Pro	Lys	Asp	170
									175					180		
gcg	cca	cct	cgc	tgg	gga	act	cga	atc	att	ggc	ctg	aaa	acc	act	cca	691
Ala	Pro	Pro	Arg	Trp	Gly	Thr	Arg	Ile	Ile	Gly	Leu	Lys	Thr	Thr	Pro	185
								190					195			
gaa	tgg	cta	aat	cca	cgc	atc	gag	cag	cgc	acc	gcc	agg	atg	ttt	gaa	739
Glu	Trp	Leu	Asn	Pro	Arg	Ile	Glu	Gln	Arg	Thr	Ala	Arg	Met	Phe	Glu	200
								205					210			
caa	ggc	ttt	gtc	gcc	gaa	gtg	gaa	cac	ctt	gtg	cag	caa	gga	ctc	atc	787
Gln	Gly	Phe	Val	Ala	Glu	Val	Glu	His	Leu	Val	Gln	Gln	Gly	Leu	Ile	215
								220					225			
gct	gac	tcc	acc	gcg	gga	cga	gca	atc	ggc	tac	tcc	caa	gta	ctg	gca	835

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Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr Ser Gln Val Leu Ala
230 235 240 245

gcc atg gca ggg gag atg acc tgg gaa gac gcc ttc gaa cgc acg gtc 883
Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala Phe Glu Arg Thr Val
250 255 260

acc gga acc aga cgc tat gtc agg cgc caa cgc agc tgg ttc aac aga 931
Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg Ser Trp Phe Asn Arg
265 270 275

gac cac cgc gtg tcc tgg gtc gac gcc tct ggc gat ccc acc gca caa 979
Asp His Arg Val Ser Trp Val Asp Ala Ser Gly Asp Pro Thr Ala Gln
280 285 290

gcc ttg gag att ttg ggt cta caa tagcgagggt gaatttgacc atc 1026
Ala Leu Glu Ile Leu Gly Leu Gln
295 300

<210> 384
<211> 301
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 384
Val Val Thr Pro Ile Ala Val Val Gly Pro Thr Ala Ser Gly Lys Ser
1 5 10 15

Ala Leu Gly Ile Ala Leu Ala His Lys Leu Asp Gly Glu Val Val Asn
20 25 30

Val Asp Ser Met Gln Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys
35 40 45

Leu Thr Val Glu Glu Arg Glu Gly Ile Ala His His Gln Leu Asp Val
50 55 60

Trp Asp Val Thr Glu Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala
65 70 75 80

Val Ala Asp Val Glu Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu
85 90 95

Val Gly Gly Ser Met Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln
100 105 110

Phe Pro Pro Thr Asp Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu
115 120 125

Ala Asp Ile Gly Val Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp
130 135 140

Pro Glu Ala Ala Ala Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val
145 150 155 160

Arg Ala Leu Glu Val Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser
165 170 175

Gln Pro Pro Lys Asp Ala Pro Pro Arg Trp Gly Thr Arg Ile Glu
180 185 190

00602039.062300

Leu Lys Thr Thr Pro Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr
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 Ala Arg Met Phe Glu Gln Gly Phe Val Ala Glu Val Glu His Leu Val
 210 215 220
 Gln Gln Gly Leu Ile Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr
 225 230 235 240
 Ser Gln Val Leu Ala Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala
 245 250 255
 Phe Glu Arg Thr Val Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg
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 Ser Trp Phe Asn Arg Asp His Arg Val Ser Trp Val Asp Ala Ser Gly
 275 280 285
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1492)
 <223> RXA02502

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 Met Val Ser Val Leu
 1 5
 atc gta ggg atg tcg cac agg tct gcg cct gtg tcg ctt ctt gaa cgt 163
 Ile Val Gly Met Ser His Arg Ser Ala Pro Val Ser Leu Leu Glu Arg
 10 15 20
 ctg agc atg gat gat tca gta cgt ggt gaa aca act caa gca ctc ctg 211
 Leu Ser Met Asp Ser Val Arg Gly Glu Thr Thr Gln Ala Leu Leu
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 ggt agg gcg tct tta agc gag gcc ctc att gtc tct acg tgt aac cgc 259
 Gly Arg Ala Ser Leu Ser Glu Ala Leu Ile Val Ser Thr Cys Asn Arg
 40 45 50
 ctg gag gtc tac acc gtc act agc agt ttc cat act ggt gtt aat gat 307
 Leu Glu Val Tyr Thr Val Thr Ser Ser Phe His Thr Gly Val Asn Asp
 55 60 65
 gtg gtg gag gtt ctc cat gag gca agt ggc gta gat att gaa act ttg 355
 Val Val Glu Val Leu His Glu Ala Ser Gly Val Asp Ile Glu Thr Leu
 70 75 80 85
 cgc gga tat ctt tat gtc cgt tac gcc gat gct gct gct gaa cac atg 403

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Arg Gly Tyr Leu Tyr Val Arg Tyr Ala Asp Ala Ala Ala Glu His Met	
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Leu Val Val Thr Ser Gly Leu Asp Ser Met Val Leu Gly Glu Gln Gln	
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atc att ggt cag gtg cgc act gcg tac caa gca gct aat gaa tat ggt	499
Ile Ile Gly Gln Val Arg Thr Ala Tyr Gln Ala Ala Asn Glu Tyr Gly	
120 125 130	
tct gtc ggt cct gct ttg cat tca ctt acc cag acc gcg ctg cat acc	547
Ser Val Gly Pro Ala Leu His Ser Leu Thr Gln Thr Ala Leu His Thr	
135 140 145	
ggc aag cgc gtg cat tcg gag act gct att gat gat gct ggt gca tcg	595
Gly Lys Arg Val His Ser Glu Thr Ala Ile Asp Asp Ala Gly Ala Ser	
150 155 160 165	
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Met Val Ser Phe Ala Val Asp Arg Ala Leu Val Gln Met Gly Leu Asp	
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tcg gag gca gaa gcc cca cta tct ggc aag aca gcc ttg gtg ttg ggc	691
Ser Glu Ala Glu Ala Pro Leu Ser Gly Lys Thr Ala Leu Val Leu Gly	
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gct ggc gcg atg agt tct ctt gca gcc act cac ctt ggt cgc gct gga	739
Ala Gly Ala Met Ser Ser Leu Ala Ala Thr His Leu Gly Arg Ala Gly	
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att tcc aac ttg atc atg gcc aac cgc act ctg gaa cgt gcc gaa agg	787
Ile Ser Asn Leu Ile Met Ala Asn Arg Thr Leu Glu Arg Ala Glu Arg	
215 220 225	
ctt gcg gag cat tcc cta gaa gcc gga gtt cct gca gag gtt gtg gaa	835
Leu Ala Glu His Ser Leu Glu Ala Gly Val Pro Ala Glu Val Val Glu	
230 235 240 245	
tac gat cag cga gct tcc gcc tac aat cgc gtt gac ctg gta gtt tcc	883
Tyr Asp Gln Arg Ala Ser Ala Tyr Asn Arg Val Asp Leu Val Val Ser	
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gcc acg gga gcg gat gat ttc acc gtg aag cct gag gat att cca gaa	931
Ala Thr Gly Ala Asp Asp Phe Thr Val Lys Pro Glu Asp Ile Pro Glu	
265 270 275	
ggt gct tcg ttg atg ttg gtg gat ttg tcc atg cca cga gac atc gat	979
Gly Ala Ser Leu Met Leu Val Asp Leu Ser Met Pro Arg Asp Ile Asp	
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Asp Ala Cys Ala Asp Leu Pro Gly Val Asp Leu Val Asn Ile Glu Arg	
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Leu His Lys Ala Ser Arg Glu Gly Gly Ser Gly Met Ala Pro Ser Glu	
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Ser Ile Ala Ile Leu Ser Ser Leu Pro Leu Ala Ser Cys Ser Thr Pro		
cca aca gat tca gag gct gtc gtt gag cat ctg gtt cca gaa att atc	25 30 35	211
Pro Thr Asp Ser Ser Glu Ala Val Val Glu His Leu Val Pro Glu Ile Ile		
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Ser Thr His Ser Ser Phe Asp Ser Thr Ser Phe Thr Gln Gly Leu Glu Leu		
gat ggc gac gag ctg att gtg gga act ggc caa tac ggt ggt tcc cga	55 60 65	307
Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln Tyr Gly Gly Ser Arg		
atc tat cgc agc tcc gtt gat ggc cag gaa tct gtt tcc caa tcg ctt	70 75 80 85	355
Ile Tyr Arg Ser Ser Val Asp Gly Gln Ser Val Ser Gln Ser Leu		
gat cca gaa ttc ttc ggt gaa ggc atc acc aag tct ggt gat gcc atc	90 95 100	403
Asp Pro Glu Phe Phe Gly Glu Gly Ile Thr Lys Ser Gly Asp Ala Ile		
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Trp Gln Leu Thr Trp Asn Glu Gly Val Ala Phe Lys Arg Asp Ala Asp		
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Thr Leu Glu Glu Leu Asp Arg Val Ser Tyr Asn Gly Gln Gly Trp Gly		

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ctc acc ttt agg gat ccg gaa acc ttt gca gag aac agc act gta gat 595
 leu thr phe arg asp pro glu thr phe ala glu asn ser thr val asp
 150 155 160 165

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 val thr leu asp gly ser pro val gly asn leu asn glu leu glu cys
 170 175 180

gtt gat gcc gag gta tat gcc aat att ttc ctc gat aca gac atc atg 691
 val asp gly glu val tyr ala asn ile phe leu asp thr asp ile met
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cga atc gat ccg aac tcc gcc gaa gtc acc gca gtg atc gat gcc tca 739
 arg ile asp pro asn ser gly glu val thr ala val ile asp ala ser
 200 205 210

aat att cct aac aac gcc aca cca gat aca aac aat gtg ctc aac gcc 787
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 215 220 225

att gca cat att ccg gat tcc gat cgt ttt tat atc act ggt aag cgt 835
 ile ala his ile pro asp ser asp arg phe tyr ile thr gly lys arg
 230 235 240 245

tgg cct gac ctc tat gag gtt aga ttc gtc cct gct gac tagaatcaag 884
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Gln Gly Leu Glu Leu Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln
 50 55 60
 Tyr Gly Gly Ser Arg Ile Tyr Arg Ser Ser Val Asp Gly Gln Glu Ser
 65 70 75 80
 Val Ser Gln Ser Leu Asp Pro Glu Phe Phe Glu Gly Ile Thr Lys
 85 90 95
 Ser Gly Asp Ala Ile Trp Gln Leu Thr Trp Asn Glu Gly Val Ala Phe
 100 105 110

05608370.052300

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 Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg
 70 75 80 85

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat 403
 Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp
 90 95 100

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg 451
 Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met
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acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc 499
 Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg
 120 125 130

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt ccg gag 547
 Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu
 135 140 145

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg 595
 Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro
 150 155 160 165

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct 643
 Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala
 170 175 180

ccg atc ggc aag cac gcg ctg gct ctg att atc ggt cgc cct ggt ggc 691
 Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly
 185 190 195

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac 739
 Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp
 200 205 210

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg 786
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 215 220

<210> 390
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 <213> Corynebacterium glutamicum

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Val Asp Val Val Glu Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu
 35 40 45

Val Ile Ser Ile Pro Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala

002240 66320930

50 55 60

Ala Glu Glu Val Asp Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser
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85 90 95

His Gln Arg Arg Asp Ile Thr Ala Ala Met Glu Glu Met Val Asp Val
100 105 110

Ile Pro Arg Thr Met Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys
115 120 125

Gly Pro Ile Thr Arg Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp
130 135 140

Gly Thr Val Pro Glu Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn
145 150 155 160

Pro Glu Asn Asp Pro Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser
165 170 175

Ser Leu Ala Ile Ala Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile
180 185 190

Gly Arg Pro Gly Gly Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu
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Gly Gln Val Gly Asp Ile Ile Gly Ala Met Leu Gln Lys
210 215 220

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<223> RXN00669

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Met Asp Asn Ser Thr
1 5

gtg cga atc cgg ctg gat cta gcg tat gac ggc acg gat ttt cat ggc 163
Val Arg Ile Arg Leu Asp Leu Ala Tyr Asp Gly Thr Asp Phe His Gly
10 15 20

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Trp Ala Lys Gln Gly Thr Ser Asp Leu Arg Thr Val Gln Lys Val Leu
25 30 35

gaa gac aat ttg agc atg gtg ctg cgt gag act gtt gaa ttg act gtg 259
Glu Asp Asn Leu Ser Met Val Leu Arg Glu Thr Val Glu Leu Thr Val
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 Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg Ser Ile Asp Gly Asp
 70 75 80 85

cca agc aag ttg gtt cgg cgc ttg ggt cgg ttg ctg ccc gat gat att 403
 Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu Leu Pro Asp Asp Ile
 90 95 100

cgg gtg cat ggc gta cgt ttt gcc gag ccc ggg ttt gat gcg cga ttt 451
 Arg Val His Gly Val Arg Phe Ala Glu Pro Gly Phe Asp Ala Arg Phe
 105 110 115

tcc gcg atg cgc agg cac tac gtt tat cgc att acg acg cat ccc gcc 499
 Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile Thr His Pro Ala
 120 125 130

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 Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala Gln Trp Pro Lys Pro
 135 140 145

gtc gaa cta gag cgg atg caa tta gcc gcc gat gca ctg ctg ggg ctg 595
 Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp Ala Leu Leu Gly Leu
 150 155 160 165

cat gat ttt gtg gcg ttt tgc aaa gct aag cca cat gcg acg acg gtg 643
 His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro His Ala Thr Thr Val
 170 175 180

cgt gaa cta caa aaa ttt gcg tgg aaa gac gtc tcc act gac atc gaa 691
 Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val Ser Thr Asp Ile Glu
 185 190 195

ccg cag gtg tat gaa gca cac gtg gtg gcc gat gct ttt tgc tgg tcg 739
 Pro Gln Val Tyr Glu Ala His Val Val Ala Asp Ala Phe Cys Trp Ser
 200 205 210

atg gtg cgc tcg ctg gtc gcc tcc tgc atg gcc gtg gcc gaa gga cgc 787
 Met Val Arg Ser Leu Val Gly Ser Cys Met Ala Val Gly Glu Gly Arg
 215 220 225

cgc gga tca ggg ttt act gca gaa ttg ett gat gca agc gaa cgc agc 835
 Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp Ala Ser Glu Arg Ser
 230 235 240 245

ccc atg gtt cca gta gca cct gcg aaa ggt ttg agc ttg gtt gcc gtg 883
 Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu Ser Leu Val Gly Val
 250 255 260

gat tat cct tcc gct gat aag tta cag gaa aga gcg ctg gaa acc cga 931
 Asp Tyr Pro Ser Ala Asp Lys Leu Gln Glu Arg Ala Leu Glu Thr Arg
 265 270 275

gct gtt cgc gag ttt ccg gac gcg tcc gcg agc cta aaa cta gat gat 979
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 280 285 290

002290.0222950

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Glu

1005

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<211> 294

<212> PRT

<213> *Corynebacterium glutamicum*

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Val Glu Leu Thr Val Ala Gly Arg Thr Asp Ala Gly Val His Ala Ala
50 55 60

Gly Gln Val Ala His Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg
65 70 75 80

Ser Ile Asp Gly Asp Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu
85 90 95

Leu Pro Asp Asp Ile Arg Val His Gly Val Arg Phe Ala Glu Pro Gly
100 105 110

Phe Asp Ala Arg Phe Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile
115 120 125

Thr Thr His Pro Ala Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala
130 135 140

Gln Trp Pro Lys Pro Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp
145 150 155 160

Ala Leu Leu Gly Leu His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro
165 170 175

His Ala Thr Thr Val Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val
180 185 190

Ser Thr Asp Ile Glu Pro Gln Val Tyr Glu Ala His Val Val Ala Asp
195 200 205

Ala Phe Cys Trp Ser Met Val Arg Ser Leu Val Gly Ser Cys Met Ala
210 215 220

Val Gly Glu Gly Arg Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp
225 230 235 240

Ala Ser Glu Arg Ser Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu
245 250 255

Ser Leu Val Gly Val Asp Tyr Pro Ser Ala Asp Lys Leu Gln Glu Arg
260 265 270

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135 140 145

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Arg	Asp	Arg	Thr	Val	Asp	Lys	Thr	Tyr	His	Ala	Leu	Val	Gln	Gly	His
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Pro	Asp	Pro	Leu	Thr	Gly	Thr	Ile	Glu	Ala	Pro	Ile	Gly	Arg	His	Pro
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tca	gca	ggt	tgg	cgt	ttc	gca	gta	aca	act	gaa	ggc	aaa	cac	gcc	gtc
Ser	Ala	Gly	Trp	Arg	Phe	Ala	Val	Thr	Thr	Glu	Gly	Lys	His	Ala	Val
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Thr	His	Tyr	Glu	Thr	Leu	Glu	Ala	Phe	Gln	Glu	Ala	Thr	Leu	Leu	Lys
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Ile	His	Leu	Glu	Thr	Gly	Arg	Thr	His	Gln	Ile	Arg	Val	His	Phe	Ser
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Ala	Leu	His	His	Pro	Cys	Cys	Gly	Asp	Pro	Met	Tyr	Gly	Ser	Asp	Pro
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Ala	Leu	Ser	Glu	Arg	Leu	Gly	Leu	Asn	Arg	Gln	Trp	Leu	His	Ala	Val
			265					270					275		
tcg	ctt	gga	ttc	aac	cac	cca	gca	gat	ggc	cga	tgg	atg	gaa	atc	gtc
Ser	Leu	Gly	Phe	Asn	His	Pro	Ala	Asp	Gly	Arg	Trp	Met	Glu	Ile	Val
		280						285				290			
tcc	cca	tat	cca	act	gat	ctc	caa	cac	gct	tta	gac	gtt	ctc	cgc	gag
Ser	Pro	Tyr	Pro	Thr	Asp	Leu	Gln	His	Ala	Leu	Asp	Val	Leu	Arg	Glu
		295				300					305				
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Gln															
310															
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Met	Asn	Asn	Arg	Gln	Ser</										

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Val Pro Gly Leu Asp Ile Leu Tyr Ser Asp Asp Asp Val Ile Ala Val 85 90 95		
Asn Lys Pro Val Glu Val Ala Ala His Pro Thr Val Gly Trp Glu Gly 100 105 110		
Pro Thr Val Val Gly Gly Leu Ala Ala Ala Gly Phe Arg Ile Ser Thr 115 120 125		
Ser Gly Pro Pro Glu Arg Lys Gly Ile Val Gln Arg Leu Asp Val Gly 130 135 140		
Thr Ser Gly Val Met Val Val Ala Ala Ser Glu Arg Gly Tyr Thr Val 145 150 155 160		
Leu Lys Arg Ala Phe Arg Asp Arg Thr Val Asp Lys Thr Tyr His Ala 165 170 175		
Leu Val Gln Gly His Pro Asp Pro Leu Thr Gly Thr Ile Glu Ala Pro 180 185 190		
Ile Gly Arg His Pro Ser Ala Gly Trp Arg Phe Ala Val Thr Thr Glu 195 200 205		
Gly Lys His Ala Val Thr His Tyr Glu Thr Leu Glu Ala Phe Gln Glu 210 215 220		
Ala Thr Leu Leu Lys Ile His Leu Glu Thr Gly Arg Thr His Gln Ile 225 230 235 240		
Arg Val His Phe Ser Ala Leu His His Pro Cys Cys Gly Asp Pro Met 245 250 255		
Tyr Gly Ser Asp Pro Ala Leu Ser Glu Arg Leu Gly Leu Asn Arg Gln 260 265 270		
Trp Leu His Ala Val Ser Leu Gly Phe Asn His Pro Ala Asp Gly Arg 275 280 285		
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<211> 2647

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2647)

<223> RXA01344

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 Val Leu Glu Gly Pro
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 Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly
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gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg 211
 Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val
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 Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly
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acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc 307
 Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala
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cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc 355
 Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile
 70 75 80 85

cag gat tac tct gga aac atg tcc ctg agc ctt tgg gag cca cgc ttc 403
 Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe
 90 95 100

gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac 451
 Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn
 105 110 115

tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc 499
 Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr
 120 125 130

ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg 547
 Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met
 135 140 145

acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc 595
 Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val
 150 155 160 165

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 Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp
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 Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg
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 Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val
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cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct 787
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Ile	Met	Met	Ser	Thr	Leu	Glu	Ser	Asp	Gly	Val	Ala	Asn	Thr	Asp	Glu	
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Ala	Leu	Leu	Glu	Ile	Tyr	Arg	Lys	Gln	Arg	Pro	Gly	Glu	Gln	Pro	Thr	
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Arg	Tyr	Asp	Leu	Ala	Arg	Val	Gly	Arg	Tyr	Lys	Ile	Asn	Arg	Lys	Leu	
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Gly	Leu	Gly	Gly	Asp	His	Asp	Gly	Leu	Met	Thr	Leu	Thr	Glu	Glu	Asp	
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Val	Met	Thr	Ser	Pro	Asn	Gly	Glu	Glu	Ile	Arg	Val	Glu	Thr	Asp	Asp	
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Gln	Asn	Gln	Val	Arg	Val	Gly	Leu	Ser	Arg	Met	Glu	Arg	Val	Val	Arg	
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Glu	Arg	Met	Thr	Thr	Gln	Asp	Ala	Glu	Ser	Ile	Thr	Pro	Thr	Ser	Leu	
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atc	aac	gtt	cgt	cct	gtc	tct	gca	gct	atc	cgt	gag	ttc	ttc	gga	act	1363
Ile	Asn	Val	Arg	Pro	Val	Ser	Ala	Ala	Ile	Arg	Glu	Phe	Phe	Gly	Thr	
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Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp
760 765 770

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Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu
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Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu
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Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu
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DISCUSSION

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys
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 Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val
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 His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro
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 Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met
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 Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg
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 Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn

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675					680					685					
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Arg	Asn	Leu	Leu	Val	Ala	Phe	Met	Pro	Trp	Glu	Gly	His	Asn	Tyr	Glu
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Ser	Ile	His	Ile	Glu	Glu	His	Glu	Ile	Asp	Ala	Arg	Asp	Thr	Lys	Leu
740					745					750					

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                               Val  Leu  Asp  Val  Asn
                               1      5

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Val  Phe  Asp  Glu  Leu  Arg  Ile  Gly  Leu  Ala  Thr  Ala  Asp  Asp  Ile  Arg
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cgt  tgg  tcc  aag  ggt  gag  gtc  aag  aag  ccg  gag  acc  atc  aac  tac  cga      211
Arg  Trp  Ser  Lys  Gly  Glu  Val  Lys  Lys  Pro  Glu  Thr  Ile  Asn  Tyr  Arg
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acc  ctc  aag  cct  gag  aag  gac  ggt  ctg  ttc  tgc  gag  cgt  atc  ttc  ggt      259
Thr  Leu  Lys  Pro  Glu  Lys  Asp  Gly  Leu  Phe  Cys  Glu  Arg  Ile  Phe  Gly
                               40      45      50

cca  act  cgc  gac  tgg  gag  tgc  gcc  tgc  ggt  aag  tac  aag  cgt  gtc  cgc      307
Pro  Thr  Arg  Asp  Trp  Glu  Cys  Ala  Cys  Gly  Lys  Tyr  Lys  Arg  Val  Arg
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Tyr  Lys  Gly  Ile  Ile  Cys  Glu  Arg  Cys  Gly  Val  Glu  Val  Thr  Lys  Ser
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aag  gtg  cgc  cgt  gag  cgc  atg  gga  cac  att  gag  ctc  gct  gca  cca  gta      403

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Lys Val Arg Arg Glu Arg Met Gly His Ile Glu Leu Ala Ala Pro Val
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Glu Arg Ile Phe Gly Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys
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Tyr Lys Arg Val Arg Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val
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 Met Asn Glu Glu Val
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ctc tcc gca aac ggc act cca atg aag ctc gcg ggt gac gac gac gac 163

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 Phe Asp Gln Ala Gly Ala Ser Ile Gly Ile Asn Leu Ser Arg Asp Glu
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 Thr Gly Ala Val Thr Gly Tyr Thr Arg His Asp Leu Ile Glu Thr Ser
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 Val Ser Gly Arg Val Leu Ala Gly Asp Ala Thr Asn Ala Ala Gly Glu
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gtt gtg ctt gct gct ggt acc gac ctg acc gag ctc aac att gac ctt 192
 Val Val Leu Ala Ala Gly Thr Asp Leu Thr Glu Leu Asn Ile Asp Leu
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 Leu Val Glu Ala Gly Ile Lys Asp Val Lys Val Arg Ser Val Leu Thr
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 Met Thr Val Leu Pro
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 Lys Asn His Asp Leu Ser Asp Thr Gln Leu Val Lys Gln Phe Ile Ser
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 Gly Asp Ser Arg Ala Phe Ser Thr Ile Ile His Arg His Glu Arg His
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 Met Met Gln Ala Ala Arg Lys Tyr Gly Arg Lys Pro Glu Asp Ala Gln
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 gac att ctc caa gaa gct ctc ttt cgc gcc agc cga aac atg cac ctt 307
 Asp Ile Leu Gln Glu Ala Leu Phe Arg Ala Ser Arg Asn Met His Leu
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 Tyr Arg Ala Glu Ala Ala Leu Gly Thr Trp Leu His Lys Leu Val Leu
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 Thr Asp Pro Leu Gly Tyr Leu Asp Val Ala Met Thr Ile Arg Ser Ala
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 atc gac caa tta cac ccc gat caa cgc atc gcc tta ata ctt gtc gac 547
 Ile Asp Gln Leu His Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp
 135 140 145
 ctc ggc ggc tac acc gta gaa gat gtg gcc gaa atc gaa gga atc aaa 595
 Leu Gly Gly Tyr Thr Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys
 150 155 160 165
 gta ggt acc gtt aaa tca cgc cga ggg cgc gca cgc aaa gcg ttg cgc 643
 Val Gly Thr Val Lys Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg
 170 175 180
 gcc ctt tta cat gca gat ttc ttc ggg ccc gaa gat ggc tcc ata cag 691
 Ala Leu Leu His Ala Asp Phe Phe Gly Pro Glu Asp Gly Ser Ile Gln
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<210> 406

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<213> Corynebacterium glutamicum
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35 40 45

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50 55 60

Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
65 70 75 80

Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
85 90 95

Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
100 105 110

Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
115 120 125

Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
130 135 140

Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
145 150 155 160

Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
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<212> DNA

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Met Thr Ala Pro Ser
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cag	cag	gat	ctc	gca	acg	act	gaa	cgt	gag	gta	gat	ccc	ggc	agg	aga	
Thr	Gln	Asp	Leu	Ala 10	Thr	Thr	Glu	Arg	Glu 15	Val	Asp	Pro	Gly	Ser 20	Arg	
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agg	ggc	caa	acc	aac	gac	aat	ccc	tcg	cag	gac	ctt	gtt	cgc	gtt	tac	
Arg	Gly	Gln	25	Asn	Asp	Asn	Pro	Ser 30	Gln	Asp	Leu	Val	Arg 35	Val	Tyr	
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ctc	aac	ggc	atc	ggc	aaa	act	gcc	ttg	ctt	acc	cgc	gag	gat	gaa	gtt	
Leu	Asn	Gly 40	Ile	Gly	Lys	Thr	Ala 45	Leu	Leu	Thr	Ala	Glu 50	Asp	Glu	Val	
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gag	ctc	gca	cag	acc	att	gag	gtt	ggc	ctt	tat	gca	gag	cac	ctt	ctg	
Glu	Leu 55	Ala	Gln	Thr	Ile	Glu 60	Val	Gly	Leu	Tyr	Ala 65	Glu	His	Leu	Leu	
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aaa	aac	tct	gaa	gag	cca	ctc	acc	cgc	gcc	atg	aag	cgc	gat	cta	aag	
Lys 70	Asn	Ser	Glu	Glu	Pro 75	Pro	Thr	Arg	Ala	Met 80	Lys	Arg	Asp	Leu 85	Lys	
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gtt	ctt	gcc	aag	gac	ggc	aag	aag	gct	cgt	tcc	cac	ctc	ctc	gag	gca	
Val	Leu	Ala	Lys 90	Gly	Lys	Lys	Ala	Ala 95	Arg	Ser	His	Leu	Leu	Glu 100	Ala	
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aac	ctg	cgc	ctg	gtg	gtg	tcc	ctt	gct	aag	cgc	tac	acc	ggc	cgc	ggc	
Asn	Leu	Arg 105	Leu	Val	Val	Ser	Leu	Ala 110	Lys	Arg	Tyr	Thr	Gly 115	Arg	Gly	
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atg	cca	ctg	ctg	gat	ctt	atc	cag	gag	ggc	aac	ctc	gga	ctg	atc	cgc	
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gcg	atg	gaa	aag	ttt	gat	tac	tcc	aag	ggc	ttt	aag	ttc	tcc	acc	tac	
Ala	Met 135	Glu	Lys	Phe	Asp	Tyr 140	Ser	Lys	Gly	Phe 145	Lys	Phe	Ser	Thr	Tyr	
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gca	acc	tgg	tgg	atc	cgc	cag	gca	atc	acc	cgc	ggc	atg	gca	gat	cag	
Ala	Thr 150	Trp	Trp	Ile	Arg 155	Gln	Ala	Ile	Thr	Arg 160	Gly	Met	Ala	Asp 165	Gln	
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tcc	cgc	acc	atc	cgc	ctc	cca	gtc	cac	ctt	gtg	gag	cag	gtg	aac	aag	
Ser	Arg	Thr 170	Ile	Arg	Leu	Pro	Val	His 175	Leu	Val	Glu	Gln	Val	Asn 180	Lys	
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ctt	tcc	cgc	atc	aag	cgc	gag	ttg	tac	cag	cac	ttg	ggc	cgt	gaa	gcc	
Leu	Ser 185	Arg	Ile	Lys	Arg	Glu	Leu	Tyr 190	Gln	His	Leu	Gly 195	Arg	Glu	Ala	
																691
acc	aat	gag	gaa	ctc	gca	gaa	gag	tcc	ggc	att	gaa	gag	tcc	aag	att	
Thr	Asn 200	Glu	Glu	Leu	Ala	Glu	Glu 205	Ser	Gly	Ile	Glu	Glu 210	Ser	Lys	Ile	
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gaa	atg	ctg	ctt	cgt	cag	tct	cgc	gat	cca	gtg	agc	ttg	gac	atg	cca	
Glu	Met 215	Leu	Leu	Arg	Gln	Ser 220	Arg	Asp	Pro	Val	Ser 225	Leu	Asp	Met	Pro	
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Val	Gly 230															

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<223> RXA00495

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                                   Leu Ala Asp Thr Glu
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cgc gag ctc gct gac ctg gta ccg cag gca acg gcg ggc gat cgt cgg 163
Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr Ala Gly Asp Arg Arg
                                   10                               15                               20

gca ttg caa aga ata atg gag att att cac ccc att gtt ttg cgt tat 211
Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro Ile Val Leu Arg Tyr
                                   25                               30                               35

gct cgc gct cgt att gga ggt gga cgc cag cca acg gca gaa gac gtt 259
Ala Arg Ala Arg Ile Gly Gly Arg Gln Pro Thr Ala Glu Asp Val
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gct caa gaa atc tgc ctg gcg gta gcc acc tcc att agg aac ttt gtc 307
Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser Ile Arg Asn Phe Val
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gac cag ggt agg ccg ttc atg gcg ttt gtc tac ggc att gca tct aac 355
Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr Gly Ile Ala Ser Asn
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aag gtc gca gat gct cac agg gcg atg tcg agg gat aaa tcg act cct 403
Lys Val Ala Asp Ala His Arg Ala Met Ser Arg Asp Lys Ser Thr Pro
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att gag gaa gtc cca gaa act tca cca gat act ttt acc ccc gaa gac 451
Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr Phe Thr Pro Glu Asp
                                   105                               110                               115

ttt gcg ctg gtc agc gat gga agt aac aga gtt agg gaa ctt ctc gat 499
Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val Arg Glu Leu Leu Asp
                                   120                               125                               130

cta ctg agt gaa aag gca cgc gac att ctt atc ttg aga gtt atc gtt 547
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                                   135                               140                               145

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Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val Gly Ser Thr Pro Gly
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gct gta cga gtt gcc caa cac agg gca ctc acg aca ctt cga agc aca 643
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 His Glu Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met
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 agc gcc ctc ccc cgc ttc gca gcg cgc tcc tcg gcg cgc acc tgg cta 240
 Ser Ala Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu
 65 70 75 80
 cta tcg cta gcc cgg cgc gtc tgg gtc gac aac atc cga cac gac atg 288
 Leu Ser Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met
 85 90 95
 gca cgc ccc cgc aaa tcc atc gtc gaa tac gaa gac acc ggt gcc acc 336
 Ala Arg Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr
 100 105 110
 gac gcg agc aac gca ggc atc tgg tcc gag tgg atc gac gtg cgc acg 384
 Asp Ala Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr
 115 120 125
 ctt atc gac gcc ctc cca ccc gaa cgc cgc gaa gcc ctc atc ctc acc 432
 Leu Ile Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr
 130 135 140
 caa gtg ttg ggc tac acc tac gaa gaa gcc gca aaa atc gcc gac gtc 480
 Gln Val Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val
 145 150 155 160
 cga gtc gga aca atc cgt tcc cgc gta gcc cgc gcc aga gcg gac ctc 528
 Arg Val Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu
 165 170 175
 att gct gca aca gct acc ggt gat tcc tca gcc gaa gat ggc aaa tcc 576
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<210> 412

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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 35 40 45

His Glu Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met
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ctc atc cag gaa ggc aac ctc ggt ctg att cgt gcc gta gag aag ttc 163
Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg Ala Val Glu Lys Phe 20

gac tac tcc aag ggc tac aag ttc tcc acc tac gca acc tgg tgg atc 211
Asp Tyr Ser Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile 35

cgt cag gca atc acc cgc gcc atg gcc gac caa gca cga acc atc cgt 259
Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln Ala Arg Thr Ile Arg 40 45 50

atc cca gtc cac atg gtt gaa gtg atc aac aaa ctt ggt cgc atc caa 307
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Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln
35 40 45
Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn Lys
50 55 60
Leu Gly Arg Ile Gln Arg Glu Leu Leu Gln Glu Leu Gly Arg Glu Pro
65 70 75 80

Thr Pro Gln Glu Leu Ser Lys Glu Met Asp Ile Ser Glu Glu Lys Val
 85 90
 Leu Glu Ile Gln Gln Tyr Ala Arg Glu Pro Ile Ser Leu Asp Gln Thr
 100 105 110
 Ile Gly Asp Glu Gly Asp Ser Gln Leu Gly Asp Phe Ile Glu Asp Ser
 115 120 125
 Glu Ala Val Val Ala Val Asp Ala Val Ser Phe Thr Leu Leu Gln Asp
 130 135 140
 Gln Leu Gln Asp Val Leu Glu Thr Leu Ser Glu Arg Glu Ala Gly Val
 145 150 155 160
 Val Lys Leu Arg Phe Gly Leu Thr Asp Gly Met Pro Arg Thr Leu Asp
 165 170 175
 Glu Ile Gly Gln Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln Ile
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 Leu Arg Asp Tyr Leu Asp
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 Met Val Glu Asn Asn
 1 5
 gta gca aaa aag acg gtc gct aaa aag acc gca cgc aag acc gca cgc 163
 Val Ala Lys Lys Thr Val Ala Lys Lys Thr Ala Arg Lys Thr Ala Arg
 10 15 20
 aaa gca gcc ccg cgc gtg gca acc cca ttg gga gtc gca tct gag tct 211
 Lys Ala Ala Pro Arg Val Ala Thr Pro Leu Gly Val Ala Ser Glu Ser
 25 30 35
 ccc att tgg gcc acc cct gcg cgc agc atc gat gga acc tca acc cct 259
 Pro Ile Ser Ala Thr Pro Ala Arg Ser Ile Asp Gly Thr Ser Thr Pro
 40 45 50
 gtt gaa gct gct gac acc ata gag acc acc gcc cct gca gcg aag gct 307
 Val Glu Ala Ala Asp Thr Ile Glu Thr Thr Ala Pro Ala Ala Lys Ala
 55 60 65

002290 63920960

cct gcg gcc aag gct ccc gct aaa aag gtt gcc aag aag aca gct cgc 355
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aag gca cct gcg aaa aag act gtc gcc aag aaa gcc aca acc gcc aag 403
 Lys Ala Pro Ala Lys Lys Thr Val Ala Lys Lys Ala Thr Thr Ala Lys
 90 95 100

gct gca cct gca act gcc aag gac gaa aac gca cct gtt gat gac gac 451
 Ala Ala Pro Ala Thr Ala Lys Asp Glu Asn Ala Pro Val Asp Asp Asp
 105 110 115

gag gag aac ctc gct cag gat gaa cag gac ttc gac ggc gat gac ttc 499
 Glu Glu Asn Leu Ala Gln Asp Glu Gln Asp Phe Asp Gly Asp Asp Phe
 120 125 130

gta gac ggc atc gaa gac gaa gaa gat gaa gac ggc gtc gaa gcc ctc 547
 Val Asp Gly Ile Glu Asp Glu Glu Asp Glu Asp Gly Val Glu Ala Leu
 135 140 145

ggt gaa gaa agc gaa gac gac gaa gag gac ggc tca tcc gtt tgg gat 595
 Gly Glu Glu Ser Glu Asp Asp Glu Glu Asp Gly Ser Ser Val Trp Asp
 150 155 160 165

gaa gac gaa tcc gca acc ctg cgt cag gca cgt aaa gat gcc gag ctc 643
 Glu Asp Glu Ser Ala Thr Leu Arg Gln Ala Arg Lys Asp Ala Glu Leu
 170 175 180

acc gct tcc gcc gac tct gtt cgc gct tac ctg aag caa atc ggt aaa 691
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 185 190 195

gtt gcc ctg ctg aac gct gaa cag gaa gtc tcc ctg goa aag cgc atc 739
 Val Ala Leu Leu Asn Ala Glu Gln Glu Val Ser Leu Ala Lys Arg Ile
 200 205 210

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 215 220 225

ttc gca gcc ggt gac aag gac gcg aaa ctc acc cca gcc gtc aag cgt 835
 Phe Ala Ala Gly Asp Lys Asp Ala Lys Leu Thr Pro Ala Val Lys Arg
 230 235 240 245

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 Asp Leu Arg Ala Ile Ala Arg Asp Gly Arg Lys Ala Lys Asn His Leu
 250 255 260

ctg gaa gcc aac ctt cgt ctg gtt gtc tcc ctg gca aag acg cta cac 931
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cgg cgg tgg cat ggc att cct gga cct cat coa gga agg caa cct cgg 979
 Arg Pro Trp His Gly Ile Pro Gly Pro His Pro Gly Arg Gln Pro Arg
 280 285 290

tct gat tgc tgc cgt aga gaa gtt cga cta ctc caa ggg cta caa gtt 1027
 Ser Asp Ser Ser Cys Arg Arg Glu Val Arg Leu Leu Gln Gly Leu Gln Val
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260 265 270

Ala Lys Thr Leu His Arg Pro Trp His Gly Ile Pro Gly Pro His Pro
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Gly Arg Gln Pro Arg Ser Asp Ser Cys Arg Arg Glu Val Arg Leu Leu
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Gln Gly Leu Gln Val Leu His Leu Arg Asn Leu Val Asp Pro Ser Gly
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Met Thr Tyr Met Lys
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Lys Lys Ser Arg Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala
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Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln
25 30 35

gca gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc 259
Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser
40 45 50

gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa 307
Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn His Asp Ala Glu
55 60 65

gac ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc 355
Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser
70 75 80 85

tac cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac 403

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 ctg cct gaa gat tat gag cgc gtt cgc ggc aat gac atc acc cca gag 499
 Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu
 120 125 130
 cag gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc 547
 Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu
 135 140 145
 gat gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt 595
 Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val
 150 155 160 165
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 Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met
 170 175 180
 ggt acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca 691
 Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala
 185 190 195
 agt ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt 739
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 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
 65 70 75 80
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
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 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys

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2025

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<213> Corynebacterium glutamicum

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 $\langle 222 \rangle \quad (1) \dots (1320)$

<223> RXN01724

<400> 421

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gcg caa act tca act gca cct gct tca gca cca tct gaa gag act ccc 96
Ala Gln Thr Ser Thr Ala Pro Ala Ser Ala Pro Ser Glu Glu Thr Pro
20 25 30

gca gct ccc gct cgt cgt gga cgt cgc cgt gta acc acc acc gcg acc 144
Ala Ala Pro Ala Arg Arg Gly Arg Arg Arg Val Thr Thr Thr Ala Thr
35 40 45

acc cca gag cca gca gcg cct gca caa tcc cag cct gca gaa gct caa 192
Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln
50 55 60

cga gca cag act cag gct gca cag caa gaa gaa ctt cct gtt gca gcg 240
Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala
65 70 75 80

aag gag tcc gca cca gct aca gaa aac act cag ggc caa gct cag ggc 288
Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr Gln Gly Gln Ala Gln Gly
85 90 95

caa gct cag ggc caa gct cag ggc gat gag cac gat gat cgt ttt gag 336
Gln Ala Gln Gly Gln Ala Gln Gly Asp Glu His Asp Asp Arg Phe Glu
100 105 110

tcc cgt tct gct gca cgc cga gca cgc cgc aac cgt cag cgc cag atc 384
 Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile
 115 120 125

cac cgc gat ggc gat gac aat gcg aat gca aac aca gag tct gag cag 432
 His Arg Asp Gly Asp Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln
 130 135 140

aac acc cct gcc cag aac gca acc gca cag gct gag tct gag cag act 480
Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr
145 150 155 160

gca gct cct gca cag gct gaa gca gct gag cag aac cag aac gat aac 528
Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn
165 170 175

Figure 1 consists of 12 diagrams illustrating the stages of chick development. The diagrams are arranged in a vertical column. Each diagram is labeled with a number (1-12) and a corresponding time point. The diagrams show the progression of the embryo from a single cell to a fully formed chick with a yolk sac.

Diagram	Time Point
1	1.0 hr
2	2.0 hr
3	3.0 hr
4	4.0 hr
5	5.0 hr
6	6.0 hr
7	7.0 hr
8	8.0 hr
9	9.0 hr
10	10.0 hr
11	11.0 hr
12	12.0 hr

agc gag tcc tcc gag aac cgc agc gat aac tac cgc aac aac aat cgt Ser Glu Ser Ser Glu Asn Arg Ser Asp Asn Tyr Arg Asn Asn Asn Arg	576		
180	185	190	
cgt tcc cgc aac aac cgg aac aat cgc aat tac cgc gat aac aac gag Arg Ser Arg Asn Asn Arg Asn Asn Arg Asn Tyr Arg Asp Asn Asn Glu	624		
195	200	205	
tcc tct gat aat gca gga cag tcc agc aat gat gat gcc gac aac aat Ser Ser Asp Asn Ala Gly Gln Ser Ser Asn Asp Asp Ala Asp Asn Asn	672		
210	215	220	
cag gca cgg tct gag gac aat aac gac gat cgc cgt tct cgt aat aac Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp Arg Arg Ser Arg Asn Asn	720		
225	230	235	240
cgt aac aac gac cgc aat gat cgt aac gat cgc aat gac cgc gac aac Arg Asn Asn Asp Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp Asn	768		
245	250	255	
gac gac aac gat gat cgc cgc aac cgt cgc gga cgc cgc aat cgc cgt Asp Asp Asn Asp Asp Arg Arg Arg Asn Arg Arg Gly Arg Arg Asn Arg Arg	816		
260	265	270	
gga cgc aac gac cgt aac gat cgc gac aac cga gat aac cgg gat aac Gly Arg Asn Asp Arg Asn Asp Arg Asp Asn Arg Asp Asn Arg Asp Asn	864		
275	280	285	
cgc gac aac agc aac gat ggc gac aac aac cag caa gat gag ctg cag Arg Asp Asn Ser Asn Asp Gly Asp Asn Asn Gln Gln Asp Glu Leu Gln	912		
290	295	300	
cag gta gca ggc atc ctg gac atc gtg gac cat aac gtc gca ttc gtg Gln Val Ala Gly Ile Leu Asp Ile Val Asp His Asn Val Ala Phe Val	960		
305	310	315	320
cgc acc acc ggt tac cac gct gca cct tct gac gtg ttt gtc agc aac Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe Val Ser Asn	1008		
325	330	335	
cag ctg atc cgc cgt atg ggt ctt cgt tcc ggt gac gcc att gaa ggt Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala Ile Glu Gly	1056		
340	345	350	
cag gtt cgt atg aac cag ggt ggt ggc aac cac aac aac cat ggt cgc Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn His Gly Arg	1104		
355	360	365	
aac cgt cag aag tac aac aac ttg gtg cgc gtg gag atg gtt aac ggt Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met Val Asn Gly	1152		
370	375	380	
ctt cct gct gaa gag act cgc aac cgt cct gag ttc ggc aag ctg act Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly Lys Leu Thr	1200		
385	390	395	400
cct ctg tac cgc aac cag cgt ctg cgt ttg gaa act gag cag aag att Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu Gln Lys Ile	1248		
405	410	415	
ctt acc act cgt gtg atc gac ttg atc atg cct att ggt aag gga cag	1296		

09602839-1052300

Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly Lys Gly Gln
 420 425 430
 ctg tgc ttt gat tgt gtc gcc acc taaggctggt aagaccaaga tcc
 Leu Cys Phe Asp Cys Val Ala Thr
 435 440
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 <212> PRT
 <213> *Corynebacterium glutamicum*
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 20 25 30
 Ala Ala Pro Ala Arg Arg Gly Arg Arg Val Thr Thr Thr Ala Thr
 35 40 45
 Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln
 50 55 60
 Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala
 65 70 75 80
 Gly Glu Ser Ala Pro Ala Thr Glu Asn Thr Gln Gly Gln Ala Gln Gly
 85 90 95
 Gln Ala Gln Gly Gln Ala Gln Gly Asp Glu His Asp Asp Arg Phe Glu
 100 105 110
 Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile
 115 120 125
 His Arg Asp Gly Asp Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln
 130 135 140
 Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr
 145 150 155 160
 Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn
 165 170 175
 Ser Glu Ser Ser Glu Asn Arg Ser Asp Asn Tyr Arg Asn Asn Asn Arg
 180 185 190
 Arg Ser Arg Asn Asn Arg Asn Asn Arg Asn Tyr Arg Asp Asn Asn Glu
 195 200 205
 Ser Ser Asp Asn Ala Gly Gln Ser Ser Asn Asp Asp Ala Asp Asn Asn
 210 215 220
 Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp Arg Arg Ser Arg Asn Asn
 225 230 235 240
 Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp Arg Asn Asp Arg Asp Asn
 245 250 255

1343

Figure 1

06-03-2007

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<223> FRXA01723
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              Val Asp Xaa Ser Arg
              1          5
gta acc acc acc acc acc acc cca pro gta cca gca gcg cct gca caa tcc 163
Val Thr Thr Thr Thr Thr Thr Pro Ala Glu Pro Ala Pro Ala Gln Ser
              10          15          20
cag cct gca gaa gct caa cca gca cag act cag gct gca cag caa gaa 211
Gln Pro Ala Glu Ala Gln Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu

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25	30	35	
gaa ctt cct gtt gca gcg aag gag tcc gca cca gct aca gaa aac act Glu Leu Pro Val Ala Ala Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr 40 45 50			259
cag ggc caa key cag ggc caa gct cag ggc saa gct cag ggc gat gag Gln Gly Gln Xaa Gln Gly Gln Ala Gln Gly Xaa Ala Gln Gly Asp Glu 55 60 65			307
cac gat gat cgy ttt gag tcc cgt tct gct gca cgc cga gca cgc cgc His Asp Asp Xaa Phe Glu Ser Arg Ser Ala Arg Arg Ala Arg Arg 70 75 80 85			355
aac cgt cag cgc cag atc cac cgc gat ggc gat gac aat gcg aat gca Asn Arg Gln Arg Gln Ile His Arg Asp Gly Asp Asp Asn Ala Asn Ala 90 95 100			403
aac aca gag tct gag cag aac acc cct gcc cag aac gca acc gca cag Asn Thr Glu Ser Glu Gln Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln 105 110 115			451
gct gag tct gag cag act gca gct cct gca cag gct gaa gca gct gag Ala Glu Ser Glu Gln Thr Thr Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu 120 125 130			499
cag aac cag aac gat aac agc gag tcc tcc gag aac cgc agc gat aac Gln Asn Gln Asn Asp Asn Ser Glu Ser Ser Glu Asn Arg Ser Asp Asn 135 140 145			547
tac cgc aac aac aat cgt cgt tcc cgc aac aac cgg aac aat cgc aat Tyr Arg Asn Asn Asn Arg Arg Ser Arg Asn Asn Arg Asn Arg Asn 150 155 160 165			595
tac cgc gat aac aac gag tcc tct gat aat gca gga cag tcc agc aat Tyr Arg Asp Asn Asn Glu Ser Ser Asp Asn Ala Gly Gln Ser Ser Asn 170 175 180			643
gat gat gcc gac aac aat cag gca cgg tct gag gac aat aac gac gat Asp Asp Ala Asp Asn Asn Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp 185 190 195			691
cgc cgt tct cgt aat aac cgt aac aac gac cgc aat gat cgt aac gat Arg Arg Ser Arg Asn Asn Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp 200 205 210			739
cgc aat gac cgc gac aac gac gac aac gat gat cgc cgc aac cgt cgc Arg Asn Asp Arg Asp Asn Asp Asp Asn Asp Asp Arg Arg Asn Arg Arg 215 220 225			787
gga cgc cgc aat cgc cgt gga ncn gca acg acc gta acg atc gcg aca Gly Arg Arg Asn Arg Arg Gly Xaa Ala Thr Val Thr Ile Ala Thr 230 235 240 245			835
acc gag ata acc ggg ata acc gcg aca aca gca acg atg gcg aca aca Thr Glu Ile Thr Gly Ile Thr Ala Thr Thr Ala Thr Met Ala Thr Thr 250 255 260			883
acc agc aag atn gag nct gca gca ggt agc agg cat cct gga cat cgt Thr Ser Lys Xaa Glu Xaa Ala Ala Gly Ser Arg His Pro Gly His Arg 265 270 275			931

00229.62200

960

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260

265

270

His Pro Gly His Arg Gly Pro
275

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<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA01724

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Val Asp His Asn Val
1 5

gca ttc gtg cgc acc acc ggt tac cac gct gca cct tct gac gtg ttt 163
Ala Phe Val Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe
10 15 20

gtc agc aac cag ctg atc cgc cgt atg ggt ctt cgt tcc ggt gac gcc 211
Val Ser Asn Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala
25 30 35

att gaa ggt cag gtt cgt atg aac cag ggt ggt ggc aac cac aac aac 259
Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn
40 45 50

cat ggt cgc aac cgt cag aag tac aac aac ttg gtg cgc gtg gag atg 307
His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met
55 60 65

gtt aac ggt ctt cct gct gaa gag act cgc aac cgt cct gag ttc ggc 355
Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly
70 75 80 85

aag ctg act cct ctg tac ccg aac cag cgt ctg cgt ttg gaa act gag 403
Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu
90 95 100

cag aag att ctt acc act cgt gtg atc gac ttg atc atg cct att ggt 451
Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly
105 110 115

aag gga cag ctg tgc ttt gat tgt gtc gcc acc taaggctggt aagaccagca 504
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tcc

507

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<211> 128

<212> PRT

002230.40000000

<213> *Corynebacterium glutamicum*

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20 25 30

Arg Ser Gly Asp Ala Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly
35 40 45

Gly Asn His Asn Asn His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu
50 55 60

Val Arg Val Glu Met Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn
65 70 75 80

Arg Pro Glu Phe Gly Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu
85 90 95

Arg Leu Glu Thr Glu Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu
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Ile Met Pro Ile Gly Lys Gly Gln Leu Cys Phe Asp Cys Val Ala Thr
115 120 125

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<212> DNA

<213> *Corynebacterium glutamicum*

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<223> RXN01725

<400> 427

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atcgacttga tcatgcctat tggtaaggga cagctgtgct ttg att gtg tgg cca 115
Leu Ile Val Ser Pro
1 5

cct aag gct ggt aag acc acg atc ctg cag aac att gcg aac gct att 163
Pro Lys Ala Gly Lys Thr Thr Ile Leu Gln Asn Ile Ala Asn Ala Ile
10 15 20

tcc acc aac aac cca gag tgc tac ctc atg gtt gtt ttg gtt gat gag 211
Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val Val Leu Val Asp Glu
25 30 35

cgt ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg 259
 Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val
 40 45 50

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[illegible]

330

<213> *Corynebacterium glutamicum*

<213> Corynebacterium glutamicum

<223> FRXA01725

231

<213> Corynebacterium glutamicum

THE UNIVERSITY OF CHICAGO

<400> 430

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<212> DNA

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<222> (101)..(673)

<223> RXA01726

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 Leu Leu Glu Leu Ala
 1 5

att gag cgt gcg aag cgc ctg gtg gag cag gcc cag gac gtc gtt gtt 163
 Ile Glu Arg Ala Lys Arg Leu Val Glu Gln Gly Gln Asp Val Val Val
 10 15 20

ctg ctt gac tcc att act cgt ttg gcc cgt gcg tac aac aac agc tca 211
 Leu Leu Asp Ser Ile Thr Arg Leu Gly Arg Ala Tyr Asn Asn Ser Ser
 25 30 35

cct gca tcg gga cgt att ttg tcc ggt ggt gtg gat tcc aat gca ctg 259
 Pro Ala Ser Gly Arg Ile Leu Ser Gly Gly Val Asp Ser Asn Ala Leu
 40 45 50

tac ccg ccg aag cgt ttc ttg ggt gct gct cga aac atc gaa aat ggt 307
 Tyr Pro Pro Lys Arg Phe Leu Gly Ala Ala Arg Asn Ile Glu Asn Gly
 55 60 65

gga tct ttg acc atc atc gca act gcc atg gtg gaa acc gcc tct gct 355
 Gly Ser Leu Thr Ile Ile Ala Thr Ala Met Val Glu Thr Gly Ser Ala
 70 75 80 85

ggt gac acc gtg atc ttc gag gag ttc aag gcc act ggt aac gct gag 403
 Gly Asp Thr Val Ile Phe Glu Glu Phe Lys Gly Thr Gly Asn Ala Glu
 90 95 100

ctg aag ctg gat cgt aag atc tct gag cgc cgc gtt ttc cca gct gtg 451
 Leu Lys Leu Asp Arg Lys Ile Ser Glu Arg Arg Val Phe Pro Ala Val
 105 110 115

gat gtt aat cct tct ggt act cgt aag gac gag ctg ttg ctc aac ccg 499
 Asp Val Asn Pro Ser Gly Thr Arg Lys Asp Glu Leu Leu Leu Asn Pro
 120 125 130

gac gag gct cgc att atg cac aag ctg cgt cgt att ctg tct gca ctt 547

00220 00230 00240 00250 00260 00270 00280 00290 00300

400> 432

Leu	Leu	Glu	Leu	Ala	Ile	Glu	Arg	Ala	Lys	Arg	Leu	Val	Glu	Gln	Gly
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Gln	Asp	Val	Val	Val	Leu	Leu	Asp	Ser	Ile	Thr	Arg	Leu	Gly	Arg	Ala
		20						25					30		
Tyr	Asn	Asn	Ser	Ser	Pro	Ala	Ser	Gly	Arg	Ile	Leu	Ser	Gly	Gly	Val
		35					40					45			
Asp	Ser	Asn	Ala	Leu	Tyr	Pro	Pro	Lys	Arg	Phe	Leu	Gly	Ala	Ala	Arg
	50					55					60				
Asn	Ile	Glu	Asn	Gly	Gly	Ser	Leu	Thr	Ile	Ile	Ala	Thr	Ala	Met	Val
				70						75					80
Glu	Thr	Gly	Ser	Ala	Gly	Asp	Thr	Val	Ile	Phe	Glu	Glu	Phe	Lys	Gly
				85					90					95	
Thr	Gly	Asn	Ala	Glu	Leu	Lys	Leu	Asp	Arg	Lys	Ile	Ser	Glu	Arg	Arg
		100						105					110		
Val	Phe	Pro	Ala	Val	Asp	Val	Asn	Pro	Ser	Gly	Thr	Arg	Lys	Asp	Glu
		115					120					125			
Leu	Leu	Leu	Asn	Pro	Asp	Glu	Ala	Arg	Ile	Met	His	Lys	Leu	Arg	Arg
		130				135					140				
Ile	Leu	Ser	Ala	Leu	Asp	Asn	Gln	Gln	Ala	Ile	Asp	Leu	Leu	Ile	Lys
				150						155					160
Gln	Leu	Lys	Lys	Thr	Lys	Ser	Asn	Ala	Glu	Phe	Leu	Met	Gln	Val	Ala
				165					170					175	
Ser	Ser	Ala	Pro	Met	Ala	Gly	Thr	Glu	Lys	Glu	Glu	Asp	Tyr	Ser	
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 <213> *Corynebacterium glutamicum*

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 <223> RXA00736

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Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val	
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ggc gat att gca ggg gcg aaa cgt cga cct gca aaa cgc cgc aac aag	144
Gly Asp Ile Ala Gly Ala Lys Arg Arg Pro Ala Lys Arg Arg Asn Lys	
35 40 45	
gtg gat cct ttg gcg ctg gag cca ggg gat ttg gtg gtt cat gaa acc	192
Val Asp Pro Leu Ala Leu Glu Pro Gly Asp Leu Val Val His Glu Thr	
50 55 60	
cac ggc att ggt cgt ttt gtg aag atg act gaa cga acc att tct gcg	240
His Gly Ile Gly Arg Phe Val Lys Met Thr Glu Arg Thr Ile Ser Ala	
65 70 75 80	
ggt gat gag acc tcg cgc cgt gaa tac att gtg ctg gag tac gcg cca	288
Gly Asp Glu Thr Ser Arg Arg Glu Tyr Ile Val Leu Glu Tyr Ala Pro	
85 90 95	
tct aag cgc gga cag ccc ggc gat cag ctg tat gtg ccg atg gat gcg	336
Ser Lys Arg Gly Gln Pro Gly Asp Gln Leu Tyr Val Pro Met Asp Ala	
100 105 110	
ctg gat atg ctc agc cgc tac gtc ggt ggc gag aag ccg acg ctg tcc	384
Leu Asp Met Leu Ser Arg Tyr Val Gly Gly Glu Lys Pro Thr Leu Ser	
115 120 125	
aaa atg ggt ggt tct gac tgg aag aac gcc aag aag aag gct cgc gct	432
Lys Met Gly Gly Ser Asp Trp Lys Asn Ala Lys Lys Lys Ala Arg Ala	
130 135 140	
gcc gtg cgt gaa atc gcc ggt gag ctg gta gaa ctc tac gct aag cgc	480
Ala Val Arg Glu Ile Ala Gly Glu Leu Val Glu Leu Tyr Ala Lys Arg	
145 150 155 160	
caa tcc gcg ccg ggt cac ccg ttt gcg ccg gat acg ccg tgg caa aaa	528
Gln Ser Ala Pro Gly His Pro Phe Ala Pro Asp Thr Pro Trp Gln Lys	
165 170 175	
gag atg gaa gat aac ttc ccc tac gtt gag acc gaa gac cag atg ttg	576
Glu Met Glu Asp Asn Phe Pro Tyr Val Glu Thr Glu Asp Gln Met Leu	
180 185 190	
gcg atc gat gcg gtc aag gag gac atg gag aaa agt gtc ccc atg gac	624
Ala Ile Asp Ala Val Lys Glu Asp Met Glu Lys Ser Val Pro Met Asp	

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210	215	220	
cgc gcg gcg ttc aag gct gtg caa gac ggc aag cag gta gcc gtt ctg Arg Ala Ala Phe Lys Ala Val Gln Asp Gly Lys Gln Val Ala Val Leu	720		
225	230	235	240
gtg ccc acc acg ttg ctt gcg cag cag cac cag tcc acg ttt gaa gag Val Pro Thr Thr Leu Leu Ala Gln Gln His Gln Ser Thr Phe Glu Glu	768		
245	250	255	
cgt atg act ggt ttc cct gtc acc atc aag gga ttg tca cgc ttt act Arg Met Thr Gly Phe Pro Val Thr Ile Lys Gly Leu Ser Arg Phe Thr	816		
260	265	270	
tgc cct gcg gaa tgc cgg gag att ctc tcc ggt ttg gct gca gga tgc Ser Pro Ala Glu Ser Arg Glu Ile Leu Ser Gly Leu Ala Ala Gly Ser	864		
275	280	285	
gtg gat atc gtc atc ggt act cac cgt ttg ctg cag act ggc gtg cag Val Asp Ile Val Ile Gly Thr His Arg Leu Leu Gln Thr Gly Val Gln	912		
290	295	300	
tgg aaa aac cta ggg ctt gtc att gtg gat gag gag cag cgt ttc ggc Trp Lys Asn Leu Gly Leu Val Ile Val Asp Glu Glu Gln Arg Phe Gly	960		
305	310	315	320
gtg gaa cat aag gag cac atc aag gct ctg cgt act cac gtg gat gtg Val Glu His Lys Glu His Ile Lys Ala Leu Arg Thr His Val Asp Val	1008		
325	330	335	
ctg acc atg tcc gcg acc ccg att ccg cgc acc ctg gaa atg tcc atg Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met	1056		
340	345	350	
gcc ggt atc cgt gag atg acc acc atg ctc acc ccg ccg gaa gat cgc Ala Gly Ile Arg Glu Met Thr Thr Met Leu Thr Pro Pro Glu Asp Arg	1104		
355	360	365	
cac coa att ctt acc tat gtg gga ccg tat gaa gac aag cag gtc gcg His Pro Ile Leu Thr Tyr Val Gly Pro Tyr Glu Asp Lys Gln Val Ala	1152		
370	375	380	
gca tca att cgc cgt gag ctg ctg cgc gat ggc cag gtc ttt ttc atc Ala Ser Ile Arg Arg Glu Leu Leu Arg Asp Gly Gln Val Phe Phe Ile	1200		
385	390	395	400
cac aac aag gtg gca gat att gag aag aag gcc cgc gag atc cgc gat His Asn Lys Val Ala Asp Ile Glu Lys Lys Ala Arg Glu Ile Arg Asp	1248		
405	410	415	
cta gtt ccc gaa gcc cga gtg gtc gtt gcc cac gcc cag atg agt gaa Leu Val Pro Glu Ala Arg Val Val Val Ala His Gly Gln Met Ser Glu	1296		
420	425	430	
gag ctg ctg gaa caa acc gtt caa ggt ttc tgg gac cgc gaa tac gat Glu Leu Leu Glu Gln Thr Val Gln Gly Phe Trp Asp Arg Glu Tyr Asp	1344		
435	440	445	

000290* 66920960

gtg ctg gtg tgt acc acc atc gtg gaa act ggt ctg gat att tcc aac 1392
Val Leu Val Cys Thr Thr Ile Val Glu Thr Gly Leu Asp Ile Ser Asn
450 455 460

gcc aac acg ctt atc gtg gaa aat gcc cac cac atg gcc ttg tct cag 1440
Ala Asn Thr Leu Ile Val Glu Asn Ala His Met Gly Leu Ser Gln
465 470 475 480

ctg cac cag ctg cgt ggc cgc gtg ggt cgt tcc cgt gag cgc ggt tac 1488
Leu His Gln Leu Arg Gly Arg Val Gly Arg Ser Arg Glu Arg Gly Tyr
485 490 495

gcc tac ttc ctg tat cca aag ggc gcg aca ctg act gaa atg tcc tac 1536
Ala Tyr Phe Leu Tyr Pro Lys Gly Ala Thr Leu Thr Glu Met Ser Tyr
500 505 510

gac cgc ctg gca acg att gcc caa aac aat gat ttg ggt gcc ggt atg 1584
Asp Arg Leu Ala Thr Ile Ala Gln Asn Asn Asp Leu Gly Ala Gly Met
515 520 525

gcg gtt gcc atg aag gat ttg gaa atg cgt ggc gcc gcc aac gtg ctg 1632
Ala Val Ala Met Lys Asp Leu Glu Met Arg Gly Ala Gly Asn Val Leu
530 535 540

ggt gca gaa caa tca ggc cat atc gct ggc gtg ggc ttt gac ctg tac 1680
Gly Ala Glu Gln Ser Gly His Ile Ala Gly Val Gly Phe Asp Leu Tyr
545 550 555 560

gtt cgc ctc gtc ggc gaa gca gtg gaa gcc tac cgc gcg ctg gct gat 1728
Val Arg Leu Val Gly Glu Ala Val Glu Ala Tyr Arg Ala Leu Ala Asp
565 570 575

ggc aaa gtt gtt gat ggc acc gtc aag gga cca aag gaa atc cgc gtg 1776
Gly Lys Val Val Asp Gly Thr Val Lys Gly Pro Lys Glu Ile Arg Val
580 585 590

gac ctt ccc gtg gat gcc cac att ccc gaa aag tac atc aac gcc gag 1824
Asp Leu Pro Val Asp Ala His Ile Pro Glu Lys Tyr Ile Asn Ala Glu
595 600 605

cgt ctg cgt ctg gaa atc tac cgc aag ctc gcg cag tcc gaa tgg gaa 1872
Arg Leu Arg Leu Glu Ile Tyr Arg Lys Leu Ala Gln Ser Glu Ser Glu
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Val Asp Leu Arg Leu
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<210> 434

<211> 629

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

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20 25 30

002290 6320960

Gly Asp Ile Ala Gly Ala Lys Arg Arg Pro Ala Lys Arg Arg Asn Lys
 35 40 45
 Val Asp Pro Leu Ala Leu Glu Pro Gly Asp Leu Val Val His Glu Thr
 50 55 60
 His Gly Ile Gly Arg Phe Val Lys Met Thr Glu Arg Thr Ile Ser Ala
 65 70 75 80
 Gly Asp Glu Thr Ser Arg Arg Glu Tyr Ile Val Leu Glu Tyr Ala Pro
 85 90 95
 Ser Lys Arg Gly Gln Pro Gly Asp Gln Leu Tyr Val Pro Met Asp Ala
 100 105 110
 Leu Asp Met Leu Ser Arg Tyr Val Gly Gly Glu Lys Pro Thr Leu Ser
 115 120 125
 Lys Met Gly Gly Ser Asp Trp Lys Asn Ala Lys Lys Lys Ala Arg Ala
 130 135 140
 Ala Val Arg Glu Ile Ala Gly Glu Leu Val Glu Leu Tyr Ala Lys Arg
 145 150 155 160
 Gln Ser Ala Pro Gly His Pro Phe Ala Pro Asp Thr Pro Trp Gln Lys
 165 170 175
 Glu Met Glu Asp Asn Phe Pro Tyr Val Glu Thr Glu Asp Gln Met Leu
 180 185 190
 Ala Ile Asp Ala Val Lys Glu Asp Met Glu Lys Ser Val Pro Met Asp
 195 200 205
 Arg Val Ile Ile Gly Asp Val Gly Tyr Gly Lys Thr Glu Val Ala Val
 210 215 220
 Arg Ala Ala Phe Lys Ala Val Gln Asp Gly Lys Gln Val Ala Val Leu
 225 230 235 240
 Val Pro Thr Thr Leu Leu Ala Gln Gln His Gln Ser Thr Phe Glu Glu
 245 250 255
 Arg Met Thr Gly Phe Pro Val Thr Ile Lys Gly Leu Ser Arg Phe Thr
 260 265 270
 Ser Pro Ala Glu Ser Arg Glu Ile Leu Ser Gly Leu Ala Ala Gly Ser
 275 280 285
 Val Asp Ile Val Ile Gly Thr His Arg Leu Leu Gln Thr Gly Val Gln
 290 295 300
 Trp Lys Asn Leu Gly Leu Val Ile Val Asp Glu Glu Gln Arg Phe Gly
 305 310 315 320
 Val Glu His Lys Glu His Ile Lys Ala Leu Arg Thr His Val Asp Val
 325 330 335
 Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met
 340 345 350

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REPORT

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<211> 1116
<212> DNA
<213> Corynebacterium glutamicum
<220>
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				Met	Lys	Val	Ser	Asp								
				1				5								
att	agg	cag	ttc	tct	gtc	gcc	gat	cag	cgc	acc	att	cca	gaa	atc	acc	163
Ile	Arg	Gln	Phe	Ser	Val	Ala	Asp	Gln	Arg	Thr	Ile	Pro	Glu	Ile	Thr	
				10					15					20		
atc	aag	agc	att	gag	att	ttc	ccg	gca	cgg	gaa	ttg	ctc	att	act	gaa	211
Ile	Lys	Ser	Ile	Glu	Ile	Phe	Pro	Ala	Arg	Glu	Leu	Leu	Ile	Thr	Glu	
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gaa	gtg	gca	tcg	cgt	gcg	gag	tct	ctt	att	tct	aag	cac	ccg	ggc	aac	259
Glu	Val	Ala	Ser	Arg	Ala	Glu	Ser	Leu	Ile	Ser	Lys	His	Pro	Gly	Asn	
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ccg	ach	ctt	gtg	gag	atg	ctg	tcg	agg	att	gcg	gat	tcc	caa	gat	ggt	307
Pro	Thr	Leu	Val	Glu	Met	Leu	Ser	Arg	Ile	Ala	Asp	Ser	Gln	Asp	Val	
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gat	ggc	atg	gag	gcg	ttg	att	ccg	gcg	ctg	acg	gat	acg	ccg	atg	ggt	355
Gly	Gly	Met	Glu	Ala	Leu	Ile	Pro	Ala	Leu	Thr	Asp	Thr	Pro	Met	Val	
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ccg	atg	ctg	gag	ctc	atg	ccg	gaa	aac	acc	cat	gtg	ttg	gtg	att	gct	403
Pro	Met	Leu	Glu	Leu	Met	Pro	Glu	Asn	Thr	His	Val	Leu	Val	Ile	Ala	
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ccg	gag	aag	gtg	cgc	cga	cgc	att	gcg	gat	ctg	gaa	gca	acc	gat	gct	451
Pro	Glu	Lys	Val	Arg	Arg	Arg	Ile	Ala	Asp	Leu	Glu	Ala	Thr	Asp	Ala	
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gag	ttt	ttg	atg	gct	ggt	tgg	gaa	gca	gct	gcg	atg	ggt	gct	gat	ggt	499
Glu	Phe	Leu	Met	Ala	Gly	Trp	Glu	Ala	Ala	Ala	Met	Gly	Ala	Asp	Gly	
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cca	gtg	gct	gcg	gaa	ggc	ctg	gac	ttg	gaa	gct	tct	agc	tat	cgc	agt	547
Pro	Val	Ala	Ala	Glu	Gly	Leu	Asp	Leu	Glu	Ala	Ser	Ser	Ser	Arg	Ser	
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tat	gaa	agt	ttg	gag	gtt	tct	gcg	tcg	aaa	agc	gat	gtg	cgt	tgg	tgg	595
Thr	Glu	Ser	Leu	Glu	Val	Ser	Ala	Ser	Lys	Ser	Asp	Val	Arg	Trp	Trp	
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act	ttc	gcg	ccg	ccg	ggc	atg	ttt	gag	gcc	tcg	gag	gag	gcg	acg	ctg	643
Thr	Phe	Ala	Pro	Pro	Gly	Met	Phe	Glu	Ala	Ser	Glu	Glu	Ala	Thr	Leu	
				170					175					180		
ccg	ctt	gat	ttt	gaa	gcc	ggg	ccg	gcg	ccg	cgc	ggt	gag	ctg	ccg	aag	691
Pro	Leu	Asp	Phe	Glu	Ala	Gly	Pro	Ala	Pro	Arg	Gly	Glu	Leu	Pro	Lys	
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atc																

200 205 210

cgg gct gcg ttt atc gcg ccg acc caa ggt gcg att aag cgc atg gtc 787
 Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala Ile Lys Arg Met Val
 215 220 225

gat cgt ttc gcg gaa aag ggc att ccc acc cat gtg gcg acc ccg ggt 835
 Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His Val Ala Thr Pro Gly
 230 235 240 245

tgg gag cca acg cct ggt caa gtg act ctt tat cat gcg ctg agc cat 883
 Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr His Ala Leu Ser His
 250 255 260

gct ggc ctg gtg ttt ccg aag gtg cgt aaa cac cgc gat ggc gct gca 931
 Ala Gly Leu Val Phe Pro Lys Val Arg Lys His Arg Asp Gly Ala Ala
 265 270 275

atg ccg ttg gtg gtt att aca gaa acc gat ctg act ggt aac cgt gtt 979
 Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val
 280 285 290

ggc gat att gca ggg cga aac gtc gac ctg caa aac gcc gca aca agg 1027
 Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln Asn Ala Ala Thr Arg
 295 300 305

tgg atc ctt tgg cgc tgg agc cag ggg att tgg tgg ttc atg aaa ccc 1075
 Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp Trp Phe Met Lys Pro
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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 35 40 45
 Lys His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala
 50 55 60
 Asp Ser Gln Asp Val Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr
 65 70 75 80
 Asp Thr Pro Met Val Pro Met Leu Glu Leu Met Pro Glu Asn Thr His
 85 90 95
 Val Leu Val Ile Ala Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu
 100 105 110

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Glu Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala
 115 120 125
 Met Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala
 130 135 140
 Ser Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser
 145 150 155 160
 Asp Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser
 165 170 175
 Glu Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg
 180 185 190
 Gly Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His
 195 200 205
 Thr Thr Gly Gly Gly Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala
 210 215 220
 Ile Lys Arg Met Val Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His
 225 230 235 240
 Val Ala Thr Pro Gly Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr
 245 250 255
 His Ala Leu Ser His Ala Gly Leu Val Phe Pro Lys Val Arg Lys His
 260 265 270
 Arg Asp Gly Ala Ala Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu
 275 280 285
 Thr Gly Asn Arg Val Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln
 290 295 300
 Asn Ala Ala Thr Arg Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp
 305 310 315 320
 Trp Phe Met Lys Pro Thr Ala Leu Val Val Leu
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<210> 437

<211> 480

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(480)

<223> FRXA00737

<400> 437

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 His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala Asp
 1 5 10 15

tcc caa gat gtt gat ggc atg gag gcg ttg att ccg gcg ctg acg gat 96
 Ser Gln Asp Val Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr Asp

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[illegible]

Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp
100 105 110

Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu
 115 120 125
 Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly
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 Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr
 145 150 155 160

<210> 439
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 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <223> RXN01872

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 Met Gly Asn Asp Gly
 1 5
 gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163
 Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
 10 15 20
 tca ggc cac cta acc gaa act gcc caa aga tta ggc atc cgc cag ccc 211
 Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
 25 30 35
 aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
 Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
 40 45 50
 ctt ttc gac cgc gcc gcc cgc aaa ctc gtc ctc aac caa cga ggc cac 307
 Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
 55 60 65
 gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355
 Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala
 70 75 80 85
 gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403
 Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg
 90 95 100
 ctg gac ttc atg cat tcc ttg gcc act tgg atg gtc ccc gaa ctt atc 451
 Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
 105 110 115
 cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499
 Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln

002240.002240

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ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly 150 155 160			595
tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp 170 175 180			643
cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr 185 190 195			691
gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc ggc acc cga Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg 200 205 210			739
ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val 215 220 225			787
ggt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala Gly Leu Val Ser Ala 230 235 240 245			835
ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat ccc tac ctt tcc aca Gly Leu Gly Val Gly Val Val Pro Met Asp Asp Pro Tyr Leu Ser Thr 250 255 260			883
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<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

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20 25 30Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
35 40 45His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
50 55 60Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
65 70 75 80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu

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85 90 95

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met
100 105 110

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu
115 120 125

Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu
130 135 140

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
145 150 155 160

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu
165 170 175

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu
180 185 190

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala
195 200 205

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly
210 215 220

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala
225 230 235 240

Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp
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Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro
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Ala Tyr Arg Glu
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<210> 441
<211> 865
<212> DNA
<213> *Corynebacterium glutamicum*

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<223> FRXA01872

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Met Gly Asn Asp Gly
1 5

gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163
Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
10 15 20

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211

00000000 00000000

Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
25 30 35

aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
40 45 50

ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac 307
Leu Phe Asp Arg Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
55 60 65

gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355
Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ser Ala
70 75 80 85

gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403
Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg
90 95 100

ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc 451
Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
105 110 115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499
Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln
120 125 130

gcg gca gca atg ctc ctg gta gat cgt gtt ttg gct gat gaa act gac 547
Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu Ala Asp Glu Thr Asp
135 140 145

ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg 595
Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly
150 155 160 165

tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat 643
Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp
170 175 180

cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act 691
His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr
185 190 195

gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc ggc acc cga 739
Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg
200 205 210

ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg 787
Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val
215 220 225

gtt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca 835
Val Phe Glu Ser Met Glu Leu Thr Thr Thr Ala Gly Leu Val Ser Ala
230 235 240 245

ggt ctc ggc gtt ggt gtg gtt ccg atg gat 865
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250 255

<221> CDS

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<223> RXA02413

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Met Thr Ser Glu Asn
1 5

tcc gaa tcc cag gac att tgg cta acc gat gag caa caa gat gtg tgg 163
Ser Glu Ser Gln Asp Ile Trp Leu Thr Asp Glu Gln Gln Asp Val Trp
10 15 20

ctc gat gtg tgg aca atg cga atc ggc ctg cct gct cgc ttg gat gct 211
Leu Asp Val Trp Thr Met Arg Ile Gly Leu Pro Ala Arg Leu Asp Ala
25 30 35

caa ctg aaa gaa gct gcg ggt gtc agc cac ttt gag tac ttc acc atg 259
Gln Leu Lys Glu Ala Ala Gly Val Ser His Phe Glu Tyr Phe Thr Met
40 45 50

gcg cag att tct atg gcc ccg gaa cat cgg gtg cgc atg agt gag ctt 307
Ala Gln Ile Ser Met Ala Pro Glu His Arg Val Arg Met Ser Glu Leu
55 60 65

gct gag ctg tcc gat atg acg cta tcg cat cta tct aga gtg gtt act 355
Ala Glu Leu Ser Asp Met Thr Leu Ser His Leu Ser Arg Val Val Thr
70 75 80 85

cgc cta gaa aag gct ggc tgg gtg aag cgt gtt ccc gat cct gat gat 403
Arg Leu Glu Lys Ala Gly Trp Val Lys Arg Val Pro Asp Pro Asp Asp
90 95 100

ggt cgc gcc acc gtt gct gtg ctc acg gac tct ggg tgg gag aaa gtt 451
Gly Arg Ala Thr Val Ala Val Leu Thr Asp Ser Gly Trp Glu Lys Val
105 110 115

aaa gca aca gcc cct ggt cat gtg aag gaa gtg cgt cgt ttg gtg ttt 499
Lys Ala Thr Ala Pro Gly His Val Lys Glu Val Arg Arg Leu Val Phe
120 125 130

gac gat ctc act cca gaa gaa ctc aag gta atg ggc acc gca atg aag 547
Asp Asp Leu Thr Pro Glu Glu Leu Lys Val Met Gly Thr Ala Met Lys
135 140 145

aag att gtg aac cga ctc gat atg tcc aac agg ctg ccc cgg gtg 592
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<210> 444

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

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Leu Pro Arg Val

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Thr Gln Leu Ile Ala Val Leu Ile Asp Asp Tyr Ser Asn Pro Trp Phe

09603639 066300

ccc tgg ctg att gaa cgg ggc acg tgc gcg cca cgt gga tagctacccc 1009
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 325 330

aaataacttgg act 1022

<210> 446

<211> 333

<212> PRT

<213> Corynebacterium glutamicum

<400> 446

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Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys
 35 40 45

Leu Asn Tyr Gln Pro Asn Arg Ala Ala Ser Asp Leu Ala Ala Lys Arg
 50 55 60

Thr Gln Leu Ile Ala Val Leu Ile Asp Asp Tyr Ser Asn Pro Trp Phe
 65 70 75 80

Ile Asp Leu Ile Gln Ser Leu Ser Asp Val Leu Thr Pro Lys Gly Tyr
 85 90 95

Arg Leu Ser Val Ile Asp Ser Leu Thr Ser Gln Ala Gly Thr Asp Pro
 100 105 110

Ile Thr Ser Ala Leu Ser Met Arg Pro Asp Gly Ile Ile Ala Gln
 115 120 125

Asp Ile Pro Asp Phe Thr Val Pro Asp Ser Leu Pro Pro Phe Val Ile
 130 135 140

Ala Gly Thr Arg Ile Thr Gln Ala Ser Thr His Asp Ser Val Ala Asn
 145 150 155 160

Asp Asp Phe Arg Gly Ala Glu Ile Ala Thr Lys His Leu Ile Asp Leu
 165 170 175

Gly His Thr His Ile Ala His Leu Arg Val Gly Ser Gly Ala Gly Leu
 180 185 190

Arg Arg Phe Glu Ser Phe Glu Ala Thr Met Arg Ala His Gly Leu Glu
 195 200 205

Pro Leu Ser Asn Asp Tyr Leu Gly Pro Ala Val Glu His Ala Gly Tyr
 210 215 220

Thr Glu Thr Leu Ala Leu Leu Lys Glu His Pro Glu Val Thr Ala Ile
 225 230 235 240

Phe Ser Ser Asn Asp Ile Thr Ala Ile Gly Ala Leu Gly Ala Ala Arg
 245 250 255

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Glu Leu Gly Leu Arg Val Pro Glu Asp Leu Ser Ile Ile Gly Tyr Asp
260 265 270

Asn Thr Pro Leu Ala Gln Thr Arg Leu Ile Asn Leu Thr Thr Ile Asp
275 280 285

Asp Asn Ser Ile Gly Val Gly Tyr Asn Ala Ala Leu Leu Leu Ser
290 295 300

Met Leu Asp Pro Glu Ala Pro His Pro Glu Ile Met His Thr Leu Gln
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Pro Ser Leu Ile Glu Arg Gly Thr Cys Ala Pro Arg Gly
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<211> 523

<212> DNA

<213> Corynebacterium glutamicum

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Met Tyr Glu Gln Gln
1 5

aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat 163
Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp
10 15 20

ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc 211
Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser
25 30 35

att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att 259
Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile
40 45 50

gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt 307
Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val
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tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag 355
Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu
70 75 80 85

atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat 403
Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp
90 95 100

can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg 451
Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser
105 110 115

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Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His
120 125 130

tct ccg acg tgg aag cgc cag ttg ggt tgc ctt ggt gga ggt aat cac 547
Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Asn His
135 140 145

ttc att gag ttg tgt ctt gat gag ttg gat cgg gtg tgg atg ttt ttg 595
Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu
150 155 160 165

cac tct ggt tcc cgc ggt gtg ggt aac aag att gcc cag aag cac atc 643
His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala Gln Lys His Ile
170 175 180

aag atc cgc cag gcc gag tgt aag aat gag gag ctt ccc gat aag gat 691
Lys Ile Ala Tyr Gln Ala Glu Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp
185 190 195

ctt gcg tac ttg acc gag ggg act gag gag ttt gag tct tac atc aag 739
Leu Ala Tyr Leu Thr Glu Gly Thr Glu Glu Phe Glu Ser Tyr Ile Lys
200 205 210

gaa ctg aat tgg gcg cag cgt ttt gcg ttc ctc aac agg gaa gaa atg 787
Glu Leu Asn Trp Ala Gln Arg Phe Ala Phe Leu Asn Arg Glu Glu Met
215 220 225

atg gac aga ttc gca cgg gag ctg ggt ttt ttc gac aag cag ctt 835
Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln Leu
230 235 240 245

gaa gag gtc gag cgc atc aac tgc cac cat aac tac acg gtc cag gag 883
Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln Glu
250 255 260

gag cac tac ggc gag acc att tgg ctc acc cgt aag ggt gcc gtg ttg 931
Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val Leu
265 270 275

gcg gac gaa ggc acg cgc gcg ttg att cgg ggg tgc atg ggc acc gcg 979
Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr Ala
280 285 290

tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgg tgc gcg 1027
Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser Ala
295 300 305

ccg cat ggg gcg ggc cgg agg atg tgc cgc aac cag gct aaa aag cgc 1075
Pro His Gly Ala Gly Arg Arg Met Ser Arg Asn Gln Ala Lys Lys Arg
310 315 320 325

ttc tgc acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac cgg 1123
Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr Arg
330 335 340

ccc gcg aag gag tgg atc gat gaa att ccc gac gct tac aaa gac atc 1171
Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp Ile
345 350 355

gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat aaa 1219
Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His Lys

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ggtccaattc atg				1137
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Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly				
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Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr				
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Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile				
	65	70	75	80
Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln				
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Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro				
	100	105	110	
Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu				
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Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg				
	130	135	140	
Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg				
	145	150	155	160
Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys				
	165	170	175	
Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val				
	180	185	190	
Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala				
	195	200	205	
Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu				
	210	215	220	
Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr				
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Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser				

245 250 255

Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly
260 265 270

Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe
275 280 285

Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly
290 295 300

Leu Thr Leu Lys Asp Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu
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Ser Glu

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 Met Ser Asp Glu Asn
 1 5

att aac gag ttt gag cag gac gag gat ctg aac ttc gcc gcg agc ttt 163
 Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn Phe Gly Ala Ser Phe
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 Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala Glu Ala Asp Val Glu
 25 30 35

gca gat gct gct gca gag gcc tct gcc ctg gaa gct gag cag gat ctg 259
 Ala Asp Ala Ala Glu Ala Ser Ala Leu Glu Ala Glu Gln Asp Leu
 40 45 50

gaa gaa gag acc cta gat gct cca gaa gaa gcc gca gaa gaa gct cct 307
 Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro
 55 60 65

gct gct gca gag tcc gaa gct cca gta gaa gag gac gaa gag gct gac 355
 Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp
 70 75 80 85

agc ctt gct cag gcg gct gct gca ctt ggt gac acc gat gag cag gac 403
 Ser Leu Ala Gln Ala Ala Ala Leu Gly Asp Thr Asp Glu Gln Asp
 90 95 100

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Thr Pro Val Asp Leu Ser Phe Asp Gln Val Glu Lys Val Ser
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cgc ggg ctg gcg ctg aca ggg gcg gcc gat cag ctt ttg tcg cag gcg 96
Arg Gly Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala
20 25 30

cgc cgc ctg atc gcc ctg aac gac gag gta tac gcc cgc ttg aac gcc 144
Arg Arg Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala
35 40 45

ggt gcc tac gag gcc gag gtg acg ctg ggc gtg cct caa gac gtg atc 192
Gly Ala Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile
50 55 60

tac ccc gtc atc ccg cgc gtc ttg cag caa ttc gcc cgc gat ttt ccc 240
Tyr Pro Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro
65 70 75 80

cgc gtg caa att cac ctg atc tcg aac ttc acg ctg atg ctg aaa gaa 288
Arg Val Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu
85 90 95

cag ttc cgc cgc gcc gaa atc gac gtg atg ctg acg acc gag gac gag 336
Gln Phe Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu
100 105 110

ctg gcc gag gcc gcc gag acg ctg gcc cag cgc gag ctg atc tgg gtc 384
Leu Gly Glu Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val
115 120 125

ggc gca ccg gcc ggg tcg gcg tgg acc cgc agg ccg ctg ccc ttg gcg 432
Gly Ala Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala
130 135 140

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Phe Glu Arg Ala Cys Ile Phe Arg Ser Phe Val Gln Arg Arg Leu Asp
145 150 155 160

gcc aac agc atc gat tgg cag atg gtg gtc agc agc gaa tcc aca cgg 528
Ala Asn Ser Ile Asp Trp Gln Met Val Val Ser Ser Glu Ser Thr Arg
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Ser Arg Thr Ile Arg Leu Pro Val His Leu Val Glu Gln Val Asn Lys
170 175 180

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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				1		
aaa	ttt	tcc	cgc	act	gct	163
Lys	Phe	Ser	Arg	Thr	Ala	
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cgc	att	aat	gag	cgc	atc	211
Arg	Ile	Asn	Glu	Arg	Ile	
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aac	ggt	gag	caa	gta	ggc	259
Asn	Gly	Glu	Gln	Val	Gly	
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gca	ttc	gac	gca	gac	cta	307
Ala	Phe	Asp	Ala	Asp	Leu	
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cct	cca	gtc	tcg	aag	atc	355
Pro	Pro	Val	Cys	Lys	Ile	
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gcc	caa	aag	gct	cgt	gag	403
Ala	Gln	Lys	Ala	Arg	Glu	
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aaa	gag	caa	aag	ctt	cgt	451
Lys	Glu	Gln	Lys	Leu	Arg	
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Lys	Lys	Asn	Asn	Val	Ile	
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gtc	acg	atc	atg	ttc	cgt	547
Val	Thr	Ile	Met	Phe	Arg	
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tac	agg	ctc	ctc	gag	cga	585
Tyr	Arg	Leu	Leu	Glu	Arg	
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gtg	gaa	acc	cgc	gca	aag	643
Val	Glu	Thr	Arg	Ala	Lys	
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Gly	Pro	Val	Arg	Lys	Gly	
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<212> PRT

<213> *Corynebacterium glutamicum*

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gct cag ggt gct cag gga gca cct tcc cag gag cgt caa ggt ggc gga 1027
 Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu Arg Gln Gly Gly Gly
 295 300 305

cgt cgt cca tcc cca gca atg atg cct cca acc cca ggt cag atg cct 1075
 Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr Pro Gly Gln Met Pro
 310 315 320 325

gct aag gca cct ggc aag ggt ggt cgt ggt ggc caa gcc ggc ggt ggc 1123
 Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly Gln Ala Gly Gly Gly
 330 335 340

gct ggt ggc gga ttc aac cgt ggt ggc gga acc ggt ggc ggc gca ggc 1171
 Ala Gly Gly Phe Asn Arg Gly Gly Gly Thr Gly Gly Ala Gly
 345 350 355

cgt ggc ggt cgt cgt ggc ggt acc gca ggt gca ttc ggc cgt cca ggt 1219
 Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala Phe Gly Arg Pro Gly
 360 365 370

ggt gct cca cgc agg gga cgt aag tgc aag cgt cag aag cgc aac gag 1267
 Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg Gln Lys Arg Asn Glu
 375 380 385

tac gaa tca atg cag gca ccg aac gtc att ggt ggc gtt cgt ttg cca 1315
 Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly Gly Val Arg Leu Pro
 390 395 400 405

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 Asp Gly Lys Gly Ala Thr Ile Arg Leu Ala Arg Gly Ala Ser Leu Ala
 410 415 420

gac ttc gct gac aag atc ggc gca gac gca gca gca ttg gtt cag gct 1411
 Asp Phe Ala Asp Lys Ile Gly Ala Asp Ala Ala Ala Leu Val Gln Ala
 425 430 435

ctg ttc aac ttg ggt gaa atg gtc acc gca act gca tgc gtt tct gat 1459
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 440 445 450

gaa acc ttg cag ctg ctc ggt gag gaa atg aac tac aag gtt cag gtt 1507
 Glu Thr Leu Gln Leu Leu Glu Glu Met Asn Tyr Lys Val Gln Val
 455 460 465

gtt tcc cca gaa gat gaa gac cgt gag ctg ctc gaa agc ttc gac ctt 1555
 Val Ser Pro Glu Asp Glu Asp Arg Glu Leu Leu Glu Ser Phe Asp Leu
 470 475 480 485

cag ttc ggt gag gac gaa ggt ggc gag gct gac ctt gct aag cgt cct 1603
 Gln Phe Gly Glu Asp Glu Gly Gly Glu Ala Asp Leu Ala Lys Arg Pro
 490 495 500

cca gtg gtt acc gtc atg ggt cac gtt gac cac ggt aag act cgt ttg 1651
 Pro Val Val Thr Val Met Gly His Val Asp His Gly Lys Thr Arg Leu
 505 510 515

ctg gat act atc cgt aag gca aat gtg ggc tcc gac gaa gcc ggc ggc 1699

002220 002220

Leu Asp Thr Ile Arg Lys Ala Asn Val Gly Ser Asp Glu Ala Gly Gly
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 Ile Thr Gln Gly Ile Gly Ala Tyr Gln Val Lys Val Asn Val Glu Asp
 535 540 545
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 Thr Glu Arg Thr Ile Thr Phe Leu Asp Thr Pro Gly His Glu Ala Phe
 550 555 560 565
 acc gca atg cgt gcc cgt ggt gca aag tcc aca gat atc gcg gtt ctg 1843
 Thr Ala Met Arg Ala Arg Gly Ala Lys Ser Thr Asp Ile Ala Val Leu
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 Asn His Ala Lys Ala Ala Asp Val Pro Ile Val Val Ala Val Asn Lys
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 Ile Asp Lys Pro Glu Ala Ser Pro Glu Lys Ile Arg Gly Gln Leu Thr
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 Asp Ile Ser Ala Lys Gln Gly Leu Asn Ile Asp Glu Leu Leu Ala Ser
 650 655 660
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 Val Cys Leu Thr Ala Asp Ala Glu Leu Asp Leu Val Ala Asn Pro Glu
 665 670 675
 atg gac gca cag ggt gtt gca att gaa gct cac ctc gac cgt ggt cgt 2179
 Met Asp Ala Gln Gly Val Ala Ile Glu Ala His Leu Asp Arg Gly Arg
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 Gly Pro Val Ala Thr Val Ile Val Gln Arg Gly Thr Leu Arg Val Gly
 695 700 705
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 Asp Ser Ile Val Ala Gly Asp Thr Tyr Gly Arg Val Arg Arg Met Val
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 730 735 740
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act gag gaa gca aac gca gaa ggc gtc gat gtt cgt tac tac acg atc Thr Glu Glu Ala Asn Ala Glu Gly Val Asp Val Arg Tyr Tyr Thr Ile 870 875 880 885			2755
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gac gat gcc acc gaa gtc tct gca ggc tac gag tgc ggt atg gtt ctg Asp Asp Ala Thr Glu Val Ser Ala Gly Tyr Glu Cys Gly Met Val Leu 970 975 980			3043
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<211> 1004

<212> PRT

<213> *Corynebacterium glutamicum*

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Pro Lys Pro Gly Ala Pro Ala Lys Pro Ala Ala Pro Ala Ala Lys Pro
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Pro Lys Pro Gly Val Gln Ala Lys Pro Ala Ala Ala Lys Pro Gly
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Gly Ser Ala Ser Lys Pro Ala Ala Ala Ala Lys Pro Ala Phe Ser Gly
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Pro Thr Pro Gly Asp Ala Ser Lys Lys Ala Glu Pro Ala Ala Lys Pro
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Gly Ala Glu Ala Pro Arg Pro Gly Gly Met Pro Arg Pro Met Gly Lys
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Pro Ala Pro Lys Pro Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro
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Phe Ser Thr Gly Gly Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly
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Pro Arg Pro Gly Gly Gly Pro Arg Pro Gly Gly Gly Pro Arg Pro Gln
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Gly Gln Gly Arg Pro Gly Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln
  245              250              255

Arg Asp Gly Gln Gly Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala
  260              265              270

Gly Gly Pro Arg Pro Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg
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Pro Gln Gly Gly Ser Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu
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 Arg Gln Gly Gly Gly Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr
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 Pro Gly Gln Met Pro Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly
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 Gln Ala Gly Gly Gly Ala Gly Gly Gly Phe Asn Arg Gly Gly Gly Thr
 340 345 350
 Gly Gly Gly Ala Gly Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala
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 Phe Gly Arg Pro Gly Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg
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 Gln Lys Arg Asn Glu Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly
 385 390 395 400
 Gly Val Arg Leu Pro Asp Gly Lys Gly Ala Thr Ile Arg Leu Ala Arg
 405 410 415
 Gly Ala Ser Leu Ala Asp Phe Ala Asp Lys Ile Gly Ala Asp Ala Ala
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 Ala Leu Val Gln Ala Leu Phe Asn Leu Gly Glu Met Val Thr Ala Thr
 435 440 445
 Ala Ser Val Ser Asp Glu Thr Leu Gln Leu Leu Gly Glu Glu Met Asn
 450 455 460
 Tyr Lys Val Gln Val Val Ser Pro Glu Asp Glu Asp Arg Glu Leu Leu
 465 470 475 480
 Glu Ser Phe Asp Leu Gln Phe Gly Glu Asp Glu Gly Gly Glu Ala Asp
 485 490 495
 Leu Ala Lys Arg Pro Pro Val Val Thr Val Met Gly His Val Asp His
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 Gly Lys Thr Arg Leu Leu Asp Thr Ile Arg Lys Ala Asn Val Gly Ser
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 Thr Val Glu Ala Ile Asn His Ala Lys Ala Ala Asp Val Pro Ile Val
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 Arg Gly Gln Leu Thr Glu Tyr Gly Leu Ile Pro Glu Glu Tyr Gly Gly
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 Glu Leu Leu Ala Ser Val Cys Leu Thr Ala Asp Ala Glu Leu Asp Leu
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 Val Ala Asn Pro Glu Met Asp Ala Gln Gly Val Ala Ile Glu Ala His
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 Leu Asp Arg Gly Arg Gly Pro Val Ala Thr Val Ile Val Gln Arg Gly
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 Val Arg Arg Met Val Asp Glu Tyr Gly Arg Asp Val Glu Glu Ala Gly
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 Pro Ser Arg Pro Val Gln Val Gln Gly Leu Asn Gly Val Pro Gly Ala
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 Gly Asp Asn Leu Leu Val Val Glu Asp Asp Arg Ile Ala Arg Gln Ile
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 Ala Asn Gln Arg Asn Ala Arg Lys Arg Asn Ala Leu Ala Ala Arg Ser
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 Arg Lys Arg Val Ser Leu Glu Asp Leu Asp Ser Val Leu Lys Glu His
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 Ser Thr Leu Asn Leu Ile Leu Lys Gly Asp Asn Ala Gly Ser Val Glu
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 Arg Tyr Tyr Thr Ile Ile Tyr Arg Ala Ile Glu Glu Val Glu Ala Ala
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 Gly Cys Met Val Glu Asp Gly Lys Val Arg Arg Asn Ala Thr Val Arg

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Ile Ile Arg Asp Gly Asn Val Ile Ala Glu Asn Ala Lys Ile Val Ser 945 950 955 960		
Leu Arg Arg Glu Lys Asp Asp Ala Thr Glu Val Ser Ala Gly Tyr Glu 965 970 975		
Cys Gly Met Val Leu Ser Tyr Pro Asp Ile Ser Val Asp Asp Lys Ile 980 985 990		
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 Val Pro Gly Lys Leu
 1 5
 cgt gta cat gag ctt gct aag caa ctc ggt att acc agc aag gaa cta 163
 Arg Val His Glu Leu Ala Lys Gln Leu Gly Ile Thr Ser Lys Glu Leu
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 ctt gcc acc ctt aag gat aaa ggc gag ttt gtt aaa acc gca tca tcc 211
 Leu Ala Thr Leu Lys Asp Lys Gly Glu Phe Val Lys Thr Ala Ser Ser
 25 30 35
 aca att gaa ccc cca gtt gtg aag agg atg cag gag cac tac ggt tcg 259
 Thr Ile Glu Pro Pro Val Val Lys Arg Met Gln Glu His Tyr Gly Ser
 40 45 50
 agc ggt tcg gat aag tcc gac acc gct gcg aag cct gca gcg gca aag 307
 Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys Pro Ala Ala Ala Lys
 55 60 65
 cct gct gcg cca aaa cca gct gcg tca gca gct cca aag cca ggt gct 355
 Pro Ala Ala Pro Lys Pro Ala Ala Ser Ala Ala Pro Lys Pro Gly Ala
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 cca gca aaa cct gca gca cct gca gca aag cct gcc cca gct gct cct 403
 Pro Ala Lys Pro Ala Ala Pro Ala Ala Lys Pro Ala Pro Ala Ala Pro
 90 95 100
 tct gca gct tct gca gca aag cca ggc gca gca cct aag cca ggc gtt 451
 Ser Ala Ala Ser Ala Ala Lys Pro Gly Ala Ala Pro Lys Pro Gly Val
 105 110 115
 cag gca aag cct gca gca gcc gct aag cca ggc gct cca gca aag cca 499

002290 50202060

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ggt gct cca cgc agg gga	cgt aag tgc aag cgt	cag aag cgc aac gag	1267
Gly Ala Pro Arg Arg Gly	Arg Lys Ser Lys Arg	Gln Lys Arg Asn Glu	
375	380	385	
tac gaa tca atg cag gca	ccg aac gtc att ggt	ggc gtt cgt ttg cca	1315
Tyr Glu Ser Met Gln Ala	Pro Asn Val Ile Gly	Gly Val Arg Leu Pro	
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gac ggc aag ggt gca acc atc	cgc ctc gcg cgc ggt	gca tct ttg gct	1363
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Lys Thr Ala Ser Ser Thr Ile Glu Pro Pro Val Val Lys Arg Met Gln			
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Glu His Tyr Gly Ser Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys			
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Pro Lys Pro Gly Val Gln Ala Lys Pro Ala Ala Ala Lys Pro Gly			
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Gly Ser Ala Ser Lys Pro Ala Ala Ala Ala Lys Pro Ala Phe Ser Gly			
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Gly Ala Glu Ala Pro Arg Pro Gly Gly Met Pro Arg Pro Met Gly Lys			
180 185 190			

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Pro Ala Pro Lys Pro Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro
195 200 205

Phe Ser Thr Gly Gly Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly
210 215 220

Pro Arg Pro Gly Gly Gly Pro Arg Pro Gly Gly Gly Pro Arg Pro Gln
225 230 235 240

Gly Gln Gly Arg Pro Gly Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln
245 250 255

Arg Asp Gly Gln Gly Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala
260 265 270

Gly Gly Pro Arg Pro Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg
275 280 285

Pro Gln Gly Gly Ser Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu
290 295 300

Arg Gln Gly Gly Gly Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr
305 310 315 320

Pro Gly Gln Met Pro Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly
325 330 335

Gln Ala Gly Gly Gly Ala Gly Gly Gly Phe Asn Arg Gly Gly Gly Thr
340 345 350

Gly Gly Gly Ala Gly Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala
355 360 365

Phe Gly Arg Pro Gly Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg
370 375 380

Gln Lys Arg Asn Glu Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly
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<223> FRXA01496

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5

10

15

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gag Glu	gaa Glu	atg Met 35	aac Asn	tac Tyr	aag Lys	ggt Val	cag Gln 40	ggt Val	ggt Val	tcc Ser	cca Pro	gaa Glu 45	gat Asp	gaa Glu	gac Asp	144
cgt Arg	gag Glu	ctg Leu 50	ctc Leu	gaa Glu	agc Ser	ttc Phe 55	gac Asp	ctt Leu	cag Gln	ttc Phe	ggt Gly 60	gag Glu	gac Asp	gaa Glu	ggt Gly	192
ggc Gly 65	gag Glu	gct Ala	gac Asp	ctt Leu	gct Ala 70	aag Lys	cgt Arg	cct Pro	cca Pro	gtg Val 75	ggt Val	acc Thr	gtc Val	atg Met	ggt Gly 80	240
cac His	ggt Val	gac Asp	cac His	ggt Gly 85	aag Lys	act Thr	cgt Arg	ttg Leu	ctg Leu 90	gat Ala Asp	act Thr	atc Ile	cgt Arg	aag Lys 95	gca Ala	288
aat Asn	gtg Val	ggc Gly	tcc Ser 100	gac Asp	gaa Glu	gcc Ala	ggc Gly	ggc Gly 105	att Ile	acc Thr	cag Gln	ggc Gly 110	att Ile	ggt Gly	gca Ala	336
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ctg Leu 130	gat Asp	acc Thr	cca Pro	ggt Gly	cac His	gag Glu 135	gcc Ala	ttc Phe	acc Thr	gca Ala 140	atg Met	cgt Arg	gcc Ala	cgt Arg	ggt Gly	432
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ggt Val	atg Met	cct Pro	cag Gln	act Thr 165	gtg Val	gaa Glu	gca Ala	atc Ile	aac Asn 170	cac His	gct Ala	aag Lys	gct Ala	gca Ala 175	gat Asp	528
gta Val	cca Pro	atc Ile 180	gtg Val	ggt Val	gca Ala	gtg Val	aac Asn	aag Lys 185	att Ile	gat Asp	aag Lys	cca Pro	gaa Glu 190	gct Ala	tct Ser	576
cca Pro	gag Glu	aag Lys 195	atc Ile	cgt Arg	ggt Gly	cag Gln	ctg Leu 200	acc Thr	gaa Glu	tac Tyr	gga Gly	ttg Leu 205	atc Ile	cct Pro	gaa Glu	624
gag Glu 210	tac Tyr	ggt Gly	ggc Ser	gac Asp	acc Thr	atc Ile 215	ttc Phe	ggt Val	gac Asp	atc Ile	tct Ser 220	gca Ala	aag Lys	cag Gln	gga Gly	672
ctg Leu 225	aac Asn	atc Ile	gat Asp	gag Glu	ctg Leu 230	ctc Leu	gct Ala	tct Ser	gtc Val	tgc Cys 235	ctg Leu	acc Thr	gca Ala	gac Asp 240	gct Ala	720
gag Glu	ctt Leu	gac Asp	ctt Leu	ggt Val 245	gct Ala	aac Asn	cca Pro	gaa Glu	atg Met 250	gac Asp	gca Ala	cag Gln	ggt Gly 255	ggt Val	gca Ala	768
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gtc	cag	cgc	ggg	acc	ctg	cgc	gtc	ggg	gac	tcc	atc	gtt	gca	ggc	gat	864
Val	Gln	Arg	Arg	Gly	Thr	Leu	Arg	Val	Gly	Asp	Ser	Ile	Val	Ala	Gly	Asp
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acc	tac	gga	cgt	gtt	cgc	cgc	atg	gtg	gac	gaa	tac	gga	cgc	gac	gtt	912
Thr	Tyr	Gly	Arg	Val	Arg	Arg	Met	Val	Asp	Glu	Tyr	Gly	Arg	Asp	Val	
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gaa	gag	gcc	gga	cct	tcc	cgt	cct	gtt	cag	gtt	cag	ggg	ctt	aac	ggg	960
Glu	Glu	Ala	Gly	Pro	Ser	Ser	Arg	Pro	Val	Gln	Val	Gln	Gly	Leu	Asn	Gly
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gtc	cca	ggc	gcc	ggc	gac	aac	ctt	ctg	gtt	gtt	gaa	gat	gac	cgc	att	1008
Val	Pro	Gly	Ala	Gly	Asp	Asn	Leu	Leu	Val	Val	Glu	Asp	Asp	Arg	Ile	
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gca	cgt	cag	att	gct	aac	cag	cgc	aac	gcc	cgc	aag	cgt	aac	gct	ctg	1056
Ala	Arg	Gln	Ile	Ala	Asn	Gln	Arg	Asn	Ala	Arg	Lys	Arg	Asn	Ala	Leu	
			340					345					350			
gca	gca	cgc	tcc	cgt	aag	cgc	gtc	tcc	ctc	gag	gat	ctg	gat	tca	gtt	1104
Ala	Ala	Arg	Ser	Arg	Lys	Arg	Val	Ser	Leu	Glu	Asp	Leu	Asp	Ser	Val	
		355					360					365				
ctt	aag	gaa	cat	agc	acc	ctt	aac	ctc	att	ctt	aag	ggc	gac	aac	gca	1152
Leu	Lys	Glu	His	Ser	Thr	Leu	Asn	Leu	Ile	Leu	Lys	Gly	Asp	Asn	Ala	
		370				375					380					
ggg	tcc	gtg	gaa	gca	ctg	gaa	gaa	gca	ttg	cta	aag	att	gag	atg	gac	1200
Gly	Ser	Val	Glu	Ala	Leu	Glu	Glu	Ala	Leu	Leu	Lys	Ile	Gly	Met	Asp	
		385			390					395					400	
gat	gaa	gtc	cag	ctc	aac	atc	atc	gac	cgc	ggg	gtg	ggg	gca	gtt	acc	1248
Asp	Glu	Val	Gln	Leu	Asn	Ile	Ile	Asp	Arg	Gly	Val	Gly	Ala	Val	Thr	
				405				410					415			
cag	acc	aac	gtc	acc	ctt	gca	gct	gca	tcc	gac	gct	gtc	atc	atc	gcc	1296
Gln	Thr	Asn	Val	Thr	Leu	Ala	Ala	Ala	Ser	Ser	Ala	Val	Ile	Ile	Ala	
			420					425					430			
ttc	aac	gtt	cgc	gct	gaa	ggg	aag	gca	act	gag	gaa	gca	aac	gca	gaa	1344
Phe	Asn	Val	Arg	Ala	Glu	Gly	Lys	Ala	Thr	Glu	Glu	Ala	Asn	Ala	Glu	
		435				440						445				
ggc	gtc	gat	gtt	cgt	tac	tac	acg	atc	atc	tac	cgt	gct	atc	gaa	gag	1392
Gly	Val	Asp	Val	Arg	Tyr	Tyr	Thr	Ile	Ile	Tyr	Arg	Ala	Ile	Glu	Glu	
		450				455					460					
gtc	gag	ggg	gcc	ctc	aag	ggc	atg	ctc	aag	cca	atc	tac	gaa	gag	cgc	1440
Val	Glu	Ala	Ala	Leu												

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gcc	aca	gtc	cgc	att	att	cgc	gac	ggc	aac	gtc	atc	gcc	gag	aat	gca	1584														
Ala	Thr	Val	Arg	Ile	Ile	Arg	Asp	Gly	Asn	Val	Ile	Ala	Glu	Asn	Ala															
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aag	atc	gtg	tcc	ctt	cgc	cgt	gag	aag	gac	gat	gcc	acc	gaa	gtc	tct	1632														
Lys	Ile	Val	Ser	Leu	Arg	Arg	Glu	Lys	Asp	Asp	Ala	Thr	Glu	Val	Ser															
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gca	ggc	tac	gag	tgc	ggt	atg	gtt	ctg	tct	tac	cca	gac	atc	tcc	gtc	1680														
Ala	Gly	Tyr	Glu	Cys	Gly	Met	Val	Leu	Ser	Tyr	Pro	Asp	Ile	Ser	Val															
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Asp	Asp	Lys	Ile	Glu	Val	Tyr	Glu	Met	Val	Glu	Val	Pro	Arg	Glu	Ala															
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<211> 576

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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Glu	Glu	Met	Asn	Tyr	Lys	Val	Gln	Val	Val	Ser	Pro	Glu	Asp	Glu	Asp
		35				40						45			

Arg	Glu	Leu	Leu	Glu	Ser	Phe	Asp	Leu	Gln	Phe	Gly	Glu	Asp	Glu	Gly
		50				55					60				

Gly	Glu	Ala	Asp	Leu	Ala	Lys	Arg	Pro	Pro	Val	Val	Thr	Val	Met	Gly
		65			70					75				80	

His	Val	Asp	His	Gly	Lys	Thr	Arg	Leu	Leu	Asp	Thr	Ile	Arg	Lys	Ala
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Asn	Val	Gly	Ser	Asp	Glu	Ala	Gly	Gly	Ile	Thr	Gln	Gly	Ile	Gly	Ala
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Tyr	Gln	Val	Lys	Val	Asn	Val	Glu	Asp	Thr	Glu	Arg	Thr	Ile	Thr	Phe
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Leu	Asp	Thr	Pro	Gly	His	Glu	Ala	Phe	Thr	Ala	Met	Arg	Ala	Arg	Gly
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Ala	Lys	Ser	Thr	Asp	Ile	Ala	Val	Leu	Val	Val	Ala	Ala	Asp	Asp	Gly
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Val	Met	Pro	Gln	Thr	Val	Glu	Ala	Ile	Asn	His	Ala	Lys	Ala	Ala	Asp
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Val	Pro	Ile	Val	Val	Ala	Val	Asn	Lys	Ile	Asp	Lys	Pro	Glu	Ala	Ser
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<212> DNA

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<223> RXA00677

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Met Ala Lys Glu Gly
1 5

gct att gaa gtt gag ggt cgc att gtc gaa cct ctg ccg aat gca atg 163
Ala Ile Glu Val Glu Gly Arg Ile Val Glu Pro Leu Pro Asn Ala Met
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ttc cga gtc gag ctc gac aac gga cac aag gta ctc gcc cac atc agt 211
Phe Arg Val Glu Leu Asp Asn Gly His Lys Val Leu Ala His Ile Ser
25 30 35

gga aag atg cgc cag cac tac atc cgt atc ctt cct gag gac cgc gtc 259
Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu Pro Glu Asp Arg Val
40 45 50

gtt gta gag ctg tgc ccc tat gat ctg act cgt gga cga atc gtt tac 307
Val Val Glu Leu Ser Pro Tyr Asp Leu Thr Arg Gly Arg Ile Val Tyr
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cgc tac aag taaaaataag cttaagcct cca 339
Arg Tyr Lys
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<210> 470

<211> 72

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 470

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 Leu Ala His Ile Ser Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu
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 Gly Arg Ile Val Tyr Arg Tyr Lys
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<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(667)

<223> RXN01284

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 Val Ala Lys Ala Lys 5
 ttc gag cgt acc aag ccc cac gta aac atc ggc acc atc ggt cac gtt 163
 Phe Glu Arg Thr Lys Pro His Val Asn Ile Gly Thr Ile Gly His Val 20
 gag cac ggt aag acc acc acc acc ggc gct atc acc aag gtt ctg gct 211
 Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile Thr Lys Val Leu Ala 35
 gag act tac cct gag ctc aac gag gct ttc gcc ttc gac tcc atc gat 259
 Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala Phe Asp Ser Ile Asp 50
 aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc cac 307
 Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser His 65
 gtt gag tac cag act gaa aag cgc cac tac gca cac gtt gac gct cca 355
 Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala Pro 85
 ggc cac gcc gac tac atc aag aac atg att acc ggc gct gct cag atg 403
 Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln Met 100
 gag ggc gca atc ctc gtt gtt gct gct acc gac ggc cca atg cct cag 451
 Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro Gln 115
 105 110

002230-6620460

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 Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Ile Ile
 135 140 145

gag ctc gtc gag atg gaa gtt cgt gaa ctt ctt gct gag cag gac tac 595
 Glu Leu Val Glu Met Glu Val Arg Glu Leu Ala Glu Gln Asp Tyr
 150 155 160 165

gac gaa gag gct cca att gtt cac atc tcc gct ctg aag gct ctt gag 643
 Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu Glu
 170 175 180

ggc gac gag aag tgg ggc aag cag 667
 Gly Asp Glu Lys Trp Gly Lys Gln
 185

<210> 472

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Val Ala Lys Ala Lys Phe Glu Arg Thr Lys Pro His Val Asn Ile Gly
 1 5 10 15

Thr Ile Gly His Val Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile
 20 25 30

Thr Lys Val Leu Ala Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala
 35 40 45

Phe Asp Ser Ile Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr
 50 55 60

Ile Asn Ile Ser His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala
 65 70 75 80

His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr
 85 90 95

Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp
 100 105 110

Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val
 115 120 125

Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu
 130 135 140

Asp Glu Glu Ile Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu
 145 150 155 160

Ala Glu Gln Asp Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala
 165 170 175

Leu Lys Ala Leu Glu Gly Asp Glu Lys Trp Gly Lys Gln

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180

185

<210> 473
 <211> 507
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (1)..(507)
 <223> FRXA01284

<400> 473
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 Val Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile Thr Lys Val Leu
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 gct gac act tac cct gag ctc aac cag gct ttc gcc ttc gac tcc atc 96
 Ala Asp Thr Tyr Pro Glu Leu Asn Gln Ala Phe Ala Phe Asp Ser Ile
 20 25 30
 gat aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc 144
 Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser
 35 40 45
 cac gtt gag tac cag act gaa aag cgc cac tac gca cac gtt gac gct 192
 His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala
 50 55 60
 cca ggc cac gcc gac tac atc aag aac atg att acc ggc gct gct cag 240
 Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln
 65 70 75 80
 atg gac ggc gca atc ctc gtt gtt gct gct acc gac ggc cca atg cct 288
 Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro
 85 90 95
 cag acc cgt gag cac gtt ctt ctt gct cgc cag gtt ggc gtt cct tac 336
 Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr
 100 105 110
 atc ctc gtt gct ctt aac aag tgc gac atg gtt gag gat gag gaa atc 384
 Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile
 115 120 125
 atc gag ctc gtc gag atg gaa gtt cgt gaa ctt ctt gct gag cag gac 432
 Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Ala Glu Gln Asp
 130 135 140
 tac gac gaa gag gct cca att gtt cac atc tcc gct ctg aag gct ctt 480
 Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu
 145 150 155 160
 gag ggc gac gag aag tgg ggc aag cag 507
 Glu Gly Asp Glu Lys Trp Gly Lys Gln
 165

<210> 474
 <211> 169

002290.062300

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Val	Asp	His	Gly	Lys	Thr	Thr	Thr	Thr	Ala	Ala	Ile	Thr	Lys	Val	Leu
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Ala	Asp	Thr	Tyr	Pro	Glu	Leu	Asn	Gln	Ala	Phe	Ala	Phe	Asp	Ser	Ile
		20						25					30		

Asp	Lys	Ala	Pro	Glu	Glu	Lys	Glu	Arg	Gly	Ile	Thr	Ile	Asn	Ile	Ser
	35						40					45			

His	Val	Glu	Tyr	Gln	Thr	Glu	Lys	Arg	His	Tyr	Ala	His	Val	Asp	Ala
	50					55					60				

Pro	Gly	His	Ala	Asp	Tyr	Ile	Lys	Asn	Met	Ile	Thr	Gly	Ala	Ala	Gln
	65				70					75					80

Met	Asp	Gly	Ala	Ile	Leu	Val	Val	Ala	Ala	Thr	Asp	Gly	Pro	Met	Pro
			85							90				95	

Gln	Thr	Arg	Glu	His	Val	Leu	Leu	Ala	Arg	Gln	Val	Gly	Val	Pro	Tyr
		100						105					110		

Ile	Leu	Val	Ala	Leu	Asn	Lys	Cys	Asp	Met	Val	Glu	Asp	Glu	Glu	Ile
	115						120					125			

Ile	Glu	Leu	Val	Glu	Met	Glu	Val	Arg	Glu	Leu	Leu	Ala	Glu	Gln	Asp
	130				135						140				

Tyr	Asp	Glu	Glu	Ala	Pro	Ile	Val	His	Ile	Ser	Ala	Leu	Lys	Ala	Leu
	145				150					155					160

Glu	Gly	Asp	Glu	Lys	Trp	Gly	Lys	Gln
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<210> 475

<211> 684

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(661)

<223> RXA00138

<400> 475

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cagacc	ccccca	tcacg	taata	ccacg	agggga	gatcac	atcc	gtg	gca	act	acc	gct		115
								Val	Ala	Thr	Thr	Ala		
								1				5		

gat	ttc	aag	aac	ggt	cta	gtt	ctc	aag	aac	gaa	ggc	aag	ctg	cag	cag
Asp	Phe	Lys	Asn	Gly	Leu	Val	Leu	Lys	Asn	Glu	Gly	Lys	Leu	Gln	Gln
				10					15				20		

atc	atc	gag	ttc	cag	cac	gtc	aag	cca	ggc	aag	ggc	cca	gca	ttc	gtg
Ile	Ile	Glu	Phe	Gln	His	Val	Lys	Pro	Gly	Lys	Gly	Pro	Ala	Phe	Val

002200.000000

25	30	35	
cga acc aaa ctc aag gac gtc gtg acc ggc aag acc atc gac aag acc Arg Thr Lys Leu Lys Asp Val Val Thr Gly Lys Thr Ile Asp Lys Thr	40	45	50
259			
tgg aac gca ggc gtc aag gtt gaa acc gca acc gtc gac cgc cgc gat Trp Asn Ala Gly Val Lys Val Glu Thr Ala Thr Val Asp Arg Arg Asp	55	60	65
307			
gtc acc tat ttg tac aac gac ggc act tcc ttc atc gtc atg gat gac Val Thr Tyr Leu Tyr Asn Asp Gly Thr Ser Phe Ile Val Met Asp Asp	70	75	80
355			85
aag act ttc gag cag tac gag ctg tcc cca gac gca ttc ggc gac gct Lys Thr Phe Glu Gln Tyr Glu Leu Ser Pro Asp Ala Phe Gly Asp Ala	90	95	100
403			
ggc cgc ttc cta ctt gaa aac atg cgc gtt cag gtc tcc ttc cac gaa Gly Arg Phe Leu Leu Glu Asn Met Arg Val Gln Val Ser Phe His Glu	105	110	115
451			
ggc gag gca ctc ttc ggc gaa ctc cca gta tct gtc gac ctc cgc gtc Gly Glu Ala Leu Phe Gly Glu Leu Pro Val Ser Val Asp Leu Arg Val	120	125	130
499			
gag cac acc gat cca ggc ctg cag ggc gac cgc tcc acc ggc ggc acc Glu His Thr Asp Pro Gly Leu Gln Gly Asp Arg Ser Thr Gly Gly Thr	135	140	145
547			
aag cca gca acc ctc gag acc ggc gct gaa atc cag gtc cca ctg ttc Lys Pro Ala Thr Leu Glu Thr Gly Ala Glu Ile Gln Val Pro Leu Phe	150	155	160
595			165
atc gag acc gga aac gta ctc aag gta gac acc cgc gac ggt tcc tac Ile Glu Thr Gly Asn Val Leu Lys Val Asp Thr Arg Asp Gly Ser Tyr	170	175	180
643			
ctc tcc cgc gtt aac aac taagattctt aaaaccttta aga Leu Ser Arg Val Asn Asn	185		
684			
<210> 476			
<211> 187			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 476			
Val Ala Thr Thr Ala Asp Phe Lys Asn Gly Leu Val Leu Lys Asn Glu	1	5	10
15			
Gly Lys Leu Gln Gln Ile Ile Glu Phe Gln His Val Lys Pro Gly Lys	20	25	30
35			
Gly Pro Ala Phe Val Arg Thr Lys Leu Lys Asp Val Val Thr Gly Lys	40	45	
50			
Thr Ile Asp Lys Thr Trp Asn Ala Gly Val Lys Val Glu Thr Ala Thr	55	60	

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<222> (101)..(457)  
<223> RXA00331
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4400> 477	cagcgcgcgac	cagcaagcga	agtactgacc	cagatttacg	aagaagtgct	cccccactc	60
	taaaatgcct	gttcgcgcac	ttcctctcgg	ggaaacagct	atg	ggt ggc	cac atg
					Met	Val Gly	His Met
					1		5
	tcg aat gat	cac cca	tac tcc	ccc gca	aaa cgc	gtc gga	aat ttc
	Ser Asn Asp	His Pro	Tyr Ser	Pro Ala	Lys Arg	Val Gly	Asn Phe
		10			15		20
	ile						
	163						
	ttc gtc tcc	ggc gct	ctt tca	gta gac	aag gac	tac caa	cca gtc
	Phe Val Ser	Gly Ala	Leu Ser	Val Asp	Lys Asp	Tyr Gln	Pro Val
		25			30		35
	211						
	ggt cgt aaa	gaa gca	ggt gat	gca gca	ctt gaa	cgc atg	cgt gaa
	Gly Arg Lys	Glu Ala	Val Asp	Ala Ala	Leu Glu	Arg Met	Arg Glu
		40		45		50	
	259						
	ctc gcc acc	gct ggt	ggt gaa	ctc aaa	gac gtt	gtg aaa	ctc act
	Leu Ala Thr	Ala Gly	Gly Glu	Leu Lys	Asp Val	Val Lys	Leu Thr
		55	60			65	
	307						
	ttt gtc acc	gac atc	agc ctg	cgc gaa	gaa tgc	aac gag	caa ttc
	Phe Val Thr	Asp Ile	Ser Leu	Arg Glu	Glu Cys	Asn Glu	Gln Phe
		70	75		80		85
	355						

gag cat ttc ctc gaa ggc cgc cgg gca cgc tct ttc gtg ggt gca tca	403
Glu His Phe Leu Glu Gly Arg Pro Ala Arg Ser Phe Val Gly Ala Ser	
90 95 100	
tcg ctt cct tat ggt gca act gtg gaa att gat gcg att gcg atg atc	451
Ser Leu Pro Tyr Gly Ala Thr Val Glu Ile Asp Ala Ile Ala Met Ile	
105 110 115	
gag gac taaccagagc atttttcgca cga	480
Glu Asp	

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<210> 478
<211> 119
<212> PRT
<213> Corynebacterium glutamicum
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<400> 478
Met Val Gly His Met Ser Asn Asp His Pro Tyr Ser Pro Ala Lys Arg
  1           5           10           15
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Val Gly Asn Phe Ile Phe Val Ser Gly Ala Leu Ser Val Asp Lys Asp
20 25 30

Tyr Gln Pro Val Val Gly Arg Lys Glu Ala Val Asp Ala Ala Leu Glu
35 40 45

Arg Met Arg Glu Arg Leu Ala Thr Ala Gly Gly Glu Leu Lys Asp Val
50 55 60

Val Lys Leu Thr Tyr Phe Val Thr Asp Ile Ser Leu Arg Glu Glu Cys
65 70 75 80

Asn Glu Gln Phe Arg Glu His Phe Leu Glu Gly Arg Pro Ala Arg Ser
85 90 95

Phe Val Gly Ala Ser Ser Leu Pro Tyr Gly Ala Thr Val Glu Ile Asp
100 105 110

Ala Ile Ala Met Ile Glu Asp
115

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<210> 479
<211> 570
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (1)..(570)  
<223> RXA02822
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<400> 479
ggt acc gag gtt agc cat ccc gcc cat ggt gcg tgg agc cag ttc aag 48
Gly Thr Glu Val Ser His Pro Ala His Gly Ala Trp Ser Gln Phe Lys
1 5 10 15

ttt qaa ggt ggc gtg cac cgt gtt cag cgt gtg cct gtt act gaa tct 96

Phe	Glu	Gly	Gly	Val	His	Arg	Val	Gln	Arg	Val	Pro	Val	Thr	Glu	Ser					
																20	25	30		
cag	gga	cgc	atc	cag	acc	tct	gct	gct	ggg	gtc	ttg	gtt	tac	cca	gaa	144				
Gln	Gly	Arg	Ile	Gln	Thr	Ser	Ala	Ala	Gly	Val	Leu	Val	Tyr	Pro	Glu					
																35	40	45		
cca	gat	gag	gtg	gaa	aac	gtt	gag	atc	gat	gag	aag	gat	att	cgc	gtc	192				
Pro	Asp	Glu	Val	Glu	Asn	Val	Glu	Ile	Asp	Glu	Lys	Asp	Ile	Arg	Val					
																50	55	60		
gat	gtg	tac	cgt	tcc	tca	ggg	aag	ggg	ggg	cag	ggc	gtt	aac	acc	act	240				
Asp	Val	Tyr	Arg	Ser	Ser	Gly	Lys	Gly	Gly	Gln	Gly	Val	Asn	Thr	Thr					
																65	70	75	80	
gac	tcc	gct	gtg	cgt	att	acc	cac	ttg	cca	act	ggg	ttg	gtg	gtg	acc	288				
Asp	Ser	Ala	Val	Arg	Ile	Thr	His	Leu	Pro	Thr	Gly	Leu	Val	Val	Thr					
																85	90	95		
tgt	cag	aag	gag	cgc	tcc	cag	att	cag	aac	cgt	gcg	cgt	gcg	atg	cag	336				
Cys	Gln	Lys	Glu	Arg	Ser	Gln	Ile	Gln	Asn	Arg	Ala	Arg	Ala	Met	Gln					
																100	105	110		
gtt	ttg	gct	gcc	cgt	tta	cag	gcg	atg	aag	gaa	gag	gaa	gcg	gcg	gct	384				
Val	Leu	Ala	Ala	Arg	Leu	Gln	Ala	Met	Lys	Glu	Glu	Glu	Ala	Ala	Ala					
																115	120	125		
gag	gct	gct	acg	gga	cgt	gct	gcg	cag	att	cgc	acc	atg	gac	cgc	tct	432				
Glu	Ala	Ala	Thr	Gly	Arg	Ala	Ala	Gln	Ile	Arg	Thr	Met	Asp	Arg	Ser					
																130	135	140		
gag	cgc	atc	cgt	acc	tac	aac	tgg	ccg	gaa	aac	cgc	atc	agc	gat	cac	480				
Glu	Arg	Ile	Arg	Thr	Tyr	Asn	Trp	Pro	Glu	Asn	Arg	Ile	Ser	Asp	His					
																145	150	155	160	
cgt	att	ggg	ttt	aag	gcg	aac	aac	ctt	gat	tcg	gtt	ctc	gat	ggg	gaa	528				
Arg	Ile	Gly	Phe	Lys	Ala	Asn	Asn	Leu	Asp	Ser	Lys	Leu	Asp	Gly	Glu					
																165	170	175		
ttg	gat	gat	ctg	ttc	acc	gcg	ttg	cag	gct	gct	gag	cgt	gca			570				
Leu	Asp	Asp	Leu	Phe	Thr	Ala	Leu	Gln	Ala	Ala	Glu	Arg	Ala							
																180	185	190		
<210> 480																				
<211> 190																				
<212> PRT																				
<213> Corynebacterium glutamicum																				
<400> 480																				
Gly	Thr	Glu	Val	Ser	His	Pro	Ala	His	Gly	Ala	Trp	Ser	Gln	Phe	Lys					
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Phe	Glu	Gly	Gly	Val	His	Arg	Val	Gln	Arg	Val	Pro	Val	Thr	Glu	Ser					
																20	25	30		
Gln	Gly	Arg	Ile	Gln	Thr	Ser	Ala	Ala	Gly	Val	Leu	Val	Tyr	Pro	Glu					
																35	40	45		
Pro	Asp	Glu	Val	Glu	Asn	Val	Glu	Ile	Asp	Glu	Lys	Asp	Ile	Arg	Val					
																50	55	60		

Asp Val Tyr Arg Ser Ser Gly Lys Gly Gly Gln Gly Val Asn Thr Thr
65 70 75 80

Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Leu Val Val Thr
85 90 95

Cys Gln Lys Glu Arg Ser Gln Ile Gln Asn Arg Ala Arg Ala Met Gln
100 105 110

Val Leu Ala Ala Arg Leu Gln Ala Met Lys Glu Glu Glu Ala Ala Ala
115 120 125

Glu Ala Ala Thr Gly Arg Ala Ala Gln Ile Arg Thr Met Asp Arg Ser
130 135 140

Glu Arg Ile Arg Thr Tyr Asn Trp Pro Glu Asn Arg Ile Ser Asp His
145 150 155 160

Arg Ile Gly Phe Lys Ala Asn Asn Leu Asp Ser Val Leu Asp Gly Glu
165 170 175

Leu Asp Asp Leu Phe Thr Ala Leu Gln Ala Ala Glu Arg Ala
180 185 190

<210> 481

<211> 480

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}...(457)

<223> RXA00011

<400> 481

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gtcgaatgtct accgctcctc cggcccaggt ggtcagttcca gtg aac acc acc gac 115
Val Asn Thr Thr Asp
1 5

tct gcc gtg cgc ctg acc cac atc cca acc ggc atc gtg gtg acc tgc 163
Ser Ala Val Arg Leu Thr His Ile Pro Thr Gly Ile Val Val Thr Cys
10 15 20

caa aac gag aaa tca cag atc caa aac aag gca tcc ggc atg cgt gtt 211
Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala Ser Ala Met Arg Val
25 30 35

ctc cag gca aaa ctg ctt gag cgt aaa cgc cag gaa gaa cgc gcc gaa 259
Leu Gln Ala Lys Leu Leu Arg Lys Arg Gln Glu Glu Arg Ala Glu
40 45 50

atg gat gcc ctc gga gct gga gcc aat gca tcc tgg ggt aac caa atg 307
Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser Trp Gly Asn Gln Met
55 60 65

cgt tcc tac gtg ctg cac cct tat caa atg gtg aag gat ctg cgc acc 355
Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val Lys Asp Leu Arg Thr

00602070.062300

70	75	80	85
aac ttt gaa gtc aac gat ccg caa aaa gtc ctt gac ggc gat atc gat	403		
Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu Asp Gly Asp Ile Asp			
90 95 100			
ggc ctt ttg gaa gca ggt att cgc tgg cga atg gct gag agc cag tcg	451		
Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met Ala Glu Ser Gln Ser			
105 110 115			
gcg gaa taaagggttgg ttttctggca gaa	480		
Ala Glu			

<210> 482
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 482
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 1 5 10 15
 Ile Val Val Thr Cys Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala
 20 25 30
 Ser Ala Met Arg Val Leu Gln Ala Lys Leu Leu Glu Arg Lys Arg Gln
 35 40 45
 Glu Glu Arg Ala Glu Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser
 50 55 60
 Trp Gly Asn Gln Met Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val
 65 70 75 80
 Lys Asp Leu Arg Thr Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu
 85 90 95
 Asp Gly Asp Ile Asp Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met
 100 105 110
 Ala Glu Ser Gln Ser Ala Glu
 115

<210> 483
 <211> 999
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> {101}..(976)
 <223> RXA00012

<400> 483
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 Met Arg Pro Glu Phe

002250.5320550

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tct	gca	gaa	ctc	tcc	gag	cta	gac	agc	acg	ctg	aca	acc	att	gaa	aaa	163															
Ser	Ala	Glu	Leu	Ser	Glu	Leu	Asp	Ser	Thr	Leu	Thr	Thr	Ile	Glu	Lys																
10																15	20														
gtg	ctg	aac	ccg	caa	gag	atg	tct	gac	cga	gtc	aga	gaa	ctt	gaa	gct	211															
Val	Leu	Asn	Pro	Gln	Glu	Met	Ser	Asp	Arg	Val	Arg	Glu	Leu	Glu	Ala																
25																30	35														
caa	gca	gct	gac	ccg	tct	ctg	tgg	gat	gac	cct	gac	cat	gca	cag	caa	259															
Gln	Ala	Ala	Asp	Pro	Ser	Leu	Trp	Asp	Asp	Pro	Asp	His	Ala	Gln	Gln																
40																45	50														
gtc	acc	tct	gag	ctg	tcc	cac	gtc	cag	gcg	gag	ctg	cgc	aaa	att	acc	307															
Val	Thr	Ser	Glu	Leu	Ser	His	Val	Gln	Ala	Glu	Leu	Arg	Lys	Ile	Thr																
55																60	65														
gat	ctg	cgc	cag	cgc	atc	gaa	gat	ctg	ccc	atc	atg	gtg	gaa	ctc	gca	355															
Asp	Leu	Arg	Gln	Arg	Ile	Glu	Asp	Leu	Pro	Ile	Met	Val	Glu	Leu	Ala																
70																75	80														
gag	gaa	gaa	gac	ggc	gat	acc	tcc	atc	gcg	gaa	gaa	gaa	ctc	gcc	gat	403															
Glu	Glu	Glu	Asp	Gly	Asp	Thr	Ser	Ile	Ala	Glu	Glu	Glu	Leu	Ala	Asp																
90																95	100														
ctg	cgt	tct	ctg	atc	gat	gcg	tgg	gaa	gta	aag	acc	atg	ctg	tcg	ggt	451															
Leu	Arg	Ser	Leu	Ile	Asp	Ala	Leu	Glu	Val	Lys	Thr	Met	Leu	Ser	Gly																
105																110	115														
gaa	tat	gat	gct	cgc	gag	gca	gtg	atc	aat	att	cga	tcc	ggt	gcc	ggt	499															
Glu	Tyr	Asp	Ala	Arg	Glu	Ala	Val	Ile	Asn	Ile	Arg	Ser	Gly	Ala	Gly																
120																125	130														
ggt	gtc	gat	gct	gcg	gac	tgg	gct	gaa	atg	ctc	atg	cgc	atg	tac	acc	547															
Gly	Val	Asp	Ala	Ala	Asp	Trp	Ala	Glu	Met	Leu	Met	Arg	Met	Tyr	Thr																
135																140	145														
cgc	tgg	gcg	gaa	aag	aac	ggc	cac	aaa	gta	gat	att	tac	gat	att	tcc	595															
Arg	Trp	Ala	Glu	Lys	Asn	Gly	His	Lys	Val	Asp	Ile	Tyr	Asp	Ile	Ser																
150																155	160														
tac	gcc	gaa	gaa	gcc	ggc	atc	aaa	tcc	gcc	acc	ttc	gtg	gtc	cac	ggc	643															
Tyr	Ala	Glu	Glu	Ala	Gly	Ile	Lys	Ser	Ala	Thr	Phe	Val	Val	His	Gly																
170																175	180														
gac	tac	atg	tac	ggc	cag	ctc	tcc	gtg	gag	caa	ggc	gca	cac	cgc	ctc	691															
Asp	Tyr	Met	Tyr	Gly	Gln	Leu	Ser	Val	Glu	Gln	Gly	Ala	His	Arg	Leu																
185																190	195														
gtg	cgc	atc	agt	cct	ttt	gat	aac	cag	ggc	agg	cgc	caa	acc	tcc	ttc	739															
Val	Arg	Ile	Ser	Pro	Phe	Asp	Asn	Gln	Gly	Arg	Arg	Gln	Thr	Ser	Phe																
200																205	210														
gcc	gag	gta	gaa	gtt	ctt	ccc	gtg	gtg	gaa	aaa	gtg	gac	tcc	atc	gac	787															
Ala	Glu	Val	Glu	Val	Leu	Pro	Val	Val	Glu	Lys	Val	Asp	Ser	Ile	Asp																
215																220	225														
atc	cct	gat	gcc	gat	gtt	cgc	gtc	gat	gtc	tac	cgc	tcc	tcc	ggc	cca	835															
Ile	Pro	Asp	Ala	Asp	Val	Arg	Val	Val	Asp	Val	Tyr	Arg	Ser	Ser	Gly																
230																235	240														

Gly Ala His Arg Leu Val Arg Ile Ser Pro Phe Asp Asn Gln Gly Arg
195 200 205

☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8
☐ 9 ☐ 10 ☐ 11 ☐ 12 ☐ 13 ☐ 14 ☐ 15

Arg Gln Thr Ser Phe Ala Glu Val Glu Val Leu Pro Val Val Glu Lys
210 215 220
Val Asp Ser Ile Asp Ile Pro Asp Ala Asp Val Arg Val Asp Val Tyr
225 230 235 240
Arg Ser Ser Ser Gly Pro Gly Gly Gln Ser Ser Glu His His Arg Leu Cys
245 250 255
Arg Ala Pro Asp Pro His Pro Asn Arg His Arg Gly Asp Leu Pro Lys
260 265 270
Arg Glu Ile Thr Asp Pro Lys Gln Gly Ile Arg Asp Ala Cys Ser Pro
275 280 285
Gly Lys Thr Ala
290

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<210> 485
<211> 741
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (1)..(741)  
<223> RXN01926
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c400> 485																
ctg	cga	agc	ttc	tac	acc	cca	gaa	caa	gcc	atc	gaa	cgc	gaa	ggc	gac	48
Leu	Arg	Ser	Phe	Tyr	Thr	Pro	Glu	Gln	Ala	Ile	Glu	Arg	Glu	Gly	Asp	
			5					10						15		
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gtc	tgg	aaa	gcc	gcc	acc	gaa	gaa	gca	gaa	ctc	ctc	gca	gct	gac	ggc	96
Val	Trp	Lys	Ala	Ala	Thr	Glu	Glu	Ala	Glu	Leu	Leu	Ala	Ala	Gly	Gly	
			20					25						30		
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gcc	gtc	cac	gac	cag	gaa	ctc	ttc	ctc	aac	tgc	acc	acc	tcc	cca	ctg	144
Ala	Val	His	Asp	Gln	Glu	Leu	Phe	Leu	Asn	Cys	Thr	Thr	Ser	Pro	Leu	
			35					40						45		
<hr/>																
atc	ttc	gcc	tcc	cgq	atg	ctc	aac	ttc	ggc	gtc	cac	caa	atc	ctg	gac	192
Ile	Phe	Ala	Ser	Ala	Met	Leu	Asn	Phe	Gly	Val	His	Gln	Ile	Leu	Asp	
			50					55						60		
<hr/>																
acc	ctc	tgc	caa	ctc	gca	cca	tcc	ccc	gcc	ggc	cgc	gac	gca	gac	ccc	240
Thr	Leu	Cys	Gln	Leu	Ala	Pro	Ser	Pro	Ala	Gly	Arg	Asp	Ala	Asp	Pro	
			65		70						75			80		
<hr/>																
aaa	gcc	ctc	gaa	gcc	gcc	acc	tcc	gca	atg	gac	gac	cac	cgc	gac	acc	288
Lys	Ala	Leu	Glu	Ala	Ala	Thr	Ser	Ala	Met	Asp	Asp	His	Arg	Asp	Thr	
			85						90						95	
<hr/>																
acc	gac	gac	pfc	tcc	ggc	gtc	gtc	ttc	aaa	gtc	caa	gcc	ggc	atg	gac	336
Thr	Asp	Asp	Phe	Ser	Gly	Val	Val	Phe	Lys	Val	Gln	Ala	Gly	Met	Asp	
			100					105						110		
<hr/>																
aaa	aac	cac	cgc	gat	acc	ctc	gcc	ttc	atg	cgc	gtc	gtc	tcc	ggc	gaa	384
Lys	Asn	His	Arg	Asp	Thr	Leu	Ala	Phe	Met	Arg	Val	Val	Ser	Gly	Glu	
			115					120						125		

ttc gac cgc gcc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc 432
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140

tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc 480
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160

gaa acc gcc ttc ccc gcc gac atc gtc ggc ctc gtc aac gcc gcc gcc 528
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175

ctc gca cca gcc gac acc atc ttc gaa gcc cga aaa atc caa tac cca 576
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190

cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa 624
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205

tca ctc gcc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac 672
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220

tcc gaa ggt gtc gtc cag atc ctc aag aac gac ctg cgt gcc gac gcc 720
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240

aac cca ggt cat gcc cgg tgt 741
 Asn Pro Gly His Gly Arg Cys
 245

<210> 486
 <211> 247
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 486
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 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110

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[illegible]

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<211> 672
<212> DNA
<213> Corynebacterium glutamicum
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<222> (1)..(672)  
<223> FRXA01926
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Leu	Arg	Ser	Phe	Tyr	Thr	Pro	Glu	Gln	Ala	Ile	Glu	Arg	Glu	Gly	Asp			
1				5					10					15				
gtc	tg	aaa	gcc	acc	gaa	gaa	gca	gaa	ctc	ctc	gca	gct	gac	ggc			96	
Val	Trp	Lys	Ala	Ala	Thr	Glu	Glu	Ala	Glu	Leu	Leu	Ala	Ala	Asp	Gly			
			20					25					30					
gcc	gtc	cac	gac	cag	gaa	ctc	ttc	ctc	aac	tgc	acc	acc	tcc	cca	ctg		144	
Ala	Val	His	Asp	Gln	Glu	Leu	Phe	Leu	Asn	Cys	Thr	Thr	Ser	Pro	Leu			
			35				40					45						
atc	ttc	gcc	tcc	gcg	atg	ctc	aac	ttc	ggc	gtc	cac	caa	atc	ctg	gac		192	
Ile	Phe	Ala	Ser	Ala	Met	Leu	Asn	Phe	Gly	Val	His	Gln	Ile	Leu	Asp			
			50			55					60							
acc	ctc	tgc	caa	ctc	gca	cca	tcc	ccc	gcc	ggc	gac	gac	gca	gac	ccc		240	
Thr	Leu	Cys	Gln	Leu	Ala	Pro	Ser	Pro	Ala	Gly	Cgc	Asp	Ala	Asp	Pro			
				70					75					80				
aaa	gcc	ctc	gaa	gcc	acc	tcc	gca	atg	gac	gac	cac	cgc	gac	acc			288	
Lys	Ala	Leu	Glu	Ala	Ala	Thr	Ser	Ala	Met	Asp	Asp	His	Arg	Asp	Thr			

[illegible]

Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
210 215 220

ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa 355
Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu

[illegible]

70	75	80	85	
ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc				403
Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly				
	90	95	100	
cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac				451
His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp				
	105	110	115	
gca gca gtc atg ctt atg cac tcc gtc				478
Ala Ala Val Met Leu Met His Ser Val				
	120	125		

<210> 490

<211> 126

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 490

Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg	
1 5 10 15	

Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu	
20 25 30	

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala	
35 40 45	

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu	
50 55 60	

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe	
65 70 75 80	

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu	
85 90 95	

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val	
100 105 110	

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val	
115 120 125	

<210> 491

<211> 394

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (17)..(394)

<223> FRXA02002

<400> 491

gctattcotta ataccatg agc aac gcc aat ccc gac acc acc gcc gcc gag	52
Met Ser Asn Ala Asn Pro Asp Thr Thr Ala Ala Glu	
1 5 10	

05602839.062300

aaa cat cgc cgc aaa aca ttc gcc gta atc gca cac ccc gac gcc ggt	100
Ala His Arg Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly	
15 20 25	
aaa tcc acc ctc acc gag gca ttg gcg ctg cat gca cac atc atc tcc	148
Lys Ser Thr Leu Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser	
30 35 40	
gaa gcc ggc gcc acc cac gcc aaa gca gcc cgc aaa gcc acc gtt tcc	196
Glu Ala Gly Ala Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser	
45 50 55 60	
gac tgg atg gaa atg gaa aaa gac cgc gcc atc tcc atc gcc tcc tcc	244
Asp Trp Met Glu Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser	
65 70 75	
gca ctc caa ttc gag tac gca cca gaa gcc cac gca gcc gag ccc ttc	292
Ala Leu Gln Phe Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe	
80 85 90	
atg atc aac ctc gtg gac acc cca gcc cac gcc gac ttc tcc gaa gac	340
Met Ile Asn Leu Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp	
95 100 105	
acc tac cgc gtc ctc atg gcc gtc gac gca gca gtc atg ctt atg cac	388
Thr Tyr Arg Val Leu Met Ala Val Asp Ala Ala Val Met Leu Met His	
110 115 120	
tcc gtc Ser Val	394
125	
<210> 492	
<211> 126	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 492	
Met Ser Asn Ala Pro Asp Thr Thr Ala Glu Ala His Arg Arg	
1 5 10 15	
Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu	
20 25 30	
Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala	
35 40 45	
Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu	
50 55 60	
Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe	
65 70 75 80	
Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu	
85 90 95	
Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val	
100 105 110	
Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val	

115	120	125	
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<213> Corynebacterium glutamicum			
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<222> (101)..(739)			
<223> RXA00896			
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gggttaaata	atctgcggaa	agcatgcttta	gaatgttgcc atg act gtc cga cca 115
			Met Thr Val Arg Pro 5
atc gtt att cat gga gat cct gtt ctc cac aac cct acc cag ctt gtt 163			
Ile Val Ile His Gly Asp Pro Val Leu His Asn Pro Thr Gln Leu Val	10	15	20
act gag gat gtc tct gaa ctg cag gaa cta att gca gat atg tac gag 211			
Thr Glu Asp Val Ser Glu Leu Gln Glu Leu Ile Ala Asp Met Tyr Glu	25	30	35
acg atg gat gtc gcc aat ggt gtg ggt ctt gcg gcc aac cag att ggt 259			
Thr Met Asp Val Ala Asn Gly Val Gly Leu Ala Ala Asn Gln Ile Gly	40	45	50
gtg tcc aag cgc att ttt gtt tat gac tgt cct gat gat gag ggc gtg 307			
Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro Asp Asp Glu Gly Val	55	60	65
atg cac aag ggt tgt ttc atc aat cct gtg ttg gaa acc tct gaa atc 355			
Met His Lys Gly Cys Phe Ile Asn Pro Val Leu Glu Thr Ser Glu Ile	70	75	85
cca gag acc atg cct gcc gat gat ggc tcc gac gag gaa ggc tgc ctg 403			
Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp Glu Glu Gly Cys Leu	90	95	100
tct gtt cct gcc gag gcc ttc ccc act gcc cgt gct cat tgg gcg aag 451			
Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg Ala His Trp Ala Lys	105	110	115
ggt act gga ctg aat gaa aag ggc gag gaa gtt tct gtt gag gct gag 499			
Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val Ser Val Glu Ala Glu	120	125	130
ggt ttc ttg gct cgt tgc ttc cag cat gag gtt ggc cac ctt gat ggt 547			
Gly Phe Leu Ala Arg Cys Phe Gln His Glu Val Gly His Leu Asp Gly	135	140	145
ttc ttg tac acc gat gtg ttg att ggt cgg tgg aag cgc atg gct aag 595			
Phe Leu Tyr Thr Asp Val Leu Ile Gly Arg Trp Lys Arg Met Ala Lys	150	155	165
aag gct att aag gcc aat ggg tgg act gag cct ggt ttg acc tgg atg 643			

Lys	Ala	Ile	Lys	A	Asn	Gly	Thr	Glu	Pro	Gly	Leu	Thr	Trp	Met	
				170					175					180	
cgc	ggt	gaa	gat	gag	gat	cct	ttc	ggg	cat	gac	gcc	tat	gtc	ttc	ccc
Pro	Gly	Gly	Ala	Asp	Glu	Asp	Pro	Phe	Gly	His	Asp	Ala	Tyr	Val	Phe
				185				190					195		
ggt	tcc	gca	gcc	aga	aac	ctg	ccg	tcg	gcg	atc	gtg	ttg	ttg	cac	gtc
Val	Ser	Ala	Ala	Arg	Asn	Leu	Pro	Ser	Ala	Ile	Val	Leu	Leu	His	Val
				200			205					210			

<210> 494
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 494
Met Thr Val Arg Pro Ile Val Ile His Gly Asp Pro Val Leu His Asn
1 5 10 15
Pro Thr Gln Leu Val Thr Glu Asp Val Ser Glu Leu Gln Glu Leu Ile
20 25 30
Ala Asp Met Tyr Glu Thr Met Asp Val Ala Asn Gly Val Gly Leu Ala
35 40 45
Ala Asn Gln Ile Gly Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro
50 55 60
Asp Asp Glu Gly Val Met His Lys Gly Cys Phe Ile Asn Pro Val Leu
65 70 75 80
Glu Thr Ser Glu Ile Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp
85 90 95
Glu Glu Gly Cys Leu Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg
100 105 110
Ala His Trp Ala Lys Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val
115 120 125
Ser Val Glu Ala Glu Gly Phe Leu Ala Arg Cys Phe Gln His Glu Val
130 135 140
Gly His Leu Asp Gly Phe Leu Tyr Thr Asp Val Leu Ile Gly Arg Trp
145 150 155 160
Lys Arg Met Ala Lys Lys Ala Ile Lys Ala Asn Gly Trp Thr Glu Pro
165 170 175
Gly Leu Thr Trp Met Pro Gly Glu Asp Glu Asp Pro Phe Gly His Asp
180 185 190
Ala Tyr Val Phe Pro Val Ser Ala Ala Arg Asn Leu Pro Ser Ala Ile
195 200 205
Val Leu Leu His Val
210

<210> 495
 <211> 630
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(607)
 <223> RXA02242

<400> 495
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 caccataggg aattattgtt gaaggagcct tcccacaacc atg gca gtt cgt gaa 115
 Met Ala Val Arg Glu
 1 5
 gtc aga tta ttt gga gat ccc gta ctt gtg agt cgg gca gat gag gtc 163
 Val Arg Leu Phe Gly Asp Pro Val Leu Val Ser Arg Ala Asp Glu Val
 10 15 20
 gtg gac ttc gat gaa tca ctg tcc acc ctg atc gat gac atg ttt gac 211
 Val Asp Phe Asp Glu Ser Leu Ser Thr Leu Ile Asp Asp Met Phe Asp
 25 30 35
 acc atg gaa gat gcc ggt ggc gtt ggt cta gca gca aac cag gtg ggt 259
 Thr Met Glu Asp Ala Gly Gly Val Gly Leu Ala Ala Asn Gln Val Gly
 40 45 50
 gtt tta agg cgc gtg ttc gtg ttt gat acc tcc cac cag gag ggt gga 307
 Val Leu Arg Arg Val Phe Val Phe Asp Thr Ser His Gln Glu Gly Gly
 55 60 65
 ttg cgc gga cat gtg atc aac ccg gtg tgg gag cct ctc act gag gac 355
 Leu Arg Gly His Val Ile Asn Pro Val Trp Glu Pro Leu Thr Glu Asp
 70 75 80 85
 acc cag act ggc aaa gag ggc tgt ttg tcc atc cct gat gtc tcg gct 403
 Thr Gln Thr Gly Lys Glu Gly Cys Leu Ser Ile Pro Asp Val Ser Ala
 90 95 100
 gag acc acc cgc tat gaa acg gtt cgg ctg tct ggc cag gac cgc gac 451
 Glu Thr Thr Arg Tyr Glu Thr Val Arg Leu Ser Gly Gln Asp Arg Asp
 105 110 115
 ggc aat cca gtg ggg ttt gtg gcc aat gga ttg ttg gcc agg tgc atc 499
 Gly Asn Pro Val Gly Phe Val Ala Asn Gly Leu Leu Ala Arg Cys Ile
 120 125 130
 caa cac gaa act gat cac ctt gat ggc gtg ctg ttt ttg aag cgc ctt 547
 Gln His Glu Thr Asp His Leu Asp Gly Val Leu Phe Leu Lys Arg Leu
 135 140 145
 gat cca gct gaa cgt aaa gca gcc atg ggc gtt att cgc gcg tct gca 595
 Asp Pro Ala Glu Arg Lys Ala Ala Met Gly Val Ile Arg Ala Ser Ala
 150 155 160 165
 tgg ttt aac aaa taatgagtgg aaagggcact tca 630
 Trp Phe Asn Lys

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<210> 496
<211> 169
<212> PRT
<213> Corynebacterium glutamicum
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<400> 496

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1 5 10 15

Arg Ala Asp Glu Val Val Asp Phe Asp Glu Ser Leu Ser Thr Leu Ile
20 25 30

Asp Asp Met Phe Asp Thr Met Glu Asp Ala Gly Gly Val Gly Leu Ala
35 40 45

Ala Asn Gln Val Gly Val Leu Arg Arg Val Phe Val Phe Asp Thr Ser
50 55 60

His Gln Glu Gly Gly Leu Arg Gly His Val Ile Asn Pro Val Trp Glu
65 70 75 80

Pro Leu Thr Glu Asp Thr Gln Thr Gly Lys Glu Gly Cys Leu Ser Ile
85 90 95

Pro Asp Val Ser Ala Glu Thr Thr Arg Tyr Glu Thr Val Arg Leu Ser
100 105 110

Gly Gln Asp Arg Asp Gly Asn Pro Val Gly Phe Val Ala Asn Gly Leu
115 120 125

Leu Ala Arg Cys Ile Gln His Glu Thr Asp His Leu Asp Gly Val Leu
130 135 140

Phe Leu Lys Arg Leu Asp Pro Ala Glu Arg Lys Ala Ala Met Gly Val
145 150 155 160

Ile Arg Ala Ser Ala Trp Phe Asn Lys
165

<210> 497

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101) .. (529)

<223> RXS02308

<400> 497

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gagcaaattcc gccaggaaat aaattaagta aggaatatcc atg agt gaa acc cag 115
Met Ser Glu Thr Gln
1 5

tcg aat tca gtg tca gcg gta atg cct gcg cag ctc cct cca ggg cct 163
Ser Asn Ser Val Ser Ala Val Met Pro Ala Gln Leu Pro Pro Gly Pro
10 15 20

Val Val Asn Ala Ala Arg Ser Arg Tyr Phe Thr Gly Glu Val Leu Pro

DEPARTMENT OF THE ARMY

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<210> 500

<211> 136

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 500

Met Thr Asp Phe Lys Leu Ile Ser Asp Thr Glu Trp Arg Glu Arg Leu
 1 5 10 15

Thr Pro Gln Glu Phe His Val Leu Arg Glu Ala Gly Thr Glu Pro Pro
 20 25 30

His Val Gly Glu Tyr Thr Asn Thr Thr Thr Glu Gly Val Tyr Ser Cys
 35 40 45

Arg Ala Cys Gly Glu Glu Leu Phe Arg Ser Thr Glu Lys Phe Glu Ser
 50 55 60

His Cys Gly Trp Pro Ser Phe Phe Ser Pro Leu Ala Gly Asp Lys Ile
 65 70 75 80

Ile Glu Lys Glu Asp Leu Ser Leu Gly Met Arg Arg Val Glu Ile Leu
 85 90 95

Cys Ala Asn Cys Gly Ser His Met Gly His Val Phe Glu Gly Glu Gly
 100 105 110

Tyr Asp Thr Pro Thr Asp Leu Arg Tyr Cys Ile Asn Ser Ile Ser Leu
 115 120 125

Lys Leu Glu Glu Lys Pro Val Ser
 130 135

<210> 501

<211> 1941

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1918)

<223> RXN02462

<400> 501

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atcgacgttc tacaacgtct tcgcacagat cgtcccacgc atg acc aag gac gtt 115
 Met Thr Lys Asp Val
 1 5

cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa 163
 His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
 10 15 20

ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca 211
 Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala
 25 30 35

002230.02220960

cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca	259
Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala	
40 45 50	
cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa	307
Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu	
55 60 65	
gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga	355
Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg	
70 75 80 85	
tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag	403
Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu	
90 95 100	
atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac	451
Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr	
105 110 115	
ttc cgc ctc tac acc aaa ctc gcc ggc atg acc ggt acc gca gag acc	499
Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr	
120 125 130	
gaa gca gca gag ctc aac cag atc tac aag ctc gac gtc atc gcg atc	547
Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile	
135 140 145	
cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac	595
Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr	
150 155 160 165	
aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa	643
Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu	
170 175 180	
cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag	691
Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu	
185 190 195	
cgc tcc gaa tac ctc tcc cag ctg ttg acc aaa cga ggc atc aag cac	739
Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His	
200 205 210	
aac gtc ctc aat gcg aag cac Cac gag Cag gaa gca cag atc gtt gct	787
Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala	
215 220 225	
cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg ggc	835
Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly	
230 235 240 245	
cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac	883
Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp	
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Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe Glu Asp Glu Glu Ser	
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002200 63820600

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ggc 310	acc Thr	gaa Glu	cgc Arg	cac His	gaa 315	tcc Ser	cga Arg	cgc Arg	atc Ile	gac 320	aac Asn	cag Gln	ctg Leu	cgc Arg	ggt Gly	1075
cgt Arg	tct Ser	gca Ala	cgt Arg	cag 330	ggc Gly	gac Asp	cca Pro	gga Gly	tcc Ser	acc Thr	cgc Arg	ttc Phe	tat Tyr	ctc Leu	tct Ser	1123
atg Met	cgc Arg	gac Asp	gac 345	ctg Leu	atg Met	gtt Val	cgc Arg	ttc Phe	gtc Val	ggc Gly	cca Pro	acc Thr	atg Met	gaa Glu	aac Asn	1171
atg Met	atg Met	aac Asn	agg Arg	ctc Leu	aac Asn	gtc Val	cca Pro	gac Asp	gat Asp	gtg Val	ccc Pro	atc Ile	gaa Glu	tcc Ser	aaa Lys	1219
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gaa Glu	cag Gln	cgc Arg	aag Lys	gtt Val	atc Ile	tac Tyr	agc Ser	gag Glu	cga Arg	cgc Arg	gaa Glu	atc Ile	ctc Leu	gaa Glu	tcc Ser	1363
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ctc Leu	gac Asp	aaa Lys	ctc Leu	tgg Trp	aac Asn	gcc Ala	ctc Leu	gaa Glu	gcc Ala	ctc Leu	tac Tyr	gac Asp	cca Pro	tcg Ser	atc Ile	1507
aac 470	tgg Trp	acc Thr	gac Asp	ctc Leu	gtc Val	gaa 475	ggc Gly	agc Ser	gaa Glu	tac Tyr	ggc 480	aaa Lys	cca Pro	ggg Gly	gag Glu	1555
ctg Leu	tcc Ser	gcc Ala	gaa Glu	gat Asp	cta Leu	cgc Arg	acc Thr	gca Ala	ctc Leu	gtc Val	aac 495	gac Asn	gcc Ala	cac His	gcc Ala	1603
gaa Glu	tac Tyr	gca Ala	aaa Lys	ctc Leu	gaa Glu	gaa Glu	gcc Ala	gta Ala	tcc Val	gca Ala	atc Ile	ggc Gly	ggc Gly	gaa Glu	gca Ala	1651
cag Gln	atc Arg	cgc Asn	atc Asn	gaa Ile	cga Arg	atg Met	gtc Val	ctc Leu	ctc Met	cca Pro	gtc Val	atc Ile	atc Asp	cgc Thr	acc Thr	1699

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Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile			
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Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys			
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gaa ggc ggc gac atg ttc aac ggc atg aaa gac ggc atc aag gaa gaa			1843
Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp Gly Ile Lys Glu Glu			
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Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr			
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Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val			
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Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala			
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Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val			
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Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr			
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cac	tac	gaa	gtc	gac	gaa	cgt	aaa	aag	acc	gtc	ggt	gtg	aaa	gaa	gaa	163
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ggc	gtc	gaa	tac	gtc	gaa	gac	caa	ctc	ggc	atc	gac	aac	ctc	tac	gca	211
Gly	Val	Glu	Tyr	Val	Glu	Asp	Gln	Leu	Gly	Ile	Asp	Asn	Leu	Tyr	Ala	
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Pro	Glu	His	Ser	Gln	Leu	Val	Ser	Tyr	Leu	Asn	Asn	Ala	Ile	Lys	Ala	
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Gln	Glu	Leu	Phe	Thr	Arg	Asp	Lys	Asp	Tyr	Ile	Val	Arg	Asn	Gly	Glu	
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 Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr
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 Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile
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 Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr
 150 155 160 165

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 Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu
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 Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu
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Asn	Gly	Tyr	Val	Glu	Asp	Trp	Asp	Leu	Asp	Lys	Leu	Trp	Asn	Ala	Leu	
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Ala	Leu	Val	Asn	Asp	Ala	His	Ala	Glu	Tyr	Ala	Lys	Leu	Glu	Glu	Ala	
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Val	Ser	Ala	Ile	Gly	Gly	Glu	Ala	Gln	Ile	Arg	Asn	Ile	Glu	Arg	Met	
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Val	Leu	Met	Pro	Val	Ile	Asp	Thr	Lys	Trp	Arg	Glu	His	Leu	Tyr	Glu	
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Met	Asp	Tyr	Leu	Lys	Glu	Gly	Ile	Gly	Leu	Arg	Ala	Met	Ala	Gln	Arg	
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Asp	Pro	Leu	Val	Glu	Tyr	Gln	Lys	Glu	Gly	Gly	Asp	Met	Phe	Asn	Gly	
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938

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Phe	Asp	Tyr		Leu	Arg	Asp	Asn	Met	Ala	Arg	Ser	Leu	Ser	Asp	Leu	Val
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Gln	Arg	Gly	His	Asn	Tyr	Ala	Ile	Val	Asp	Glu	Val	Asp	Ser	Ile	Leu	
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Ile	Asp	Glu	Ala	Arg	Thr	Pro	Leu	Ile	Ile	Ser	Gly	Thr	Ser	Arg	Arg	
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Phe	Ala	Asn	Leu	Thr	Asp	Glu	Glu	Leu	Lys	Ala	Lys	Thr	Ala	Glu	Phe	
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Val Asn Asp Tyr Leu Ala Lys Arg Asp Ala Glu Met Met Gly Arg Val
 130 135 140

His Arg Tyr Leu Gly Leu Glu Val Gly Val Ile Leu Ser Asp Met Arg
 145 150 155 160

Pro Asp Glu Arg Arg Glu Ala Tyr Ala Ala Asp Ile Thr Tyr Gly Thr
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Asn Asn Glu Leu Gly Phe Asp Tyr Leu Arg Asp Asn Met Ala Arg Ser
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Leu Ser Asp Leu Val Gln Arg Gly His Asn Tyr Ala Ile Val Asp Glu
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Ala Leu Ala Asp Arg Glu Gln Leu Leu Gly Ala Gly Ile Arg Val Leu	
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Lys Arg Met Val Gly Arg Arg Gln Tyr Gly Gly Ser Ser Thr Tyr Leu	
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Pro Leu Lys Val Asn Gln Ala Gly Val Ile Pro Val Ile Phe Ala Ser	
265 270 275	
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Ser Leu Ile Tyr Met Pro Val Leu Ile Thr Gln Ile Val Asn Ser Gly	
280 285 290	
tcg ctg gaa gtg tct gat aac tgg tgg cag cgc aac atc att gcg cac	1027
Ser Leu Glu Val Ser Asp Asn Trp Trp Gln Arg Asn Ile Ile Ala His	
295 300 305	
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Thr Ile Phe Phe Ser Tyr Phe Tyr Val Ser Val Gln Tyr Asp Pro Ala
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gag cag gct gaa aac atg aag aag tac ggt gga ttt atc cct ggt att 1171
Glu Gln Ala Glu Asn Met Lys Lys Tyr Gly Gly Phe Ile Pro Gly Ile
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cgt cgg ggc cgc cgc act gct gag tac ttg gga ttc gtc atg aac cgc 1219
Arg Pro Gly Arg Pro Thr Ala Glu Tyr Leu Gly Phe Val Met Asn Arg
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ctg ctg ttt gtt ggt tcc ctg tac ctg gct gtc att gct gtg ctg cca 1267
Leu Leu Phe Val Gly Ser Leu Tyr Leu Ala Val Ile Ala Val Leu Pro
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aac att atg ctg gat cta ggt gtt gac gcc ggt tgg gcc gga gca act 1315
Asn Ile Met Leu Asp Leu Gly Val Asp Ala Gly Ser Ala Gly Ala Thr
390          395          400          405

cca ttc ggc gga acc gca atc ttg att ctt gta tct gtt gca ctg acc 1363
Pro Phe Gly Gly Thr Ala Ile Leu Ile Leu Val Ser Val Ala Leu Thr
          410          415          420

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Thr Val Lys Gln Ile Glu Ser Gln Leu Leu Gln Ser Asn Tyr Glu Gly
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Leu Leu Lys
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Ile Phe Phe Thr Ile Ala Met Ile Val Leu Tyr Arg Ile Gly Ala Gln
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Ile Pro Ser Pro Gly Val Asp Tyr Ala Thr Ile Ser Gly Arg Leu Arg
          35          40          45

Asp Leu Thr Gln Asp Gln Ser Ser Val Tyr Ser Leu Ile Asn Leu Phe
          50          55          60

Ser Gly Gly Ala Leu Leu Gln Leu Ser Ile Phe Ala Ile Gly Ile Met
          65          70          75          80

Pro Tyr Ile Thr Ala Ser Ile Ile Val Gln Leu Leu Thr Val Val Ile
          85          90          95

Pro His Phe Glu Glu Leu Lys Lys Glu Gly Gln Ser Gly Gln Ala Lys

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Ser	Ser	Gly	Ile	Val	Ala	Leu	Ala	Asp	Arg	Glu	Gln	Leu	Leu	Gly
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Gly	Ile	Arg	Val	Leu	Ser	Ala	Asp	Arg	Asn	Phe	Phe	Asp	Leu	Ile
		145					150					155		
Leu	Val	Ile	Thr	Met	Thr	Ala	Gly	Ala	Val	Leu	Val	Met	Trp	Met
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Glu	Leu	Ile	Thr	Glu	Lys	Gly	Val	Gly	Asn	Gly	Met	Ser	Leu	Ile
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Phe	Ala	Gly	Ile	Ala	Thr	Arg	Leu	Pro	Thr	Asp	Gly	Met	Asn	Ile
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Ile	Leu	Val	Ile	Gly	Val	Val	Phe	Val	Glu	Gln	Gly	Gln	Arg	Arg
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Ser	Ser	Thr	Tyr	Leu	Pro	Leu	Lys	Val	Asn	Gln	Ala	Gly	Val	Ile
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Val	Ile	Phe	Ala	Ser	Ser	Leu	Ile	Tyr	Met	Pro	Val	Leu	Ile	Thr
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Ile	Val	Asn	Ser	Gly	Ser	Leu	Glu	Val	Ser	Asp	Asn	Trp	Trp	Gln
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Asn	Ile	Ile	Ala	His	Leu	Gln	Thr	Pro	Ser	Ser	Trp	Gln	Tyr	Ile
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Leu	Tyr	Phe	Ala	Leu	Thr	Ile	Phe	Phe	Ser	Tyr	Phe	Tyr	Val	Ser
				325					330					335
Gln	Tyr	Asp	Pro	Ala	Glu	Gln	Ala	Glu	Asn	Met	Lys	Lys	Tyr	Gly
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Phe	Ile	Pro	Gly	Ile	Arg	Pro	Gly	Arg	Pro	Thr	Ala	Glu	Tyr	Leu
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Phe	Val	Met	Asn	Arg	Leu	Leu	Phe	Val	Gly	Ser	Leu	Tyr	Leu	Ala
				370					375					
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Ser	Ala	Gly	Ala	Thr	Pro	Phe	Gly	Gly	Thr	Ala	Ile	Leu	Ile	Leu
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Ser	Val	Ala	Leu	Thr	Thr	Val	Lys	Gln	Ile	Glu	Ser	Gln	Leu	Gln
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Met Ala Leu Thr Leu
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caa atc atc ctc gtc gtc gcc agc ctg ctc atg acg gtt ttc gtc ttg 163
Gln Ile Ile Leu Val Val Ala Ser Leu Leu Met Thr Val Phe Val Leu
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Leu His Lys Gly Lys Gly Gly Leu Ser Ser Leu Phe Gly Gly Gly
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Val Gln Ser Asn Leu Ser Gly Ser Thr Val Val Glu Lys Asn Leu Asp
40 45 50
cgc gtc acc att ttg gtt gcc gtt atc tgg att gtg tgc att gtc gca 307
Arg Val Thr Ile Leu Val Ala Val Ile Trp Ile Val Cys Ile Val Ala
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<213> Corynebacterium glutamicum

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Leu Phe Gly Gly Gly Val Gln Ser Asn Leu Ser Gly Ser Thr Val Val
35 40 45
Glu Lys Asn Leu Asp Arg Val Thr Ile Leu Val Ala Val Ile Trp Ile
50 55 60

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Val Cys Ile Val Ala Leu Asn Leu Ile Gln Thr Tyr Ser
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<212> DNA

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Met Asp Leu Asn Thr
1 5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
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gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
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cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
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Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
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gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
70 75 80 85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
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act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
105 110 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
120 125 130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547
Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
135 140 145

ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595
Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
150 155 160 165

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gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu
 170 175 180

tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691
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 185 190 195

gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739
 Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val
 200 205 210

ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787
 Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser
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ctg ttg cac tagcacttag tccagcgctg cac 819
 Leu Leu His
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 35 40 45

Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser
 50 55 60

Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly
 65 70 75 80

Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val
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Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro
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Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp
 115 120 125

Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu
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Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly
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Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu
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Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly

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180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
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Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
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Gly Gln Phe Ala Ser Leu Leu His
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Met Asp Leu Asn Thr
1 5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
10 15 20

gtg caa got ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
25 30 35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
His Val Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
40 45 50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307
Gly Gly Tyr Gly Gly Leu Gln Asp Ile Arg Ser Ile Ser Asn Arg Val
55 60 65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
70 75 80 85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
90 95 100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
105 110 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
120 125 130

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Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu
130 135 140

[illegible]

Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly
 145 150 155 160

Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu
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Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
 180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
 195 200 205

Asn Ala Ile Ile Val Gly Thr Gly Ile Thr Asp Pro Gly Phe Ile Thr
 210 215 220

Gly Gln Phe Ala Ser Leu Leu His
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 His Glu Ala Ile Arg Gln Ala Gln Asp Ser Gly Ala Pro Asn Asp Glu
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ctt att cct ggt gag atg tgg tca gat aag gtc gag tta ccc tca acg 144
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Ser Thr
 35 40 45

att gat aaa gca gct gct gat gaa gct gag ata gct att gca cag caa 192
 Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln
 50 55 60

cag tcc caa ccc cag gcg aga gga cta gcc gct gct gca gcg tgt cag 240
 Gln Ser Gln Pro Gln Ala Arg Gly Leu Ala Ala Ala Ala Cys Gln
 65 70 75 80

aca ttt tgg ccg tca cct tat caa gtt tgt ggt gct atc tta gag cgc 288
 Thr Phe Trp Pro Ser Pro Tyr Gln Val Cys Gly Ala Ile Leu Glu Arg
 85 90 95

tat atc cag cag ggt gcc cag ttt ggg tgg atg ttg ttg ctt act gaa 336
 Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Leu Thr Glu
 100 105 110

ggc caa gcg ctt aac cct gat ggt cag gga tat cgt cag cgg ttt atg 384
 Gly Gln Ala Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met

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130	135	140	
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Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp			
145	150	155	160
atg ggg tat ccc act ggt ggt gaa gtc cct gtg tct ggg tct aat ccg	528		
Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Ser Gly Ser Asn Pro			
165	170	175	
att gat ggt gag ttg agt ggg tgg gtg caa acc ttc caa ggt ggg cga	576		
Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg			
180	185	190	
gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat	624		
Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn			
195	200	205	
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Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp			
210	215	220	
ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt	720		
Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly			
225	230	235	240
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac	768		
Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His			
245	250	255	
gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa	816		
Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu			
260	265	270	
gga gct gag agt ggg gaa ttc ggt tac cct atc gcc gat cca gaa aag	864		
Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys			
275	280	285	
tat aca gaa aac atg gct aat cag gta ttc gaa aaa gcc gaa ctt gca	912		
Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala			
290	295	300	
gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc	960		
Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro			
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ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca	1008		
Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser			
325	330	335	
aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att	1056		
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caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac	1104		
Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp			
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 370 375 380

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gag 1445

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Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Ser Thr
 35 40 45

Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln
 50 55 60

Gln Ser Gln Pro Gln Ala Arg Gly Leu Ala Ala Ala Ala Cys Gln
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Thr Phe Trp Pro Ser Pro Tyr Gln Val Cys Gly Ala Ile Leu Glu Arg
 85 90 95

Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Leu Leu Thr Glu
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Gly Gln Ala Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met
 115 120 125

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Asn Gly Phe Ile Tyr Trp His Pro Ser Thr Gly Ala His Ala Val Asn
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 145 150 155 160
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Ser Gly Ser Asn Pro
 165 170 175
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg
 180 185 190
 Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn
 195 200 205
 Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp
 210 215 220
 Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly
 225 230 235 240
 Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His
 245 250 255
 Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu
 260 265 270
 Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys
 275 280 285
 Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala
 290 295 300
 Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro
 305 310 315 320
 Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser
 325 330 335
 Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile
 340 345 350
 Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp
 355 360 365
 Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp
 370 375 380
 Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile
 385 390 395 400
 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln
 405 410 415
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
 420 425 430
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
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00220-5020960

Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
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Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
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<211> 826

<212> DNA

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Met His Ser Lys Glu
1 5

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val
10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala
25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn
40 45 50

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 Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn
 55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala
70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp
90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp
105 110 115

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499
Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp
120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg
135 140 145

acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gta cct ggc 595

069068

Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly
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 cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag 643
 Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln
 170 175 180
 aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac 691
 Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn
 185 190 195
 atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac 739
 Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp
 200 205 210
 tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca 787
 Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr
 215 220 225
 ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc 826
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 230 235 240
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 Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
 35 40 45
 Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
 50 55 60
 Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
 65 70 75 80
 Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
 85 90 95
 Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
 100 105 110
 Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
 115 120 125
 Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
 130 135 140
 Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp
 145 150 155 160
 Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly

000250 6620960

165 170 175

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Leu
180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe
195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala
210 215 220

Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val
225 230 235 240

Ala Ala

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<212> DNA
<213> Corynebacterium glutamicum

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Met His Ser Lys Glu
1 5

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val
10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala
25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn
40 45 50

tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat 307
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn
55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala
70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp
90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp

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<213> Corynebacterium glutamicum

<221> CDS

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cgc atc gct gca cca gcc atc gcg ctg gga att gcg atg tcc acc att 163
Arg Ile Ala Ala Pro Ala Ile Ala Leu Gly Ile Ala Met Ser Thr Ile
10 15 20

gtc acg cca tcc acc gca ggc gct gcc gaa gta acc cca gca gac gtt 211
Val Thr Pro Ser Thr Ala Gly Ala Ala Glu Val Thr Pro Ala Asp Val
25 30 35

gct ggc gat act gca cta tcc acc atc tcc gat agt gct cct gca gat 259
Ala Gly Asp Thr Ala Leu Ser Thr Ile Ser Asp Ser Ala Pro Ala Asp
40 45 50

gaa gcc tct gca cct cgc tgg cgc gca cac gtc aac gca gca gac gag 307
Glu Ala Ser Ala Pro Arg Trp Arg Ala His Val Asn Ala Ala Asp Glu
55 60 65

cgc gtc aaa gaa atg tgg gca tac tcc cct tcc atg gac cgc aat gtg 355
 Arg Val Lys Glu Met Trp Ala Tyr Ser Pro Ser Met Asp Arg Asn Val
 70 75 80 85

cca ctg gta gtt ata act gcc gat gag tcc gca ggt cct cgt cct gtg 403
Pro Leu Val Val Ile Thr Ala Asp Glu Ser Ala Gly Pro Arg Pro Val
90 95 100

att tac ctt ctt aac ggt ggc gac ggt ggc gaa ggt gcc gct aac tgg 451
Ile Tyr Leu Leu Asn Gly Gly Asp Gly Gly Glu Gly Ala Ala Asn Trp
105 110 115

ggt atg cag act gac gtt ctg gat ttc tac cta gaa aag aac gtt aac 499
Val Met Gln Thr Asp Val Leu Asp Phe Tyr Leu Glu Lys Asn Val Asn
120 125 130

ggt gtt att cca atg gaa ggc aag ttt tcc tac tac acc gac tgg gta 547
Val Val Ile Pro Met Glu Gly Lys Phe Ser Tyr Tyr Thr Asp Trp Val
135 140 145

gaa gag aat gcg tcc ctc ggt ggc aag caa atg tgg gaa acc ttc ctg 595
Glu Glu Asn Ala Ser Leu Gly Gly Lys Gln Met Trp Glu Thr Phe Leu
150 155 160 165

gtg aag gaa ctt cca gga cca ttg gaa gaa aag ctc aac act gac ggt 643
Val Lys Glu Leu Pro Gly Pro Leu Glu Glu Lys Leu Asn Thr Asp Gly
170 175 180

cag cgt gca att gct ggc atg tcc atg tcc gca act act tcc cta ctc 691
Gln Arg Ala Ile Ala Gly Met Ser Met Ser Ala Thr Thr Ser Leu Leu

Figure 1

[illegible]

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<211> 365

<212> PRT

<213> Corynebacterium glutamicum

<400> 524

Met Lys Leu Leu Arg Arg Ile Ala Ala Pro Ala Ile Ala Leu Gly Ile
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20 25 30

Thr Pro Ala Asp Val Ala Gly Asp Thr Ala Leu Ser Thr Ile Ser Asp
35 40 45

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<400> 525
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atc ggc gga aat aag aat tct tct ggt tgg atc aat ggt ggc gag ggt 64
Ile Gly Gly Asn Lys Asn Ser Ser Gly Trp Ile Asn Gly Gly Glu Gly
170 175 180

Figure 1. The structure of the proposed system.

ccg aag gtt ttc gcg gat gaa aat gtg act gta gta atg ccg ttg ggt 691
Pro Lys Val Phe Ala Asp Glu Asn Val Thr Val Val Met Pro Leu Gly
185 190 195

gct gct tca tcc atg tac tcg gat tgg ttg gaa gag gac cct gcg cta 739
Ala Ala Ser Ser Met Tyr Ser Asp Trp Leu Glu Glu Asp Pro Ala Leu
200 205 210

ggg cgc atc aag tgg gaa act ttt atc gtc gag gag ctc gcg ccc ctg 787
Gly Arg Ile Lys Trp Glu Thr Phe Ile Val Glu Glu Ala Pro Leu
215 220 225

ctt gag gct gag gaa gag ctg aac ttc aat ggt cac cgt ggc atc ggc 835
Leu Glu Ala Glu Glu Leu Asn Phe Asn Gly His Arg Gly Ile Gly
230 235 240 245

gga tta tcc atg ggt gct act ggt gcg gtt cat tta gct aac tcg aac 883
Gly Leu Ser Met Gly Ala Thr Gly Ala Val His Leu Ala Asn Ser Asn
250 255 260

cct gat ctc ttt gat gga gtc att ggc atc tct ggt tgc tac tcc acg 931
Pro Asp Leu Phe Asp Gly Val Ile Gly Ile Ser Gly Cys Tyr Ser Thr
265 270 275

ctt gat ccc att gga caa acc acg gtg tca cta att gtt aat tct cgc 979
Leu Asp Pro Ile Gly Gln Thr Thr Val Ser Leu Ile Val Asn Ser Arg
280 285 290

ggt ggc aat gta gaa aat atg tgg ggt ccc act ggt tct gaa act tgg 1027
Gly Gly Asn Val Glu Asn Met Trp Gly Pro Thr Gly Ser Glu Thr Trp
295 300 305

aaa gct cac gat gtc aca tca aat cct gag ggg ctg cgc gac atg gct 1075
Lys Ala His Asp Val Thr Ser Asn Pro Glu Gly Leu Arg Asp Met Ala
310 315 320 325

gtc tat ttg tca gct gcg aac gga gtt gta gat gac atc gat ttg gcg 1123
Val Tyr Leu Ser Ala Ala Asn Gly Val Val Asp Asp Ile Asp Leu Ala
330 335 340

gat tcc gag aaa gag cct 1141
Asp Ser Glu Lys Glu Pro
345

<210> 526

<211> 347

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<213> *Corynebacterium glutamicum*

<400> 526

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20 25 30

Ser Val Leu Ser Ser Glu Asp Ser Ser Ala Thr Asn Ser Glu Gln Asp
35 40 45

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Phe Glu Lys Ser Ser Glu Ser Gly Ser Ser Ala Gln Asp Phe Ile Ala
 50 55 60
 Leu Ser Thr Ala Asn Pro Asp Leu Thr Gly Gly Ser Val Glu Gly Leu
 65 70 75 80
 Leu Ser Ser Met Ser Leu Ile Gly Ser Ser Gln Leu Pro Leu Gly Gly
 85 90 95
 Pro Leu Leu Ser Ser Asp Ser Asn Tyr Pro Leu Glu Thr Asp Pro Ser
 100 105 110
 Ile Thr Glu Ala Arg Ile Val Glu Lys Arg Val Leu Asn Gly Leu Arg
 115 120 125
 Leu Glu Lys Trp Ser Val Ala Ser Pro Ser Met Gln Arg Asn Val Asp
 130 135 140
 Val Gln Ile Met Lys Ser Ala Glu Ala Asp Ser Pro Ala Pro Met Leu
 145 150 155 160
 Tyr Met Leu Asp Gly Ile Gly Gly Asn Lys Asn Ser Ser Gly Trp Ile
 165 170 175
 Asn Gly Gly Glu Gly Pro Lys Val Phe Ala Asp Glu Asn Val Thr Val
 180 185 190
 Val Met Pro Leu Gly Ala Ala Ser Ser Met Tyr Ser Asp Trp Leu Glu
 195 200 205
 Glu Asp Pro Ala Leu Gly Arg Ile Lys Trp Glu Thr Phe Ile Val Glu
 210 215 220
 Glu Leu Ala Pro Leu Leu Glu Ala Glu Glu Glu Leu Asn Phe Asn Gly
 225 230 235 240
 His Arg Gly Ile Gly Gly Leu Ser Met Gly Ala Thr Gly Ala Val His
 245 250 255
 Leu Ala Asn Ser Asn Pro Asp Leu Phe Asp Gly Val Ile Gly Ile Ser
 260 265 270
 Gly Cys Tyr Ser Thr Leu Asp Pro Ile Gly Gln Thr Thr Val Ser Leu
 275 280 285
 Ile Val Asn Ser Arg Gly Gly Asn Val Glu Asn Met Trp Gly Pro Thr
 290 295 300
 Gly Ser Glu Thr Trp Lys Ala His Asp Val Thr Ser Asn Pro Glu Gly
 305 310 315 320
 Leu Arg Asp Met Ala Val Tyr Leu Ser Ala Ala Asn Gly Val Val Asp
 325 330 335
 Asp Ile Asp Leu Ala Asp Ser Glu Lys Glu Pro
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<210> 527

<211> 373

<212> DNA

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<213> *Corynebacterium glutamicum*

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<223> RXA01798

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Met His Arg Lys Lys
1 5

gaa gag tta aca atg cgt aaa gga att tcc cgc atc ctc tcg gta gcg 163
Glu Glu Leu Thr Met Arg Lys Gly Ile Ser Arg Ile Leu Ser Val Ala
10 15 20

ggt gct agt tct att gga ttc ggt tcg gtg ttg tct gga acc ggc atc 211
Val Ala Ser Ser Ile Gly Phe Gly Ser Val Leu Ser Gly Thr Gly Ile
25 30 35

gca gca gct caa gac tct gca ttt gac tac ggt atg gat cct agc atg 259
Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Ser Met
40 45 50

aac tac aac ccg atc gac gac atg aag gat cgt ccc caa ggg tta tcc 307
Asn Tyr Asn Pro Ile Asp Asp Met Lys Asp Arg Pro Gln Gly Leu Ser
55 60 65

aac ctt ccc tac ttc gga agc aaa cta acc agc tgg ggc tca tca gat 355
Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Asp
70 75 80 85

gcc acc gcc tca tcc ggc 373
Ala Thr Ala Ser Ser Gly
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<210> 528

<211> 91

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 528

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20 25 30

Ser Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly
35 40 45

Met Asp Pro Ser Met Asn Tyr Asn Pro Ile Asp Asp Met Lys Asp Arg
50 55 60

Pro Gln Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser
65 70 75 80

Tro Gly Ser Ser Asp Ala Thr Ala Ser Ser Gly

EFFECTS OF

90

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<222> (101)..(1087)
<223> RYA01818
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				Met	Gly	Tyr	Pro	Ile																					
				1																									
ggg	ggg	gaa	gtc	cct	gtt	tcg	ggg	tcg	aat	ctc	att	gac	ggg	gag	atc	163													
Gly	Gly	Glu	Val	Pro	Val	Ser	Gly	Ser	Asn	Leu	Ile	Asp	Gly	Glu	Ile														
				10											20														
aat	ggg	tgg	gtg	caa	acg	ttc	caa	ggg	ggg	cgg	gtc	tat	cgt	acc	cgg	211													
Asn	Gly	Trp	Val	Gln	Thr	Phe	Gln	Gly	Gly	Arg	Val	Tyr	Arg	Thr	Pro														
				25											35														
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Met	Leu	Glu	Gly	Phe	Gln	Ile	Ala	Ser	Ile	Asn	Gly	Met	Ile	Leu	Asn														
				40											50														
aga	tgg	ttg	gct	att	ggc	ggg	cgg	gat	agc	gct	ctt	ggg	ttt	ccc	att	307													
Arg	Trp	Leu	Ala	Ile	Gly	Gly	Pro	Asp	Ser	Ala	Leu	Gly	Phe	Pro	Ile														
				55											65														
gcc	gat	gaa	gct	gtt	gca	tcc	gat	ggg	gtg	ggg	cga	ttt	agt	gtt	ttc	355													
Ala	Asp	Glu	Ala	Val	Ala	Ser	Asp	Gly	Val	Gly	Arg	Phe	Ser	Val	Phe														
				70											85														
cga	aat	ggg	gta	ctt	tac	tgg	cac	cct	aat	cac	gga	gca	tgg	gaa	atg	403													
Gln	Asn	Gly	Val	Leu	Tyr	Trp	His	Pro	Asn	His	Gly	Ala	Trp	Glu	Met														
				90											100														
acc	gga	ttt	att	gaa	gaa	gta	tgg	aaa	atg	cga	ggg	ggc	ttg	gat	tct	451													
Thr	Gly	Phe	Ile	Glu</																									

Asn Leu Ile Leu Glu Tyr Phe Gly Tyr Leu Gly Phe Asp Phe Pro Gly
 170 175 180
 agc tct tct cga gag ttg gtg caa gac cat tct aaa tca gac ttg atg 691
 Ser Ser Ser Arg Glu Leu Val Gln Asp His Ser Lys Ser Asp Leu Met
 185 190 195
 act ctt agg gct agt aga tgt gcg ctc aag gat tct tct cag gca agt 739
 Thr Leu Arg Ala Ser Arg Cys Ala Leu Lys Asp Ser Ser Gln Ala Ser
 200 205 210
 ttc ggt ggg gtg acg att cct agc cac tat gac tac tgg gga tgt ctt 787
 Phe Gly Gly Val Thr Ile Pro Ser His Tyr Asp Tyr Trp Gly Cys Leu
 215 220 225
 gac aag tcc gac cga ccc gac cct gat gct tat ggg cgc cat gac tac 835
 Asp Lys Ser Asp Arg Pro Asp Pro Asp Ala Tyr Gly Arg His Asp Tyr
 230 235 240 245
 tgc act ctt tcg cct gat tcg tat ggt ccc cta ggg aag aag gct gag 883
 Cys Thr Leu Ser Pro Asp Ser Tyr Gly Pro Leu Gly Lys Lys Ala Glu
 250 255 260
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 265 270 275
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 280 285 290
 atg agc aca gtt tgt act acc aac tat gct gag gat gct aat ttc aag 1027
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 295 300 305
 aag ggc tgt gtg aat acc gcg aag gcc tac tat aag gca gtc caa tta 1075
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<213> Corynebacterium glutamicum

<400> 530

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 20 25 30

Val Tyr Arg Thr Pro Met Leu Glu Gly Phe Gln Ile Ala Ser Ile Asn
 35 40 45

Gly Met Ile Leu Asn Arg Trp Leu Ala Ile Gly Gly Pro Asp Ser Ala
 50 55 60

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Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Ala Ser Asp Gly Val Gly
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 Gly Ala Trp Glu Met Thr Gly Phe Ile Glu Glu Val Trp Lys Met Arg
 100 105 110
 Gly Gly Leu Asp Ser Gln Trp Gly Tyr Pro Thr Ser Ala Pro Val Leu
 115 120 125
 Asp Ser Asp Ala Pro Val Glu Ile Ala Gln Asn Phe Ser Gly Gly Val
 130 135 140
 Phe Asp Leu Ala Thr Glu Ile Glu Asp Ala Gly Phe Ser Pro Ile Glu
 145 150 155 160
 Asp Lys Glu Met Ser Asn Leu Ile Leu Glu Tyr Phe Gly Tyr Leu Gly
 165 170 175
 Phe Asp Phe Pro Gly Ser Ser Arg Glu Leu Val Gln Asp His Ser
 180 185 190
 Lys Ser Asp Leu Met Thr Leu Arg Ala Ser Arg Cys Ala Leu Lys Asp
 195 200 205
 Ser Ser Gln Ala Ser Phe Gly Gly Val Thr Ile Pro Ser His Tyr Asp
 210 215 220
 Tyr Trp Gly Cys Leu Asp Lys Ser Asp Arg Pro Asp Pro Asp Ala Tyr
 225 230 235 240
 Gly Arg His Asp Tyr Cys Thr Leu Ser Pro Asp Ser Tyr Gly Pro Leu
 245 250 255
 Gly Lys Lys Ala Glu Phe Ser Gly Ala Cys Ala Arg His Asp Leu Cys
 260 265 270
 Met Asp Ala Val Asp Ala Asn Gly Thr Gly Tyr Ala Pro Cys His Pro
 275 280 285
 Ala Phe Tyr Thr Trp Met Ser Thr Val Cys Thr Thr Asn Tyr Ala Glu
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 Asp Ala Asn Phe Lys Lys Gly Cys Val Asn Thr Ala Lys Ala Tyr Tyr
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 Lys Ala Val Gln Leu Lys Asn Pro Asn
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<211> 342

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> {101}..(319)

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Phe Arg Ser Ile Lys Ala Lys Ala Gln Ala Lys Arg Arg Ser Leu Trp
10 15 20

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Ile Ala Ala Gly Ala Val Pro Thr Ala Ile Ala Leu Thr Met Ser Leu
25 30 35

gca cct atg gct tcg gct cag tcc agc aac ctt tcc tct gat gcc gtt 259

Ala Pro Met Ala Ser Ala Gln Ser Ser Asn Leu Ser Ser Asp Ala Val
40 45 50

att ggc agc atc gcg cag ggc gtc acc gat ggc ctg act gac tac ctg 307

Ile Gly Ser Ile Ala Gln Gly Val Thr Asp Gly Leu Thr Asp Tyr Leu
55 60 65

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Lys Pro Arg Val
70

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<213> *Corynebacterium glutamicum*

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20 25 30

Leu Thr Met Ser Leu Ala Pro Met Ala Ser Ala Gln Ser Ser Asn Leu
35 40 45

Ser Ser Asp Ala Val Ile Gly Ser Ile Ala Gln Gly Val Thr Asp Gly
50 55 60

Leu Thr Asp Tyr Leu Lys Pro Arg Val
65 70

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06-09-2017

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Ala Met	Pro Pro	Arg Pro	Ile Lys	Val Val	Gln Leu	Leu Leu	Pro Arg	Asp	35
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Trp Tyr	Ser Ser	Pro Asn	Arg Glu	Phe Pro	Glu Ile	Trp Ala	Leu Asp		40
		40		45					50
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Gly Leu	Arg Ala	Ile Glu	Glu Gln	Ser Gly	Trp Thr	Ile Glu	Thr Asn		55
		60							65
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Ile Glu	Gln Tyr	Tyr Ala	Asp Lys	Asn Ala	Ile Val	Val Val	Leu Pro	Val	70
		75						85	
ggt ggc	gag agc	tcc ttc	tac tct	gac tgg	gaa ggg	cca aac	aac ggc		403
Gly Gly	Glu Ser	Ser Phe	Tyr Ser	Asp Trp	Glu Gly	Pro Asn	Asn Gly		90
		90							100
aag aac	tac cag	tgg gag	acc ttc	ctg act	cag gag	ctc gca	ccg atc		451
Lys Asn	Tyr Gln	Trp Trp	Glu Thr	Phe Leu	Thr Thr	Gln Val	Leu Ala	Pro Ile	105
		105							115
ctg gac	aag ggt	ttc cgt	tct aac	acc gat	cgc gcc	atc acc	ggt atc		499
Leu Asp	Lys Gly	Phe Arg	Ser Asn	Thr Asp	Arg Arg	Ile Thr	Gly Ile		120
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tcc atg	ggc ggt	acc gct	gcg gtt	aac atc	gca acc	cac cac	cca gac		547
Ser Met	Gly Gly	Thr Thr	Ala Ala	Val Asn	Ile Ala	Thr His	His Pro	Asp	135
		140							145
atg ttt	aag gtc	gtc ggt	tcc ttc	tcc ggc	tat ctg	gac acc	gct tcc		595
Met Phe	Lys Phe	Val Gly	Ser Phe	Ser Gly	Tyr Thr	Leu Asp	Thr Thr	Ser	150
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gct ggc	atg cca	atc gct	att tcc	gca gcc	ctg gca	gac gcc	ggc gga		643
Ala Gly	Met Pro	Ile Ala	Ile Ser	Ala Ala	Leu Ala	Asp Ala	Gly Gly		170
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tac gat	gcc aac	gca atg	tgg gga	cca gtc	ggt tct	gag cgc	tgg cag		691
Tyr Asp	Ala Asn	Ala Met	Trp Gly	Pro Val	Gly Ser	Glu Arg	Trp Gln		185
		185							190
gaa aac	gat cca	aag agc	aac gta	gac aag	ctc aag	ggc aag	acc atc		739
Glu Asn	Asp Pro	Lys Ser	Asn Val	Alp Val	Lys Leu	Lys Gly	Lys Thr	Ile	200
		200							205
tac gtt	tcc tct	ggt aac	ggt gca	gat gac	ttc ggt	aag gaa	ggc tct		787

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

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Ala	Asp	Ala	Gly	Gly	Tyr	Asp	Ala	Asn	Ala	Met	Trp	Gly	Pro	Val	Gly	
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Ser	Glu	Arg	Trp	Gln	Glu	Asn	Asp	Pro	Lys	Ser	Asn	Val	Asp	Lys	Leu	
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Gly	Leu	Glu	Val	Ile	Ser	Arg	Met	Thr	Ser	Gln	Thr	Phe	Val	Asp	Arg	
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Val	His	Ser	Trp	Glu	Tyr	Trp	Gln	Phe	Glu	Met	Thr	Gln	Ala	Phe	Pro	
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His	Ile	Ala	Asn	Ala	Leu	Gly	Met	Ser	Thr	Glu	Asp	Arg	Gly	Val	Glu	
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Cys	Ala	Pro	Val	Gly	Ala	Ile	Ala	Asp	Ala	Val	Ala	Asp	Gly	Ala	Met	
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Asp	Phe	Ala	Asn	Gly	Arg	Ala	Tyr	Trp	Ser	Ala	Asn	Thr	Gly	Ala	Phe	
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Met Lys Leu Phe Ser
1 5
aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163
Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile
10 15 20
gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac 211
Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp
25 30 35
caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct 259
Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro
40 45 50
gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307
Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile
55 60 65
cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355
His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu
70 75 80 85
ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr

090630Z FEB 80

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 Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala
 345 350 355

gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc 1219
 Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro
 360 365 370

ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca 1267
 Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser
 375 380 385

aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att 1315
 Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile
 390 395 400 405

caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac 1363
 Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp
 410 415 420

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 Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp
 425 430 435

tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att 1459
 Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile
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tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa 1507
 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln
 455 460 465

ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt 1555
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
 470 475 480 485

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 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
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 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
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gag 1704

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 <213> Corynebacterium glutamicum

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 Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
 35 40 45
 Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
 50 55 60
 Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
 65 70 75 80
 Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
 85 90 95
 Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
 100 105 110
 Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
 115 120 125
 Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
 130 135 140
 Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met
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 Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
 165 170 175
 Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
 180 185 190
 Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
 195 200 205
 Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
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 Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
 225 230 235 240
 Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln
 245 250 255
 Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly
 260 265 270
 Gly Pro Asp Ser Asp Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr
 275 280 285
 Ala Asp Gly Val Gly Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr
 290 295 300
 Trp His Pro Gln His Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser
 305 310 315 320
 Ile Trp Arg Glu Glu Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile
 325 330 335
 Gly Asp Pro Glu Lys Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu

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340 345 350

Lys Gly Glu Leu Ala Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe
355 360 365

Ile Glu Phe Leu Pro Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe
370 375 380

Glu Asn Gly Leu Ser Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala
385 390 395 400

Lys Lys Asp Ser Ile Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val
405 410 415

Arg Thr Lys Ser Asp Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe
420 425 430

Lys Ala Arg Met Asp Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val
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Gly Tyr Gly Trp Ile Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala
450 455 460

Ala Tyr Ala Gln Gln Phe Gly Asn Arg Asn Ser Val Val Gln Thr
465 470 475 480

Asn Leu Glu Ala Gly Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly
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Thr Ser Tyr Phe Gln Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln
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Met Lys Leu Phe Ser
1 5
aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163
Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile
10 15 20
gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac 211
Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp
25 30 35

caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct 259
 Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro
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gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307
 Val Val Asp Gly Val Gly Gly Tyr Thr Glu Glu Ile Ala Glu Ile
 55 60 65

cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355
 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Lys Ala Pro Asn Glu Glu
 70 75 80 85

ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr
 90 95 100

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 Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln
 105 110 115

caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag 499
 Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Cys Gln
 120 125 130

acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc 547
 Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg
 135 140 145

tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa 595
 Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu
 150 155 160 165

ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg 643
 Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met
 170 175 180

aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat 691
 Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn
 185 190 195

aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg 739
 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp
 200 205 210

atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg 787
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro
 215 220 225

att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga 835
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg
 230 235 240 245

gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat 883
 Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn
 250 255 260

ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac 931
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<213> *Corynebacterium glutamicum*

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 35 40 45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
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Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
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180 185 190																
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Gly	Phe	Gly	Leu	Asp	Gly	Gly	Pro	Ile	Pro	Val	Tyr	Asn	Pro	Asn	Gly	
195 200 205																
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Val	Ser	Ser	Ser	Glu	Ser	Ser	Ser	Glu	Leu	Ser	Ser	Asp	Val	Ser	Leu	
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0896

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<213> *Corynebacterium glutamicum*

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Thr Gly Ser Phe Tyr Glu
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<212> DNA

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<222> (1)..(675)

<223> FRXA02904

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Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu Glu Arg Phe Val Gly
20 25 30

gtt gac ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg 144
Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met
35 40 45

gga cgc acc att cct cta gtc tgg gtc gtg cca gaa gac aac acc gtg 192
Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val
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cct ggc cca acg gtc tac gca ctc ggc ggc ggc gac ggt ggc caa ggc 240
Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly
65 70 75 80

ggc caa aac tgg gtc acc cgc acc gac ctt gat gag ttg acc agt gaa 288
Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp Glu Leu Thr Ser Glu
85 90 95

aac aac atc aac ctc atc atg ccc atg ctc gga tct ttt agt ttc tac 336
Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr
100 105 110

gct gac tgg gca ggc gaa agc gaa tcc atg ggt ggt gcg caa cag tgg 384
Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly Gly Ala Gln Gln Trp
115 120 125

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Glu Thr Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile
130 135 140

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Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly
145 150 155 160

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Gly	Ser	Phe	Ser 180	Gly	Cys	Ala	Glu	Thr 185	Asn	Ser	Trp	Met	Gly 190	Arg	Arg	
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ggc	atc	gca	gcc	act	gcc	tac	aac	ggc	aat	gtc	gtg	cct	gag	caa	atc	
Gly	Ile	Ala 195	Ala	Ala	Thr	Ala	Tyr 200	Gly	Asn	Val	Val	Pro 205	Glu	Gln	Ile	
															624	
ttt	ggt	gaa	gta	gac	agt	gat	tac	tct	cgc	tat	aac	gat	cct	agt	att	
Phe	Gly 210	Glu	Val	Asp	Ser	Asp 215	Tyr	Ser	Arg	Tyr	Asn 220	Asp	Pro	Ser	Ile	
															672	
cta	tagtgtcaccc	t														
Leu 225																688

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<210> 544
<211> 225
<212> PRT
<213> Corynebacterium glutamicum
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400> 544																	
Thr	Asp	Pro	Arg	Tyr	Pro	Leu	Gly	Lys	Asp	Asp	Leu	Pro	Lys	Ala	Thr		
1				5					10					15			
Ile	Asp	Met	Glu	Pro	Glu	Ala	Leu	Ala	Arg	Leu	Glu	Arg	Phe	Val	Gly		
			20					25					30				
Val	Asp	Gly	Asp	Arg	Ile	Arg	Gln	Ile	Asn	Ala	Tyr	Ser	Pro	Ser	Met		
		35					40					45					
Gly	Arg	Thr	Ile	Pro	Leu	Val	Trp	Val	Val	Pro	Glu	Asp	Asn	Thr	Val		
	50					55					60						
Pro	Gly	Pro	Thr	Val	Tyr	Ala	Leu	Gly	Gly	Gly	Asp	Gly	Gly	Gln	Gly		
	65				70					75				80			
Gly	Gln	Asn	Trp	Val	Thr	Arg	Thr	Asp	Leu	Asp	Glu	Leu	Thr	Ser	Glu		
			85					90						95			
Asn	Asn	Ile	Asn	Leu	Ile	Met	Pro	Met	Leu	Gly	Ser	Phe	Ser	Phe	Tyr		
		100						105					110				
Ala	Asp	Trp	Ala	Gly	Glu	Ser	Glu	Ser	Met	Gly	Gly	Ala	Gln	Gln	Trp		
		115					120					125					
Glu	Thr	Phe	Leu	Met	His	Glu	Leu	Pro	Glu	Pro	Leu	Glu	Ala	Ala	Ile		
	130					135					140						
Gly	Ala	Asp	Gly	Gln	Arg	Ser	Ile	Val	Gly	Met	Ser	Met	Ser	Gly	Gly		
	145				150					155				160			
Ser	Val	Leu	Asn	Phe	Ala	Thr	His	Asp	Pro	Asn	Phe	Tyr	Ser	Ser	Val		
			165					170					175				

400> 545																																										
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					Met	Ala	Trp	Phe	Phe	5																																
					1																																					
gca ccc gaa ccc	gtg atg gtt acc	gct gat gag gcg	ctt aaa ggt ggc	163																																						
Ala Pro Glu Pro	Val Met Val Thr	Ala Asp Glu Ala	Leu Lys Gly Gly	20																																						
	10	15	20																																							
agg cat cct gtt	tta gaa aat cct	gcg ccg cac act	gtg ttg gga act	211																																						
Arg His Pro Val	Leu Glu Asn Pro	Ala Pro His Thr	Val Leu Gly Thr	35																																						
	25	30	35																																							
cct gtg act ggt	ccg tgg aaa gaa	ggc cag cag cga	att tgg att ggc	259																																						
Pro Val Thr Gly	Pro Trp Lys Glu	Gly Gln Gln Arg	Ile Trp Ile Gly	50																																						
	40	45	50																																							
ctt ggt tgt ttc	tgg ggt gtg gag	caa atg tat tgg	cag atg gat ggc	307																																						
Leu Gly Cys Phe	Trp Gly Val Glu	Gln Met Tyr Trp	Gln Met Asp Gly	60																																						
	55	60	65																																							
gtt gag gga act	tcg gtt ggt tac	gcc gcc ggt ttc	acc cct aat ccc	355																																						
Val Glu Gly Thr	Ser Val Gly Tyr	Ala Gly Gly Phe	Thr Pro Asn Pro	85																																						
	70	75	80																																							
act tat cgc gag	gtg tgt tct ggg	cgc acc gcc ggc	cac act gaa atc	403																																						
Thr Tyr Arg Glu	Val Cys Ser Gly	Arg Thr Gly His	Thr Glu Ile Val	100																																						
	90	95	100																																							
gag gtt gtt tac	gat cct tcg aag	att tcc ctc gag	cag ctt gtt gcc	451																																						

gat gtg gga acg cag tac cgc tct gct tat tac acc gag aac gaa gag 547
 Asp Val Gly Thr Gln Tyr Arg Ser Ala Tyr Tyr Thr Glu Asn Glu Glu
 135 140 145
 gac gct gcg cgc gta aaa gcc gtg gtc gat gcc tat ggt gag acg ctg 595
 Asp Ala Ala Arg Val Lys Ala Val Val Asp Ala Tyr Gly Glu Thr Leu
 150 155 160 165
 aag cag cac ggt ttt ggt gaa atc acc acg gaa atc ggt gtc att agc 643
 Lys Gln His Gly Phe Gly Glu Ile Thr Thr Glu Ile Gly Val Ile Ser
 170 175 180
 ccg tct gac tac ttc ctc gcc gag gat tac cac cag caa tac ctg gac 691
 Pro Ser Asp Tyr Phe Leu Ala Glu Asp Tyr Thr His Gln Gln Tyr Leu Asp
 185 190 195
 aag aat ccc gat gcc tac tgc cct cat cac tcc acg gcc atc ccg tgc 739
 Lys Asn Pro Asp Gly Tyr Cys Pro His His Ser Thr Gly Ile Pro Cys
 200 205 210
 ggg gta gaa gct taaaagattt ttgcttttcg acg 774
 Gly Val Glu Ala
 215

<210> 546

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 546

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Ala Leu Lys Gly Gly Arg His Pro Val Leu Glu Asn Pro Ala Pro His
 20 25 30

Thr Val Leu Gly Thr Pro Val Thr Gly Pro Trp Lys Glu Gly Gln Gln
 35 40 45

Arg Ile Trp Ile Gly Leu Gly Cys Phe Trp Gly Val Glu Gln Met Tyr
 50 55 60

Trp Gln Met Asp Gly Val Glu Gly Thr Ser Val Gly Tyr Ala Gly Gly
 65 70 75 80

Phe Thr Pro Asn Pro Thr Tyr Arg Glu Val Cys Ser Gly Arg Thr Gly
 85 90 95

His Thr Glu Ile Val Glu Val Val Tyr Asp Pro Ser Lys Ile Ser Leu
 100 105 110

Glu Gln Leu Val Ala Arg Gly Leu Glu Ala His Asp Pro Thr Gln Gly
 115 120 125

Phe Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Ser Ala Tyr Tyr
 130 135 140

Thr Glu Asn Glu Glu Asp Ala Ala Arg Val Lys Ala Val Val Asp Ala
 145 150 155 160

002250 00220960

Tyr Gly Glu Thr Leu Lys Gln His Gly Phe Gly Glu Ile Thr Thr Glu
165 170 175

Ile Gly Val Ile Ser Pro Ser Asp Tyr Phe Leu Ala Glu Asp Tyr His
180 185 190

Gln Gln Tyr Leu Asp Lys Asn Pro Asp Gly Tyr Cys Pro His His Ser
195 200 205

Thr Gly Ile Pro Cys Gly Val Glu Ala
210 215

<210> 547

<211> 444

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle$ (101) .. (421)

<223> RXA01431

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attccccagg agtcccgta ttgttaattt aggagaaacc atg agc aat gtt gtt 115
Met Ser Asn Val Val
1 5

gca gta acc gag cag acc ttc aag tcc acc gtc atc gat tcc gac aag 163
Ala Val Thr Glu Gln Thr Phe Lys Ser Thr Val Ile Asp Ser Asp Lys
10 15 20

cca gtc atc gtt gac ttc tgg gca gaa tgg tgt ggc ccc tgc aag aag 211
Pro Val Ile Val Asp Phe Trp Ala Glu Trp Cys Gly Pro Cys Lys Lys
25 30 35

ctc agc ccc atc att gag gaa atc gca ggc gag tac ggc gac aag gca 259
Leu Ser Pro Ile Ile Glu Glu Ile Ala Gly Glu Tyr Gly Asp Lys Ala
40 45 50

gtc gtt gcc agc gtc gac gtc gat gca gag cgt acc ttg ggt gcc atg 307
Val Val Ala Ser Val Asp Val Asp Ala Glu Arg Thr Leu Gly Ala Met
55 60 65

ttc cag att atg tcg att cct tct gtt ctc att ttc aaa aat ggt gca 355
Phe Gln Ile Met Ser Ile Pro Ser Val Leu Ile Phe Lys Asn Gly Ala
70 75 80 85

aaa gtc gag gaa ttt gtc ggt ctg cgc ccc aag aac gaa att gtg gaa 403
Lys Val Glu Glu Phe Val Gly Leu Arg Pro Lys Asn Glu Ile Val Glu
90 95 100

aaa cta gag aag cac ctc tagctggtat tcttactgca gtc 444
Lys Leu Glu Lys His Leu
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<210> 548

069874

<211> 107
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Gly Pro Cys Lys Lys Leu Ser Pro Ile Ile Glu Glu Ile Ala Gly Glu
 35 40 45
 Tyr Gly Asp Lys Ala Val Val Ala Ser Val Asp Val Asp Ala Glu Arg
 50 55 60
 Thr Leu Gly Ala Met Phe Gln Ile Met Ser Ile Pro Ser Val Leu Ile
 65 70 75 80
 Phe Lys Asn Gly Ala Lys Val Glu Glu Phe Val Gly Leu Arg Pro Lys
 85 90 95
 Asn Glu Ile Val Glu Lys Leu Glu Lys His Leu
 100 105

<210> 549
 <211> 1074
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1051)
 <223> RXA01432

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 gtgatgtcgc acttttacgt ttactacttt gagggaaaca atg tct gaa gaa caa 115
 Met Ser Glu Glu Gln
 1 5
 tct gcc gta gca cca aag att cat gat gtc gcc atc atc ggc tcc ggt 163
 Ser Ala Val Ala Pro Lys Ile His Asp Val Ala Ile Ile Gly Ser Gly
 10 15 20
 cca gct ggc tat acc gca gca gta tat gca gcc cgc gct gac ctc aac 211
 Pro Ala Gly Tyr Thr Ala Ala Val Tyr Ala Ala Arg Ala Asp Leu Asn
 25 30 35
 ccc atc atg ttc gag ggc tat gaa tac ggt gga tct ttg atg acc act 259
 Pro Ile Met Phe Glu Gly Tyr Glu Tyr Gly Gly Ser Leu Met Thr Thr
 40 45 50
 act gac gtg gaa aac ttc cca ggc ttt gaa aag gga atc ctg ggc cca 307
 Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys Gly Ile Leu Gly Pro
 55 60 65
 gag ctc atg gaa aac atg cgc gct cag gcc gag cgt ttc ggc acc gag 355

000290 68820960

Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu Arg Phe Gly Thr Asp
 70 75 80 85
 atg cac atg gag ctt gtc gac cgc gtt gat ctc acc ggc gac atc aag 403
 Met His Met Glu Leu Val Asp Arg Val Asp Leu Thr Gly Asp Ile Lys
 90 95
 aag ctg tgg gtc ggc gac gat gag tac cac gcg cgt gct gtc atc ttg 451
 Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala Arg Ala Val Ile Leu
 105 110 115
 tcc atg ggt tct gca cct cgc tac ttg ggt gtg aag ggc gag cag gaa 499
 Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val Lys Gly Glu Gln Glu
 120 125 130
 ctg ctc ggc cgc ggc gtt tct gca tgt gca acc tgc gat ggt ttc ttc 547
 Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr Cys Asp Gly Phe Phe
 135 140 145
 ttc cgc gat cag gac atc gcc gtg atc ggt ggt ggc gac tcc gcg atg 595
 Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly Asp Ser Ala Met
 150 155 160 165
 gag gaa gca acc ttc ctc acc aag ttc gct cgc agt gtc acc atc gtg 643
 Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg Ser Val Thr Ile Val
 170 175 180
 cac cgc cgc gaa gag ttc cgc gcc agc gcc atc atg ctg gag cgt gct 691
 His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile Met Leu Glu Arg Ala
 185 190 195
 cag aag aac gag aag att cgc ttc gtc acc aac aag act gtc gaa gag 739
 Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn Lys Thr Val Glu Glu
 200 205 210
 gtc atc gag gca gac ggc aag gtc agc ggt ctg aag ctc aac gac acc 787
 Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu Lys Leu Asn Asp Thr
 215 220 225
 gtc act ggt gaa gat tcc gtc ttg gat gtc acc gcc atg ttc gtt gcc 835
 Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr Ala Met Phe Val Ala
 230 235 240 245
 atc ggc cat gat cca cgc tct gaa atc ctc gca ggt cag gtc gag gtt 883
 Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala Gly Gln Val Glu Val
 250 255 260
 gat cct tcc aac tac gtt ttg gtt cag gag cct tcc acc cgc acc aac 931
 Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro Ser Thr Arg Thr Asn
 265 270 275
 ctt gat ggt gtt ttc gct gct ggc gac ctg gtg gac agc cac tac cag 979
 Leu Asp Gly Val Phe Ala Ala Gly Asp Leu Val Asp Ser His Tyr Gln
 280 285 290
 cag gcc atc acc gca gct ggt tcc ggt tgc cgc gca gcg atc gat gca 1027
 Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Arg Ala Ala Ile Asp Ala
 295 300 305
 gag cat tac cta gct tct ctg gcc taattcacag ttagccttaa acc 1074
 Glu His Tyr Leu Ala Ser Leu Ala

00502077-052300

315

<213> *Corynebacterium glutamicum*

Met Ser Glu Glu Gln Ser Ala Val Ala Pro Lys Ile His Asp Val Ala
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Ile Ile Gly Ser Gly Pro Ala Gly Tyr Thr Ala Ala Val Tyr Ala Ala
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Arg Ala Asp Leu Asn Pro Ile Met Phe Glu Gly Tyr Glu Tyr Gly Gly
35 40 45

Ser Leu Met Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys
50 55 60

Gly Ile Leu Gly Pro Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu
65 70 75 80

Arg Phe Gly Thr Asp Met His Met Glu Leu Val Asp Arg Val Asp Leu
85 90 95

Thr Gly Asp Ile Lys Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala
100 105 110

Arg Ala Val Ile Leu Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val
115 120 125

Lys Gly Glu Gln Glu Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr
130 135 140

Cys Asp Gly Phe Phe Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly
145 150 155 160

Gly Asp Ser Ala Met Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg
165 170 175

Ser Val Thr Ile Val His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile
180 185 190

Met Leu Glu Arg Ala Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn
195 200 205

Lys Thr Val Glu Glu Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu
210 215 220

Lys Leu Asn Asp Thr Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr
225 230 235 240

Ala Met Phe Val Ala Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala
245 250 255

Gly Gln Val Glu Val Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro
260 265 270

Ser Thr Arg Thr Asn Leu Asp Gly Val Phe Ala Ala Gly Asp Leu Val

[illegible]

0902634

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 552

Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr
 1 5 10 15

Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro
 20 25 30

Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr
 35 40 45

Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala
 50 55 60

Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp
 65 70 75 80

Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu
 85 90 95

Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg
 100 105 110

Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala
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<210> 553

<211> 146

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(123)

<223> FRXA00937

<400> 553

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 Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu
 1 5 10 15

gtc aac cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc 96
 Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val
 20 25 30

gca gag cag cag ggt tct gca gag gca taagcttcca attgtgtttt 143
 Ala Glu Gln Gln Gly Ser Ala Glu Ala
 35 40

ggt 146

<210> 554

<211> 41

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 554

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Ala Asp Ala Leu Lys Gln Trp Thr Asp Gln Val Val Gln Ala Val Gly

09602830 0E2300

135	140	145	
gga cag ctg gaa gga ctg cca gag gag gcc aca gac ggc gaa caa gaa			595
Gly Gln Leu Glu Gly Leu Pro Glu Glu Ala Thr Asp Gly Glu Gln Glu			
150	155	160	165
gac gct cct gtg gaa gac ccc cgc ttc gat gct gcc act gat gct cta			643
Asp Ala Pro Val Glu Asp Pro Arg Phe Asp Ala Ala Thr Asp Ala Leu			
170	175		180
aac cgt ggc gct ttc gat gag gcg att gcg gtt tat gag tcc att ttg			691
Asn Arg Gly Ala Phe Asp Glu Ala Ile Ala Val Tyr Glu Ser Ile Leu			
185	190		195
gcg cag gag cca aac aac gct gat gcg aag caa gca ccg cga tac cgc			739
Ala Gln Glu Pro Asn Asn Ala Asp Ala Lys Gln Ala Pro Arg Tyr Arg			
200	205		210
aaa gct gtt ggg ccg gct tgc cac ccg tgg atc ctt ccg tgg atg ttg			787
Lys Ala Val Gly Pro Ala Cys His Arg Trp Ile Leu Arg Trp Met Leu			
215	220		225
tcg ctg ctg cag atg ctg atc caa caa acg ttg atc tgg cct aca caa			835
Ser Leu Leu Gln Met Leu Ile Gln Gln Thr Leu Ile Trp Pro Thr Gln			
230	235		240
gca act gac gcg gct gtt gtt gcg ggt gat cct gag			871
Ala Thr Asp Ala Ala Val Val Ala Gly Asp Pro Glu			
250	255		
<210> 556			
<211> 257			
<212> PRT			
<213> <i>Corynebacterium glutamicum</i>			
<400> 556			
Val Thr Ser Pro His Asn Phe Val Ser Gly Ala Ile Asp Leu Gly Glu			
1	5	10	15
Val Lys Ala Arg Ala Asp Ala Arg Gln Lys Ala His Glu Gln Gly Pro			
20	25		30
Val Thr Gln Gly Ile Ala Ser Ser Leu Asp Val Thr Met Glu Asn Leu			
35	40		45
Glu Asn Glu Val Leu Arg Arg Ser Thr Gln Val Pro Val Ile Val Leu			
50	55		60
Val Gly Thr Pro Arg Ser Pro Asp Ser Glu Gln Leu Lys Ser Asp Leu			
65	70		75
Thr Thr Leu Ala Ala Glu Ser Gly Arg Lys Phe Ile Phe Gly Tyr Val			
85	90		95
Asn Ala Asp Thr Asp Ala Asp Val Ala Gln Val Phe Gly Val Gln Gly			
100	105		110
Leu Pro Ser Val Ile Ala Val Ala Ala Gly Arg Pro Leu Ala Asp Phe			
115	120		125

00229.62200

Gln Gly Gly Gln Pro Ala Asp Ala Leu Lys Gln Trp Thr Asp Gln Val
 130 135 140
 Val Gln Ala Val Gly Gly Gln Leu Glu Gly Leu Pro Glu Glu Ala Thr
 145 150 155 160
 Asp Gly Glu Gln Glu Asp Ala Pro Val Glu Asp Pro Arg Phe Asp Ala
 165 170 175
 Ala Thr Asp Ala Leu Asn Arg Gly Ala Phe Asp Glu Ala Ile Ala Val
 180 185 190
 Tyr Glu Ser Ile Leu Ala Gln Glu Pro Asn Asn Ala Asp Ala Lys Gln
 195 200 205
 Ala Pro Arg Tyr Arg Lys Ala Val Gly Pro Ala Cys His Arg Trp Ile
 210 215 220
 Leu Arg Trp Met Leu Ser Leu Leu Gln Met Leu Ile Gln Gln Thr Leu
 225 230 235 240
 Ile Trp Pro Thr Gln Ala Thr Asp Ala Ala Val Val Ala Gly Asp Pro
 245 250 255
 Glu

<210> 557
 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(658)
 <223> RXA00824

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 agggagcacc tgctgaaaaat ggcaggaatg tagaaaaacaa atg aca agc agt gca 115
 Met Thr Ser Ser Ala
 1 5
 aag tgg tcc atc gtt gga gtt gtc gcc atc ctg gct gtg atc gtt gcg 163
 Lys Trp Ser Ile Val Gly Val Val Ala Ile Leu Ala Val Ile Val Ala
 10 15 20
 tta atc ccg cag ctt gtg ggt gga gaa agc gca gag gaa gcg cag ggg 211
 Leu Ile Pro Gln Leu Val Gly Gly Glu Ser Ala Glu Glu Ala Gln Gly
 25 30 35
 gag acg tcg aca agc aaa att acg acg cgt cct gac tgc gtg gcc tct 259
 Glu Thr Ser Thr Ser Lys Ile Thr Thr Arg Pro Asp Cys Val Ala Ser
 40 45 50
 ggc gcg gcg ggt gtg gat ctg ccc tgc ttg ggc gcc gcc aac gcc gtc 307
 Gly Ala Ala Gly Val Asp Leu Pro Cys Leu Gly Gly Ala Asn Gly Val
 55 60 65

002299.062700

ggc aac gag ctg gcc acc gtg gtg aat ctg tgg gcg tgg tgg tgc gaa 355
Gly Asn Glu Leu Ala Thr Val Val Asn Leu Trp Ala Trp Trp Cys Glu
70 75 80 85

ccg tgc cgc gcg gag ctg ccg att ttt gat gaa ttc gcc acc acc cac 403
Pro Cys Arg Ala Glu Leu Pro Ile Phe Asp Glu Phe Ala Thr Thr His
90 95 100

ccc gaa ctc aac gtc att ggc gtg cat gca gac caa aac gca gcc aac 451
Pro Glu Leu Asn Val Ile Gly Val His Ala Asp Gln Asn Ala Ala Asn
105 110 115

ggc gcc gca ctc ctt gag gat ctg ggc gtg aat ctt gca agc tac caa 499
Gly Ala Ala Leu Leu Glu Asp Leu Gly Val Asn Leu Ala Ser Tyr Gln
120 125 130

gac gat tcc aac ctg ttc gca ggc acc ctt ggg ctg ccg ggc gtc gtg 547
Asp Asp Ser Asn Leu Phe Ala Gly Thr Leu Gly Leu Pro Gly Val Val
135 140 145

ccg atc acc atc gtg gtt tct cca gac ggc aat gta gtg gac acc ttc 595
Pro Ile Thr Ile Val Val Ser Pro Asp Gly Asn Val Val Asp Thr Phe
150 155 160 165

ccg cag cct ttc gaa acc atc gat gac ctc gaa acc gct gtg gca ggg 643
Pro Gln Pro Phe Glu Thr Ile Asp Asp Leu Glu Thr Ala Val Ala Gly
170 175 180

gcg ctg cag aat gcg taactaccct gatttaccgc atg 681
Ala Leu Gln Asn Ala
185

<210> 558

<211> 186

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 558

Met Thr Ser Ser Ala Lys Trp Ser Ile Val Gly Val Val Ala Ile Leu
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Ala Val Ile Val Ala Leu Ile Pro Gln Leu Val Gly Gly Glu Ser Ala
20 25 30

Glu Glu Ala Gln Gly Glu Thr Ser Thr Ser Lys Ile Thr Thr Arg Pro
35 40 45

Asp Cys Val Ala Ser Gly Ala Ala Gly Val Asp Leu Pro Cys Leu Gly
50 55 60

Gly Ala Asn Gly Val Gly Asn Glu Leu Ala Thr Val Val Asn Leu Trp
65 70 75 80

Ala Trp Trp Cys Glu Pro Cys Arg Ala Glu Leu Pro Ile Phe Asp Glu
85 90 95

Phe Ala Thr Thr His Pro Glu Leu Asn Val Ile Gly Val His Ala Asp
100 105 110

Gln Asn Ala Ala Asn Gly Ala Ala Leu Leu Glu Asp Leu Gly Val Asn

0960203060300

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Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val
40 45 50

090367

ggt Gly	tat Tyr	act Thr	tta Leu 55	caa Gln	act Thr	gtc Val	gac Asp	ccc Pro 60	gag Glu	cct Pro	tta Leu	gat Asp	atg Met 65	gac Asp	tta Leu	248
att Ile	tat Tyr	cgt Arg 70	aga Arg	ctt Leu	gat Asp	gaa Glu	att Ile 75	cca Pro	aat Asn	ctg Leu	cga Arg	acg Thr 80	atg Met	tca Ser	att Ile	296
aca Thr	ggt Gly	ggc Gly	gaa Glu	cca Pro	atg Met	ttt Phe 90	tct Ser	aaa Lys	aag Lys	tct Ser	att Ile 95	aga Arg	aat Asn	gtt Val	gtt Val	344
aaa Lys 100	cct Pro	cta Leu	tta Leu	aag Lys	tat Tyr 105	gca Ala	cat His	cat His	cga Arg	ggg Gly 110	ata Ile	tat Tyr	aca Thr	caa Gln	atg Met 115	392
aat Asn	tca Ser	aac Asn	cta Leu	aca Thr 120	ttg Leu	cct Pro	caa Gln	gat Asp	cgt Arg 125	tat Tyr	tta Leu	gat Asp	att Ile	gct Ala 130	gaa Glu	440
tat Tyr	atc Ile	gat Asp 135	gtt Val	atg Met	cat His	atc Ile	tca Ser	cat His 140	aac Asn	tgg Trp	gga Gly	aca Thr	act Thr 145	gat Asp	gaa Glu	488
ttc Phe	gca Ala	aat Asn 150	gtt Val	ggc Gly	ttt Phe	ggc Gly 155	gca Ala	atg Met	aag Lys	aag Lys	caa Gln	cca Pro 160	cgg Pro	tta Leu	aaa Lys	536
gct Ala	aag Lys 165	tta Leu	aaa Lys	tta Leu	tat Tyr	gaa Glu 170	caa Gln	atg Met	att Ile	tcg Ser 175	aat Asn	gca Ala	cgt Arg	aca Thr	tta Leu	584
tca Ser 180	gaa Glu	caa Gln	gga Gly	atg Met	ttt Phe 185	gta Val	tct Ser	gcg Ala	gaa Glu	aca Thr 190	atg Met	ctc Leu	aat Asn	caa Gln	agt Ser 195	632
acg Thr	cta Leu	cca Pro	cat His	tta Leu 200	cga Arg	aaa Lys	ile Ile	cat His	caa Gln 205	gtc Glu	gtt Val	cat Val	his His	gat Asp 210	atg Met	680
aaa Lys	tgt Cys	agc Ser	aga Arg 215	cac His	gag Glu	att Ile	cac His	cct Pro 220	atg Met	tat Tyr	cca Pro	gct Ala	gac Asp 225	ttt Phe	gca Ala	728
agt Ser	caa Gln	tta Leu 230	aat Asn	gtg Val	tta Leu	act Thr	cta Ala 235	gcg Glu	gaa Glu	atg Met	aaa Lys 240	aag Lys	aca Thr	att Ile	cat His	776
gat Asp	ata Ile	ttg Leu 245	gat Asp	ttc Phe	aga Arg	asp Asp 250	gaa Glu	gat Asp	att Ile	tgg Trp	atg Met 255	tta Leu	ttt Phe	ggt Gly	act Thr	824
ttg Leu 260	cct Pro	gtg Val	ttt Phe	cca Pro	tgc Cys 265	tta Leu	aag Lys	gat Asp	gat Asp	gaa Glu 270	gat Asp	caa Gln	aag Lys	tta Leu	cta Leu 275	872
tca Ser	cgt Arg	tta Leu	aga Arg	aat Asn 280	gct Ala	aac Asn	aat Asn	gta Val	acg Thr 285	act Thr	aga Arg	aat Asn	gac Asp	ccg Pro	gat Asp 290	920

Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro

DECEMBER 2006

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145          150          155          160
Pro Leu Lys Ala   Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala
    165                               170                               175

Arg Thr Leu Ser   Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu
    180                               185                               190

Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val
    195                               200                               205

His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala
    210                               215                               220

Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys
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Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu
    245                               250                               255

Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln
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Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn
    275                               280                               285

Asp Pro Asp Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn
    290                               295                               300

Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile
    305                               310                               315                               320

Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp
    325                               330                               335

Leu Ala Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly
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Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys
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Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
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<213> Corynebacterium glutamicum

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<223> FRXA01863

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Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile Asp Ile Asp Glu Gln	170										175										180																			
acc agc gag agc cta gat agt gct gga gta aaa gtg ttg ggc acc aat																															691									
Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys Val Leu Gly Thr Asn	185										190										195																			
gcg gtg cgc gta tcc gcc gaa ggt gat ggc ctg tct gtg gaa ctg tcc																															739									
Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu Ser Val Glu Leu Ser	200										205										210																			
gaa ggc gat cat tta agc tgc gac aac atc gtg gtg gca tct cgt cca																															787									
Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val Val Ala Ser Arg Pro	215										220										225																			
ctg gtg gat ggc acg ctg tac acc caa ctt ggt ggt cag atg gaa gaa																															835									
Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly Gly Gln Met Glu Glu	230										235										240										245									
aac ccg atg ggc agg ttc att cca ggt acc caa acc ggg cgc act cct																															883									
Asn Pro Met Gly Val Arg Phe Ile Pro Gly Thr Gln Thr Gly Arg Thr Pro	250										255										260																			
att gaa ggt gtg tgg gct gcc gga aac gcg caa gct ccc atg gcg atg																															931									
Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln Ala Pro Met Ala Met	265										270										275																			
gtc tat ggt tcc gct gct caa ggc gtg atg gct gga gca gag atc aac																															979									
Val Tyr Gly Ser Ala Ala Gln Gly Val Met Ala Gly Ala Glu Ile Asn	280										285										290																			
ttt gat ctg atc ctg gaa gat att tcc gtg gca agc gcg cag agc																															1024									
Phe Asp Leu Ile Leu Glu Asp Ile Ser Val Ala Ser Ala Gln Ser	295										300										305																			
taaactgcgt gaggtgtgg cct																										1047														
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Met Ser Ser His Asp Leu Val Asp Val Val Val Val Gly Ala Gly Ala	1										5										10										15									
Ala Gly Leu Ala Ala Ala Val Ala Leu Gly Arg Ser Leu Arg Ser Val	20										25										30																			
Ile Val Ile Asp Ala Gly Gln Pro Arg Asn Ser Tyr Ala His Ala Ala	35										40										45																			
His Asn Val Leu Gly Gln Glu Gly Ile Ala Pro Ala Glu Leu Leu Glu	50										55										60																			
Lys Gly Arg Ala Glu Ala Arg Ser Tyr Gly Val Thr Ile Ala Pro Gly	65										70										75										80									

Arg Val Ala Lys Val Glu Arg Thr Gly Ser Thr Phe Ala Ile Thr Leu
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Asp Asp Ala Ser Leu Leu His Ser Arg Arg Ile Ile Leu Ala His Gly
100 105 110

Ala Val Asp Asp Leu Pro Glu Val Glu Gly Leu Ser Asp Phe Trp Gly
115 120 125

Thr Lys Val Leu His Cys Ala Tyr Cys His Gly Phe Glu Ala Arg Asp
130 135 140

Ser Glu Ile Val Val Val Gly Thr Ser Pro Met Ala Ala His Gln Ala
145 150 155 160

Leu Met Phe Ser Gln Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile
165 170 175

Asp Ile Asp Glu Gln Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys
180 185 190

Val Leu Gly Thr Asn Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu
195 200 205

Ser Val Glu Leu Ser Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val
210 215 220

Val Ala Ser Arg Pro Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly
225 230 235 240

Gly Gln Met Glu Glu Asn Pro Met Gly Arg Phe Ile Pro Gly Thr Gln
245 250 255

Thr Gly Arg Thr Pro Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln
260 265 270

Ala Pro Met Ala Met Val Tyr Gly Ser Ala Ala Gln Gly Val Met Ala
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Ser Ala Gln Ser
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<210> 567

<211> 354

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(331)

<223> RXA01072

<400> 567

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tagcgctcaac cgctaaagcc gataaggagg ggtccaaaaa atg gca atc acc gtt 115

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Met Ala Ile Thr Val
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tac acc aag cca gct tgc gtc cag tgc aat gcc acc aag aag gcc ctc 163
Tyr Thr Lys Pro Ala Cys Val Gln Cys Asn Ala Thr Lys Lys Ala Leu
10 15 20

gac cgc gct ggt ctt gag tat gac ctc gtt gat atc agc ctt gat gaa 211
Asp Arg Ala Gly Leu Glu Tyr Asp Leu Val Asp Ile Ser Leu Asp Glu
25 30 35

gag gca cgt gag tac gtc ctc gca ctt ggc tac ctg cag gca cca gtt 259
Glu Ala Arg Glu Tyr Val Leu Ala Leu Gly Tyr Leu Gln Ala Pro Val
40 45 50

gtc gtt gca gat ggc tcc cac tgg tcc ggt ttc cgc cca gag cgc atc 307
Val Val Ala Asp Gly Ser His Trp Ser Gly Phe Arg Pro Glu Arg Ile
55 60 65

cgt gaa atg gca acc gca gct gcc taaactgcac ttogtggcac gac 354
Arg Glu Met Ala Thr Ala Ala
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<210> 568
 <211> 77
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Thr Lys Lys Ala Leu Asp Arg Ala Gly Leu Glu Tyr Asp Leu Val Asp
20 25 30

Ile Ser Leu Asp Glu Glu Ala Arg Glu Tyr Val Leu Ala Leu Gly Tyr
35 40 45

Leu Gln Ala Pro Val Val Val Ala Asp Gly Ser His Trp Ser Gly Phe
50 55 60

Arg Pro Glu Arg Ile Arg Glu Met Ala Thr Ala Ala Ala
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<210> 569
 <211> 684
 <212> DNA
 <213> *Corynebacterium glutamicum*

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<222> (101)..(661)
<223> RXA02436

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cgtttttota agaccccaca ttagtaaaag catggggacat gtg gtt ggc att tcg 115
Val Val Gly Ile Ser

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00602030.002700

cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc 307
 Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr
 55 60 65
 gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg 355
 Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala
 70 75 80 85
 ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc 403
 Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser
 90 95 100
 aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc 451
 Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr
 105 110 115
 gtg acc gtc aac ctg acc acc gcc cag ggc aac atc ggc atg gaa ctt 499
 Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu
 120 125 130
 gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct 547
 Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala
 135 140 145
 tcc gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct 595
 Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser
 150 155 160 165
 ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc 643
 Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly
 170 175 180
 ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act 691
 Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr
 185 190 195
 gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc 739
 Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala
 200 205 210
 aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga 787
 Asn Ala Gly Ala Asp Thr Asn Glu Leu Pro Val Leu Pro Gln Leu Arg
 215 220 225
 gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga 835
 Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu Arg Pro Asp His Arg
 230 235 240 245
 aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac 877
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<210> 572

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr
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Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile
 35 40 45

Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp
 50 55 60

Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu
 65 70 75 80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
 85 90 95

Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val
 100 105 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn
 115 120 125

Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala
 130 135 140

Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His
 145 150 155 160

Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser
 165 170 175

Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro
 180 185 190

Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly
 195 200 205

Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
 210 215 220

Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
 225 230 235 240

Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg
 245 250 255

Ser Trp His

<210> 573

<211> 416

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(393)

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<223> FRXA01837

<400> 573

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Ser	Glu	Gly	Tyr	Tyr	Asn	Asp	Thr	Val	Cys	His	Arg	Ile	Thr	Thr	Ser	
1				5					10					15		

ggc	att	tac	gtt	ctc	cag	tgc	ggc	gat	cca	agc	agc	acc	ggc	gca	ggc	96
Gly	Ile	Tyr	Val	Leu	Gln	Cys	Gly	Asp	Pro	Ser	Ser	Thr	Gly	Ala	Gly	
			20					25					30			

ggc	cca	ggg	ttc	agc	ttc	gcc	aac	gaa	tac	cca	acc	gac	gaa	gca	act	144
Gly	Pro	Gly	Phe	Ser	Phe	Ala	Asn	Glu	Tyr	Pro	Thr	Asp	Glu	Ala	Thr	
		35						40				45				

gac	cta	acc	acc	cca	gtc	atc	tac	gag	cgc	ggc	acc	atc	gcc	atg	gcc	192
Asp	Leu	Thr	Thr	Pro	Val	Ile	Tyr	Glu	Arg	Gly	Thr	Ile	Ala	Met	Ala	
	50					55					60					

aac	gct	ggc	gct	gac	acc	aac	ggc	tcc	cag	ttc	ttc	ctc	aac	tac	gag	240
Asn	Ala	Gly	Ala	Asp	Thr	Asn	Gly	Ser	Gln	Phe	Phe	Leu	Asn	Tyr	Glu	
65				70				75						80		

gat	tcc	cca	ctg	gca	ccg	aac	tac	acc	tac	ttc	ggc	cag	atc	acc	gaa	288
Asp	Ser	Pro	Leu	Ala	Pro	Asn	Tyr	Thr	Tyr	Phe	Gly	Gln	Ile	Thr	Glu	
			85					90					95			

gaa	ggc	ctt	gca	acc	ctc	gac	gcc	atc	gca	gaa	gtt	ggc	act	gaa	ggc	336
Glu	Gly	Leu	Ala	Thr	Leu	Asp	Ala	Ile	Ala	Glu	Val	Gly	Thr	Glu	Gly	
		100					105					110				

gga	acc	ggc	gac	gga	gca	cca	gcg	caa	gag	gtt	cgc	att	gaa	tcc	gca	384
Gly	Thr	Gly	Asp	Gly	Ala	Pro	Ala	Gln	Glu	Val	Arg	Ile	Glu	Ser	Ala	
		115					120					125				

gct	gtt	gcg	taagtcttaa	gccctctctt	ttt											416
Ala	Val	Ala														
		130														

<210> 574

<211> 131

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 574

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Gly	Ile	Tyr	Val	Leu	Gln	Cys	Gly	Asp	Pro	Ser	Ser	Thr	Gly	Ala	Gly
			20					25					30		

Gly	Pro	Gly	Phe	Ser	Phe	Ala	Asn	Glu	Tyr	Pro	Thr	Asp	Glu	Ala	Thr
		35					40					45			

Asp	Leu	Thr	Thr	Pro	Val	Ile	Tyr	Glu	Arg	Gly	Thr	Ile	Ala	Met	Ala
	50					55					60				

Asn	Ala	Gly	Ala	Asp	Thr	Asn	Gly	Ser	Gln	Phe	Phe	Leu	Asn	Tyr	Glu
65						70				75				80	

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Asp Ser Pro Leu Ala Pro Asn Tyr Thr Tyr Phe Gly Gln Ile Thr Glu
85 90 95

Glu Gly Leu Ala Thr Leu Asp Ala Ile Ala Glu Val Gly Thr Glu Gly
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Gly Thr Gly Asp Gly Ala Pro Ala Gln Glu Val Arg Ile Glu Ser Ala
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Ala Val Ala
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Met Thr Asp Tyr Thr
1 5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
10 15 20

tgg tgg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
25 30 35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Arg Arg Ile Ala
40 45 50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
55 60 65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tgg tat gaa 355
Gln His Pro Arg Gly Val Trp Arg Thr Thr Leu Glu Ser Tyr
70 75 80 85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat cgc ttg gcg 403
Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
90 95 100

gag gat gag gcc gaa aac tgg gta tgg aag gcc gcg gtt gtg cgc tgg 451
Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
105 110 115

cgg gag ttt gat cgg gcg ttg gtg aag ttc tgg cgg gcc ggg gct gat 499
Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
120 125 130

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Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp
615 620

tac tac gaa aac acc gag ggc ggc cat gcc ggc gcg gcg gat aac aag 2035
Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys
630 635 640 645

cag acc gcg ttt gtg gaa tcg ctg atc tac acc tgg atc gag aag act 2083
Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr
650 655 660

ttg gat cag cag ggt agc att taatacctat gattatgcga agg 2127
Leu Asp Gln Gln Gly Ser Ile
665

<210> 576

<211> 668

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu
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20 25 30

Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
50 55 60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
65 70 75 80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
85 90 95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
100 105 110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
115 120 125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
130 135 140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
145 150 155 160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
165 170 175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
180 185 190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
195 200 205

002290.062000

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
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 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
 225 230 235 240
 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
 245 250 255
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
 370 375 380
 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
 385 390 395 400
 Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
 405 410 415
 Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
 420 425 430
 Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
 435 440 445
 Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
 450 455 460
 Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
 465 470 475 480
 Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
 485 490 495
 His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
 500 505 510
 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
 515 520 525
 Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln

0500237.042300

105

110

115

gca taattttctt tactgcgcta aac
Ala

477

<210> 580
<211> 118
<212> PRT
<213> *Corynebacterium glutamicum*

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20 25 30

Gly Gly Glu Val Glu Val His Tyr Val Gly Val Asp Phe Glu Thr Gly
35 40 45

Glu Glu Phe Asp Ser Ser Trp Asp Arg Gly Gln Thr Ser Gln Phe Pro
50 55 60

Leu Asn Gly Leu Ile Ala Gly Trp Gln Glu Gly Ile Pro Gly Met Lys
65 70 75 80

Val Gly Gly Arg Arg Gln Leu Thr Ile Pro Pro Glu Ala Ala Tyr Gly
85 90 95

Pro Glu Gly Ser Gly His Pro Leu Ser Gly Arg Thr Leu Val Phe Ile
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<223> RXA00568
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Val Lys Ser Ser Val
1 5

gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt 163
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe
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tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag 211
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln

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atc gac gca cgc ttc ggc cgt ggt gcg gtt ctg gag cag gtt gtc aac Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn 55 60 65			307
gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile 70 75 80 85			355
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gag ctc gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu 105 110 115			451
ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val Pro Ala Ile Lys Ala 120 125 130			499
gac gaa gag gca atc gaa gca gag ctc gag acc ctg cgt gca cgt ttc Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr Leu Arg Ala Arg Phe 135 140 145			547
tcc acc ttg aag gat cac aac cac aag ctg aag aag ggt gag ttc gtc Ser Thr Leu Lys Asp His Asn His Lys Leu Lys Lys Gly Glu Phe Val 150 155 160 165			595
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ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu 265 270 275			931

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 Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala Ala Ala Leu Gly Glu
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gct gac ttc gct ctg cca cag tcc atc gtt gac gag cag gca cac tcc 1027
 Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp Glu Gln Ala His Ser
 295 300 305

cag ctg cac cag ctc ctc ggc gag ctt gca cac gac gat gct gca ctg 1075
 Gln Leu His Gln Leu Leu Gly Glu Leu Ala His Asp Asp Ala Ala Leu
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 Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg Glu Glu Phe Asp Lys
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aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg 1171
 Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu
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gac acc ctc tct gag gtt gag gag cct gag gtt tcc cag cag gag ctc 1219
 Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu
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 Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn
 375 380 385

cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctc ttc 1315
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 Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val
 410 415 420

aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc 1411
 Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe
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<212> PRT

<213> Corynebacterium glutamicum

<400> 582

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 20 25 30

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260					265					270					
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Ala	Ala	Leu	Gly	Glu	Ala	Asp	Phe	Ala	Leu	Pro	Gln	Ser	Ile	Val	Asp
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325					330					335					
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340					345					350					
Thr	Gln	Leu	Phe	Leu	Asp	Thr	Leu	Ser	Glu	Val	Glu	Glu	Pro	Glu	Val
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Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr
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Gly Met Asp Pro Asn Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln
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Ile Ala Asn Leu Phe Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln
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<212> DNA

<213> *Corynebacterium glutamicum*

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<222> {101}..(409)

<223> RXN03040

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Met Ser Xaa Gly Asp
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aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg 163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly
10 15 20

ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct 211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala
25 30 35

gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca 259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro
40 45 50

acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc 307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe
55 60 65

ttc cgg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg 355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro
70 75 80 85

atc tat aac cct aac ggt gtg acc tcc agc gag tct tct ntc aga act 403
Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu Ser Ser Xaa Arg Thr
90 95 100

002290.002300

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Val Phe

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His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn
35 40 45
Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu
50 55 60
Ala Leu His Arg Phe Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp
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Gly Gly Pro Ile Pro Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu
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Ser Ser Xaa Arg Thr Val Phe
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<211> 835
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(835)
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Met Arg Ser Asp Val 5
1
atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu 10 15 20
gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc 211
Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr 25 30 35
ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att 259
Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile 40 45 50

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 Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro
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ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt 355
 Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser
 70 75 80 85

gaa ttt ttt ggt gga gcc atc tat tgg cac cca gac aca ggc gct tat 403
 Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr
 90 95 100

gca gtg acc ttg gac ggt ttg cga cag tgg ggg acc ttg aac tgg gaa 451
 Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu
 105 110 115

tca ggg cca ttg ggg tac cca acc tct ggt ccg atg gat aca aac tat 499
 Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr
 120 125 130

ccc ctt act cag cga cag act ttt caa ggt ggt gac aac tac tac aac 547
 Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn
 135 140 145

cca ttg act ggc ggt gct gtg tgg ggc gat att aaa cag cgc tac gaa 595
 Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu
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gaa ctt ggc ggc tgc aat cat gcc att ggc atc ccg atc act aat gag 643
 Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu
 170 175 180

cta cct agc ggt act gag tat ttt tac aat aat ttc tcc aat gga aca 691
 Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Ser Asn Gly Thr
 185 190 195

att tgc tgg cga aat gat cgt cag aca cgg ttt atg tat ttg gct acg 739
 Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr
 200 205 210

cag cgg gtg tgg gat gcg ttg ggt cgg gag acg ggt cgt tta ggt ttt 787
 Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe
 215 220 225

cct gaa gca gat gaa aca cct gag gtt tct ggt cta ttc cat gtg gcg 835
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<210> 586

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

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0002250-69920950

Leu Met Ala Thr Thr Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser
 35 40 45
 Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu
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 Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly
 65 70 75 80
 Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro
 85 90 95
 Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly
 100 105 110
 Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro
 115 120 125
 Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly
 130 135 140
 Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile
 145 150 155 160
 Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile
 165 170 175
 Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn
 180 185 190
 Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe
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 Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr
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<212> DNA

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1	5	
ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc		163
Phe Gln Gly Asn Ala Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly	10	20
gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc		211
Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val	25	35
tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca		259
Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro	40	50
tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag		307
Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu	55	65
gca gca gca agc ctg gaa acc acc gtc ctg tgc atc tcc aag gat		355
Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp	70	85
ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac		403
Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn	90	100
gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc		451
Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly	105	115
atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc		499
Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val	120	130
atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat		547
Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp	135	145
gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac		595
Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn	150	165
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06987

<213> Corynebacterium glutamicum

<400> 590

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35 40 45Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
50 55 60Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
65 70 75 80Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
85 90 95Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
100 105 110Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
115 120 125Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
130 135 140Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
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<212> DNA

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<223> RXN01676

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Met Ile Leu His Gly
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Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
10 15 20ggc ggc gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc 211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
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<213> *Corynebacterium glutamicum*

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Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
35 40 45

Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
50 55 60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
65 70 75 80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
85 90 95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
100 105 110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
115 120 125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
130 135 140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
145 150 155 160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
165 170 175

Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
180 185 190

Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
195 200 205

Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
210 215 220

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Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
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<213> Corynebacterium glutamicum

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<222> (101) .. (721)

<223> RXN00380

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cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta	10 15 20	163
Leu Ala Ala Thr 10 Gly Cys Val Thr 15 Leu Ser Gly Leu Ala Leu Val 20		
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc gcc	25 30 35	211
Ala Cys Ser 25 Asp Ser Thr Ala Gly Thr Asp Ala Val 35 Val Gly		
gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac	40 45 50	259
Gly Thr Phe 40 Gln Phe His Ser 45 Asp Gly Lys Met Glu 50 Ile Phe Tyr		
gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc	55 60 65	307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu	55 60 65	
atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt	70 75 80 85	355
Met Glu Glu Gly Thr 75 Ile Asn Leu Ser Asp Phe Glu Asn Gln Val 85		
gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa	90 95 100	403
Val Ile Leu Asn Ala Trp 90 Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu 100		
tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac	105 110 115	451
Ser Asp Asp 105 Leu Gln Ile Ile His Glu Glu Leu Ala Ala Gly Lys 115		
ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac	120 125 130	499
Gly Asp Thr 120 Pro Gly Gly Thr 125 Val Leu Gly Ile Asn Val 130 Arg Asp Tyr		
tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac	135 140 145	547
Ser Arg Asp Ile Ala Gln Asp 140 Phe Val Thr Asp Asn Gly Leu Asp Tyr	135 140 145	
cca agc att tac gat cca ttt atg aca gca gca tcc ctc ggt ggt	150 155 160 165	595
Pro Ser Ile Tyr Asp 155 Pro Phe Met Thr Ala Ala Ser Leu Gly Gly 165		
gtt ccc gca tgc gtg atc cca acc acc atc gtg ctg gat aaa cag cac	170 175 180	643
Val Pro Ala Ser Val 170 Ile Pro Thr Thr 175 Val Leu Asp Lys Gln His 180		
cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg	185 190 195	691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu	185 190 195	
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Leu	Asp	Lys	Gln	His	Arg	Pro	Ala	Ala	Val	Phe	Leu	Arg	Glu	Val	Thr
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Ser	Lys	Asp	Val	Leu	Asp	Val	Ala	Leu	Pro	Leu	Val	Asp	Glu	Ala	
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Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg
250 255 260

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Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala
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115 120 125Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe
130 135 140Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys
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 Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg
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gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt 547
 Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val
 135 140 145

tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca cgc atg gaa 595
 Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu
 150 155 160 165

aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc 643
 Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile
 170 175 180

gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac 691
 Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr
 185 190 195

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Trp	Asp	Arg	Glu	Lys	Ala	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly		
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att	gct	gtc	atc	cgc	gtt	ggt	gca	gca	act	gaa	acc	gaa	gtc	aac	gac	1267
Ile	Ala	Val	Ile	Arg	Val	Gly	Ala	Ala	Thr	Glu	Thr	Glu	Val	Asn	Asp	
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Arg	Lys	Leu	Arg	Val	Glu	Asp	Ala	Ile	Asn	Ala	Ala	Arg	Ala	Ala	Ala	
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caa	gaa	ggc	gtt	atc	gct	ggt	ggc	ggt	tcc	gct	tgt	cag	atc	gct		1363
Gln	Glu	Gly	Val	Ile	Ala	Gly	Gly	Gly	Ser	Ala	Leu	Val	Gln	Ile	Ala	
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Glu	Thr	Leu	Lys	Ala	Tyr	Ala	Glu	Glu	Phe	Glu	Gly	Asp	Gln	Lys	Val	
				425				430					435			
ggc	gtt	cgc	gca	ctg	gct	act	gct	tgt	ggc	aag	cca	gcg	tac	tgg	atc	1459
Gly	Val	Arg	Ala	Leu	Ala	Thr	Ala	Leu	Gly	Lys	Pro	Ala	Tyr	Trp	Ile	
				440			445					450				
gcc	tcc	aac	gca	ggt	ctt	gac	ggc	tct	ggt	ggt	ggt	gca	cgc	act	gct	1507
Ala	Ser	Asn	Ala	Gly	Leu	Asp	Gly	Ser	Val	Val	Val	Ala	Arg	Thr	Ala	
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gct	ctg	cca	aac	ggc	gag	ggc	ttc	aac	gct	gca	act	tgt	gaa	tac	gga	1555
Ala	Leu	Pro	Asn	Gly	Glu	Gly	Phe	Asn	Ala	Ala	Thr	Leu	Glu	Tyr	Gly	
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Asn	Thr	Asp	Ser	Thr	Trp	Asp	Arg	Glu	Lys	Ala	Glu	Glu	Arg	Leu	Ala
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Lys	Leu	Ser	Gly	Gly	Ile	Ala	Val	Ile	Arg	Val	Gly	Ala	Ala	Thr	Glu
	370					375					380				
Thr	Glu	Val	Asn	Asp	Arg	Lys	Leu	Arg	Val	Glu	Asp	Ala	Ile	Asn	Ala
					390					395					400
Ala	Arg	Ala	Ala		Gln	Glu	Gly	Val		Ile	Ala	Gly	Gly	Gly	Ala
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Leu	Val	Gln	Ile	Ala	Glu	Thr	Leu	Lys	Ala	Tyr	Ala	Glu	Glu	Phe	Glu
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Gly	Asp	Gln	Lys	Val	Gly	Val	Arg	Ala	Leu	Ala	Thr	Ala	Leu	Gly	Lys
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Pro	Ala	Tyr	Trp	Ile	Ala	Ser	Asn	Ala	Gly	Leu	Asp	Gly	Ser	Val	Val
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Val	Ala	Arg	Thr	Ala	Ala	Leu	Pro	Asn	Gly	Glu	Gly	Phe	Asn	Ala	Ala
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Thr	Leu	Glu	Tyr	Gly	Asn	Leu	Ile	Asn	Asp	Gly	Val	Ile	Asp	Pro	Val
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Lys	Val	Thr	His	Ser	Ala	Val	Val	Asn	Ala	Thr	Ser	Val	Ala	Arg	Met
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Val	Leu	Thr	Thr	Glu	Ala	Ser	Val	Val	Glu	Lys	Pro	Ala	Glu	Glu	Ala
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ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg 1795
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 585 590 595

gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat 1939
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Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
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Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
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Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala
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Leu	Ser	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg
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Thr	Lys	Thr	Pro	Phe	Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val
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Lys	Arg	Leu	Leu	Ser	Glu	Pro	Asn	Val	Thr	Glu	Ala	Thr	Pro	Val	Tyr	
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 Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly
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atc tac ctt gtt ggt gga gga tcc tgc ctc cca ctc gtt tcc agg ttg 1075
 Ile Tyr Leu Val Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu
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 Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser
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 Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu
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 His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro Leu Ile Ala Pro Asp
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 Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr Lys Ala Val His Asn
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 Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp Asn Gly Val Ala Ser
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 Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
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 Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
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 Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
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 Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
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 Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
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 Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Thr Phe Asp Ser Ser
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 Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
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 Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
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 225 230 235 240
 Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
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 Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Ile Thr
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 Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
 290 295 300
 Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Ser Ser Leu Pro
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 Leu Ile Ala Pro Asp Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr
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 Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr
 405 410 415
 Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile
 420 425 430
 Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile
 435 440 445
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 Met Ile Phe Glu Leu
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 Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
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 Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
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 Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
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Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
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Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
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Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
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Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
 115 120 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
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Thr Asp Ala Leu Tyr Asp Arg Asp Ala Leu Glu Asp Arg Val Glu
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Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
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Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
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Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
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Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln																		
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Pro	Ser	Thr	Val	Leu	Pro	Asn	Trp	Ala	Phe	Phe	Val	Glu	Cys	Glu	Ile	
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Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu	
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 Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
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 Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
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 Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
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 Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
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 Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
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 Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
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 Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
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 Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
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 Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
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 Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
 210 215 220

 Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
 225 230 235 240

 Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
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 Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
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 Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe
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Phe	Glu	Ser	Ala	His	Pro	Glu	Val	Val	Ile	Glu	Tyr	His	Glu	His	Val			
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 Pro Glu Val Ser Gly Leu Phe His Val Val Asn Phe Ala Glu Arg Gly
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Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val
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Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala Pro Gln Trp Val Thr
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 Glu Gln Leu Glu Asp Phe Glu Ser Ala His Pro Glu Val Val Ile Glu
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 Tyr His Glu His Val Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro
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 Cys Glu Ala Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu
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 Asp Ala Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro
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 Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu
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 Phe Val Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala
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 Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser
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 Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro
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 225 230 235 240
 Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu
 245 250 255
 Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu
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 Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile
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 Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro
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 Asp Thr Pro Leu Gly Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu
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 Ser Leu Glu Gln Glu Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp
 385 390 395 400
 Ala Leu Thr Trp Ile Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe
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 Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg
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 Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp
 485 490 495
 Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met
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 Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro
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 Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys
 530 535 540
 Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala
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 Pro Gln Trp Val Thr Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala
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 Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr
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Met Leu Ala Ile Ile
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Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala Ala Ala Gly Thr Gln
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Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro Val Ala Val Gln Asn

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Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val Val Val Glu Asp Ala
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gca gtc acc gcc cag ggt gaa ggc gga ggc gct cgc acc gtc aag gaa 307
Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala Arg Thr Val Lys Glu
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Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala Leu Thr Trp Thr Gly
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Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val Asn Glu Asp Gln Gly
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Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala Asp Ala Ala Ala Ala
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Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp Ala Ala Glu Ala Ala
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cca gca gca gaa cct gca cca gct gaa gca cca gtc gag gaa gct cct 643
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170 175 180

gca cct gtc gca gaa cca gca cca gct gct gaa cct atc gct gag cca 691
Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu Pro Ile Ala Glu Pro
185 190 195

Figure 1. Schematic diagram of the experimental setup.

739	Val	Ala	Asp	200	Tyr	Ser	Ala	Asn	Val	Asp	Gly	Leu	Ala	Pro	Leu	Pro	Ser	Asn
787	Tyr	Gly	115	Asp	Ile	Gln	Pro	Val	Ala	Asp	Val	Asp	Asp	Gly	Leu	Ala	Asn	Ala
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883	Ala	Asp	Thr	Asp	Gly	Met	Pro	Lys	Val	Ile	255	Tct	ogt	gct	ggt	tgg	ggt	260
931	Ala	Asp	Glu	265	Ser	Leu	Arg	Cys	Ser	Asn	270	Pro	Thr	Ile	Asp	Gly	Val	275
979	Ser	Ala	Ile	280	Thr	Ile	His	His	Act	Thr	Ala	Gly	Ser	Asn	Asn	Tyr	Thr	Glu
1027	Ala	Gln	Ala	295	Ala	Gln	Val	Arg	Ser	Ala	Tyr	Ser	305	Tac	Ser	His	Gcc	aag
1075	Asn	Leu	Gly	310	Trp	Cys	Asp	Ile	Gly	Tyr	Gln	Ser	320	Ttg	Gtt	Val	Asp	325
1123	Gly	Asn	Ile	330	Tyr	Glu	Gly	Arg	Ala	Gly	Gly	Met	335	acc	aat	Gct	Gtt	340
1171	Gly	Gct	Ala	345	His	Gly	Gly	Phe	Asn	Gln	Asn	Act	350	tgg	Gca	atc	Tcc	atg
1219	Ile	Gly	Asp	360	Tat	Tcc	Tac	Aac	Gct	Ccc	Cct	Cag	365	Gaa	acc	atc	Aat	Gct
1267	Val	Gly	Glu	375	Gag	Ctt	Gct	Ggt	Tgg	Cgt	Gca	Aag	380	Gtt	Gcc	Ggt	Ttc	385
1315	Thr	Gly	Thr	390	Act	Thr	His	Tyr	Tcg	Gag	Ggt	Act	400	Tct	Tac	Gcg	Aag	Tac
1363	Ser	Tyr	Gly	410	Acc	Cga	Gtg	Tca	Ctt	Cct	Aat	Atc	415	Ttg	Gct	Cac	Cgc	420
1411	Val	Gly	Leu	425	Thr	Ala	Cys	Pro	Ggc	Gat	Gct	Ggc	430	Tat	Gcg	Caa	Atg	435

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Val Val Glu Asp Ala Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala
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Arg Thr Val Lys Glu Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala
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Leu Thr Trp Thr Gly Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu
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Gln Glu Asp Gly Thr Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val
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Asn Glu Asp Gln Gly Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro
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Thr Asn Lys Ile Gln Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala
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Asp Ala Ala Ala Ala Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp
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Val Glu Glu Ala Pro Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu
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Pro Leu Pro Ser Asn Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp
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Asp Gly Leu Asn Ala Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val
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Leu Pro Thr Ser Asn Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp
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Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly
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Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser
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Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser
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Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp
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00602839.062300

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									Met	Thr	Thr	Pro	Leu									
									1				5									
cgc	gta	gcc	gtc	atc	gga	gct	ggc	cct	gct	ggc	att	tac	gca	tcc	gac	163						
Arg	Val	Ala	Val	Ile	Gly	Ala	Gly	Pro	Ala	Gly	Ile	Tyr	Ala	Ser	Asp							
				10					15					20								
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Leu	Leu	Ile	Arg	Asn	Glu	Glu	Arg	Glu	Val	Phe	Val	Asp	Leu	Phe	Glu							
				25				30					35									
caa	atg	cct	gca	ccg	ttc	gga	ctc	atc	cgt	tac	ggc	gtt	gct	cca	gac	259						
Gln	Met	Pro	Ala	Pro	Phe	Gly	Leu	Ile	Arg	Tyr	Gly	Val	Ala	Pro	Asp							
				40			45					50										
cac	cca	cgc	atc	aag	ggc	atc	gtt	aag	tcc	ctg	cac	aac	gtg	ttg	gac	307						
His	Pro	Arg	Ile	Lys	Gly	Ile	Val	Lys	Ser	Leu	His	Asn	Val	Leu	Asp							
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Lys	Pro	Arg	Leu	Arg	Leu	Gly	Asn	Ile	Glu	Ile	Gly	Lys	Asp	Ile								
						75			80					85								
acc	gtc	gaa	gaa	ctc	cgc	gac	tac	tac	gat	gca	gtc	gtg	ttc	tcc	acc	403						
Thr	Val	Glu	Glu	Leu	Arg	Asp	Tyr	Tyr	Asp	Ala	Val	Val	Phe	Ser	Thr							
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Gly	Ala	Val	Ala	Asp	Arg	Asp	Leu	Asn	Ile	Pro	Gly	Ile	Glu	Ala	Glu							
				105				110				115										
ggc	tcc	ttc	ggt	qcc	ggc	gaq	ttc	gtt	ggc	ttc	tac	gac	ggc	aac	cca	499						

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the experimental group. The experimental group was divided into two subgroups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the experimental group. The experimental group was divided into two subgroups: the control group and the experimental group.

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 ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc 643
 Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Arg Ser
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 cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac 739
 Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His
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 tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac 787
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 Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro
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 His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln
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 Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp
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002300-66200000

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 Ser Asp Leu Glu Gly Ser Trp Gly Ala Gly Glu Phe Val Gly Phe Tyr
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 Thr Trp Asp Met Gln Ser Val Tyr Arg Ala Val Gly Tyr Arg Ser Asp
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APPENDIX A: DNA SEQUENCES

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>RXA00019-upstream
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>RXA00019

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>RXA0019-downstream
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>RXA0046-upstream
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>RXA0046
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>RXA0046-downstream
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>RXA0053-upstream
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>RXA0053

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>RXA00053-downstream
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>RXA00057-upstream
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>RXA00057
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>RXA00057-downstream
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>RXA00069-upstream
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>RXA00069
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>RXA00102-upstream
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>RXA00102
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>RXA00107-upstream
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>RXA00107
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>RXA00107-downstream
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>RXA00124-upstream
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>RXA00124
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>RXA00125
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>RXA00209
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>RXA00210-upstream
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>RXA00210
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>RXA00210-downstream
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>RXA00217-upstream
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>RXA00217
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>RXA00217-downstream
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>RXA00227-upstream
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>RXA00227
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>RXA00263
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>RXA00263-downstream
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>RXA00265-upstream
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>RXA00265
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>RXA00280-upstream
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>RXA00280
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>RXA00304-upstream
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>RXA00314

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>RXA00758-downstream
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>RXA00824-upstream
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>RXA00824
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>RXA00824-downstream
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>RXA00896-upstream
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>RXA00896
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RXA00927-upstream
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>RXA00927
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>RXA00928-upstream
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>RXA00928
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>RXA00928-downstream
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>RXA00929-upstream
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>RXA00929
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>RXA00935
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>RXA00937

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>RXA00938-upstream

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>RXA00938

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>RXA00938-downstream

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>RXA00966-upstream

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>RXA00966

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>RXA00968

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>RXA00975-upstream

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>RXA00975

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>RXA00976-upstream

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>RXA00976

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>RXA00976-downstream

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>RXA00985-upstream

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>RXA00985

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>RXA00998-upstream

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>RXA00998

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>RXA00998-downstream
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>RXA01020-upstream

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>RXA01020

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>RXA01020-downstream
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>RXA01061-upstream

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>RXA01061

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>RXA01061-downstream
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>RXA01072-upstream

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>RXA01072

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>RXA01124
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>RXA01179-upstream
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>RXA01179
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>RXA01199-upstream
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>RXA01199
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>RXA01223-upstream

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>RXA01223

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>RXA01223-downstream

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>RXA01226-upstream

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>RXA01226

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>RXA01228-upstream

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>RXA01228

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>RXA01252-upstream

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>RXA01387

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>RXA01388-upstream

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>RXA01388

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>RXA01388-downstream

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>RXA01398

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>RXA01431-upstream

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>RXA01431

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>RXA01431-downstream

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>RXA01432-upstream

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>RXA01432

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>RXA01432-downstream

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>RXA01433-upstream

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00602539-062300

>RXA01433

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>RXA01443-upstream
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>RXA01443
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>RXA01490

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>RXA01490-downstream

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>RXA01496
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>RXA01541
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>RXA01556
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>RXA01725
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>RXA01726
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>RXA01730
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>RXA01784

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>RXA01837
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>RXA01841-upstream
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>RXA01841

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>RXA01852-upstream

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>RXA01862

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>RXA01926

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>RXA01954-upstream

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>RXA01954

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>RXA01975
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>RXA02167
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>RXA02204

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RXA02228-upstream

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RXA02243-upstream
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>RXA02252-upstream
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>RXN02543-upstream
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>RXN03070
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>RXN03102

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>RXN03118

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>RXN03121-upstream

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>RXN03121

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09502839.062700

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>RXN03130

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>RXN03130-downstream

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>RXN03161-upstream

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>RXN03161

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>RXN03165

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>RXN03168-upstream

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>RXN03168

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>RXN03169

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>RXS00061 - upstream

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>RXS00061

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>RXS00061 - downstream
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>RXS00170 - upstream

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>RXS02308
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>RXS02308 - downstream
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>RXS02476 - upstream
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>RXS02476
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>RXS02476 - downstream
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>RXS02641 - upstream
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>RXS02641
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>RXS02641 - downstream
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>RXS02650 - upstream
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>RXS02650
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 GAGCAGGTCACTGAGATCCGTGATGTAAGCGCAAGCTGGTTAAGCGTAAGTTGCTGCCGGGCTACGTT
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 GTGGGTAACGAGGGCAGTCAACTCTGTGAAGCACCAGGATGTTGCGAAGTCTTGTGATGCTCAGGAG
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>RXS02760 - downstream
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>RXS02830
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>RXS02830 - downstream
TAACCTCTATTATG

>RXS02990 - upstream
GAAGACTAAGCACCAGTTTAAACAAGCAGGGACAATCCACACACTTAAACCATGATGTGGCTTGTTC
TGCTTTTCGTCAACGAAGGGCAACAACGCG

>RXS02990
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ACGCGCGCGGCGGTGGCGCTGAAAAGGCGCGCTCAGAGACCAAGATTCCGAGGACCGCGCCGATAC
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CTTGCGCGGGAGCGCTAGACGCGCAATCGAGGATTGAAAAAC

>RXS02990 - downstream
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>RXS03098 - upstream
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>RXS03098
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>RXS03098 - downstream
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>RXS03175
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GATGTGCGCAGTAACCGTGGCATCTCTTTACCTCCCTCAGGTTACGCGGCACTGACGACGAGGATGAA
AAGTACCGCTTCTCGATGAATCGAAGGGTTCTTGACACGCGCTAAAGAAGCGCTCCACATGGTC

Appendix B: AMINO ACID SEQUENCES

> RXA00005 (1-1608, translated) 536 residues
 MHHEQEPEGCE VGIIRRTIPEE SRTAFLDMIN QMGSLGAAST AVGVSEFTGR KWAKAAGVKL
 TRGPRGGNAF DTAEKLEIAA SMLEKGC LPR EIGEYVGMTR ANISLWRKQG PDKLRQRAAT
 LRTGKRAAEF IHAPVMGPYY GPRTLHQVLR EDYITLFDL SALGLPAQVC GALLHLAPP
 SLRFSYMSCV VPLFADEIKV VQGGRSLSE EKMMIQRFDH TGVSAAEIGR RLGRQCRTIS
 RELRRGQDDD GRYRARDSYE GAIRKLARPK TPKLDANRRL RAVVVEALNN KLSPEQISGL
 LAPEHANDSS MQISHETIYQ ALYVQGGKAL RDELKVEKFL RTGRKGRKQP SKLPSRGKFW
 VEGALISQRP YGAVDRAVPG HWEGDLVIG ENQATALVTL VERTSRLTLI KRLGVNHEAS
 TVTDALVEMM GDLPAQLRRS LTWDQGVEMA EHARFVSVTK CPVFFCDPHS PWQRGSNENT
 NGLVRDFEFK GTNFAKVSDE EVQRAQDLLN YRPRKMHGFK SATQVYEKIV VGASTD

> RXA00011 (1-357, translated) 119 residues
 VNITDSAVRL THIPTGIVVT CQNEKSIQN KASAMRVLQA KLLERKRQEE RAEMDALGAG
 GNASWGNQMR SVYLFHPYQM KDLRTNFEVN DPQKVLDDGI DGLLEAGIRW RMAESQSAE

> RXA00012 (1-876, translated) 292 residues
 MRPEFSAELS ELDSTLTITIE KVLNPEQMSD RVRELEAQAA DPSLWDDPDH AQQVTSLSH
 VQAEIRKINT LRQRIEDLPI MVELAEEEDG DTSIAEEELA DLRLSLDALE VKTMLSGEYD
 AREAVINRS GAGGYDAADW AEMLMRMYTR WAEKNNGHKV TYDTSYAEBA GIKSATFVVH
 GDYMYGQLSV EOGAHRVLRI SPFDNQGRQ TSFAEVEVLV VVEKVSIDI PDADVRVDVY
 RSSGPGGQSS EHHRLCRAPD PHPNRHRGDL PKREITDPKQ GIRDACSPGK TA

> RXA00016 (1-894, translated) 298 residues
 VTRFRFVDDA RKTYSVKRIC DVLKLNRSY YKWKSTAFTR EKRLSDAIL GVQVKTVFTT
 HSGCYGAKRI AAELKDQIGH DLANHKKRVAR IMRSLKLFQY TKKRKVTTTV PDKTKTVFPD
 LVGRKFTADK PNQLYVGDI YLPQDGSNM YLATVIDCYS RRLVGFSIAD HMRTSLVQDA
 LLMAKDQRGN LKGAIFHSDH GSVYTSHAFO ETCKKLGIRO SMGSIGTSAD NALAEFNA
 MKREVLDQSK TFENQLCCRR DVFRWCTRYN TVRRHWCYRY LAPVVEERG PAIRLAS

> RXA00017 (1-294, translated) 98 residues
 MPKRTYTEEF KRDAVALYEN SAGTSIQKTA NDLGINRMFL KNWITYKGAN STPHGANTAT
 ALSEAEIRIQ LEKENALLRE ERDILRKAAK YFAEETNW

> RXA00019 (1-1860, translated) 620 residues
 MTVTSPAAAL LSDMSYVDII KKKRGWTFE FHSTINTGET TPLPDSDBRA TALIHDIHTK
 AQEITITITDF DMDGISAGVI AYAGLAELGA QVNMVVPDYR GERNVTSADI DRALELTICG
 SLIITCDVGI GSHEGIARAH ERSIAVLVTD HHMEVEPCQA DVVLNPNRDI SDYPNKDIPAT
 AQVIFATLSD YARRYRADKI IDINLLAVFS GIGALADVMP LTRDTRPTVK QAIALLRLAI
 PQVSKNRFEG WDTYAARSVN PDTSTLMHIV NASQHDHREI AAFQGISILL GELIAQKKLV
 NIDNISESFI GFTLGPMEFA TRRVGDMMDH SFLVFAPHAH LASQPSMNPEN RHAATSRID
 NNERRKELSK SSYAAVHSSD QPYAPFVWLS EAPSGILGLI ASQLTRESDD PAIVINPDTL
 SGSARSPEWA PIITQVNTLS AQHGGGIHAA GHEYACGMRF DNHDDIVTFV ATFLDALDKNT
 PREAQPADLH LVDIDHARVP LDNPSLTQEL STVDAVDAV QLLVLIDQLD QLQPFPGHGT
 YPRIDVTRF AETEFKVMGQ HHQHLKVITH SGLTLLWNK AQQLDEIAQS ELVTMSVELD
 VNMFRGFISF QGIVSACTVI

> RXA00046 (1-696, translated) 232 residues
 MDLNTQRSKL YAQLOQLIV SVQAPDGHAM RDHTLTHVA AACVDGGAPA IRCGGYGGLE
 DIRISINRVD VPVFGLTKEG SEGVYITPTR DSVRAVAESG ATVVVCADAT RRPDGGSTFA
 ELVTVAHDSG ILLMADCATP EEVLSAHKAG ADFVSTTLG YTEHREKTVG PDFDCLEAR
 ELVPDAFLIG EGRFSNPADV AHGRLIGANA IIVGTGITDP GFITGQFASL LH

RXA00053 (1-393, translated) 131 residues
 VKKRINVTGA VLVKENRILA AQRGPEMSLP GYWEFFPGGKI EQGETPEASL ARELKEELL
 DATVGEHLTT TEHEYDFGIV VLSYFCTLN DAEPQLTEHA EIRWVAGHEL ESLEWAPANI
 PAVKLIVLEQL A

> RXA00057 (1-99, translated) 33 residues

LGSIGTSADN ALAESFNAAL RREVLQDSKT FAN

RXA00069 (1-1383, translated) 461 residues
 VAQSSIITDV VNLCKRRGLV YPCGEIYGGT RSAWDYDGLG VELKENIKRK WWRSMVTSRSP
 DVVGVDTSVI LPRQWVWTSG HVEVETDPLV ESLNTHKRYR ADHLLQEQYEE KHGHPPPVNGL
 ADINDPETGQ PGNWTEPKAF SGLLKTFLGP VDDEEGLHYL RPETAQKIFV NFKNVMNSTR
 MKPPFGIANI GKSFRNEITP GNFIPTRTREF EQMEMEFFVK PGEDEEWHQV NIDTRLQWYI
 NLGIKPENLR LYEHQPEKLS HYSKRTVDIE YAFNFANTKW GELEGIANRT DYDLRVHSEG
 SGEDLSFDDQ ETNERWIPFV IEPAGLGRA MMFLMDAYH EDEAPNSKGG VDKRVVLKLD
 RRLAPVKVAV LPLSKKDTLT PLAELKLAEL REFVNVVDYT SGAIGRRYRR QDEIGTFFCV
 TVDFDSLEDN AVTVRERDTM EQVRVPLDEL QGYLAQRLIG C

RXA00102 (1-768, translated) 256 residues
 MPEGDSVFQL SRKLQFMRGR EVLETSLRVP SVALHDFDTGO TVNRVWPYKG HLFMQFGEEI
 LHTHLMEGT WAVHRKGDWR RKPGHRTARV LVLSENIEV GHSGLFVVRV PANRYSEEIA
 YLGPDLVAEE FDIINTARNNI ASNPSTRTIGE ALLDQSNLAG VGNEYRAETC KFMGVHPATQ
 VGVVDVEKAL KITRRLMWN RNSPIRVTTG VRRAGESTYV FGRNNKPCRR CRTPIVKAEI
 GERIHWPCPR CQPLNS

> RXA00107 (1-237, translated) 79 residues
 MSNVTIYATD WCPYCRSLK GLDQOEYDLI DVDQDEEAGE WVKSVNDGNR IVPTVRYSDG
 THATNPLAAE VAKIEALA

> RXA00124 (1-732, translated) 244 residues
 MTKDVHYEVD ERKKTIVGKE EGVYVEDQL GIDNLYAPEH SQLVSYLNA IKAQELFTRD
 KDYIVRNGEV MIVDGTGRV LAGRRYNEGM HQATEAKERV EIKNENQTLA TTVTLQNYFRL
 YTKLAGMTGT AETEAALNQ YTKLDVIAIP TNRPNQREDL TDLVYKTQEA KFMGVHPATQ
 ERTEKGQPV L VGTVSVERSE YLSQLLTKRG IKHNVLNKHA HEQEAQIVAQ AGLPGAVTVA
 TNMA

> RXA00125 (1-765, translated) 255 residues
 VFGLSKVLVR GEGRAVKRLH KIADQVIALE DKFANLTDEE LKAKTAEFKE RIAGGEGLDE
 IFLEAFATAR EAAWRVLGQK HYHVQIMGGA ALHFGNVAM RTGEGKTLTC VLPAYLNALE
 GKGVHVVTVN DYLAKRDAEM MGRVHRYLGL EVGVILSDMR PDERREAYAA DITYGTNNEL
 GFDFYLRDNMA ESKLDLVQRG HNYAIVDEV D SILIDEARTP LIISGTSRRH IAVLQRLRTD
 RPTHQDQGRSL RSRRT

> RXA00138 (1-561, translated) 187 residues
 VATTADFKNQ LVLKNEGLKQ QIEFQHVKP GKGPAFVRTK LKDVTVTGKI DKTWNAGVKV
 ETATVDRRDV TYLYNDGTSF IVMDDKTFEQ YELSPDAFGD AGRFLENNMR YQVSFHGEA
 LFGLPLSVSD LRVEHTDPGL QGDRSTGGTK PATLETGAEI QVFLFIETGN VLKVDTRDGS
 YLSRVNN

> RXA00172 (1-450, translated) 150 residues
 MFGSSFKQET TNPSQRVS YLRVSSDQNL ARQREAVNHS GHIDREFTDE LSGGAKSHRP
 GLEDCINYL R EDDVLVVASI DRLARSLVDL RVIDRITDK GASVIFLKEN LTFAAGRDDP
 RANMLGILG SFAEFERSII RERQAEGLA

> RXA00184 (1-1173, translated) 391 residues
 MSTVHDEMVG MNTTVKFLHS SLDQIGMTWR FLSDEAQAARF DDDRIRAIK MGKIARKNQC
 EFIVLAGDVF EHNSLEQRTT GRALEALRSL KLPVYLLPGN HDPLTADSLF YRAKDIDGVT
 ILSDTTPHGV APGVEIIGAP LLHKMATS DL VAEALKDLEP TSNVRIAVGH QGAERTTHD
 RADLLDNVT EAKLDGTD YLALGDTHSA QPVGTSKGVW FSGAPETTFD HDLDPDRVGG
 EVNSGKVLIV SASKGDVSVE EVEVGKWTFF ALSKEITSGT DVEDFLDTLQ AYPKSRATVI
 KYGLRGITIL EQNRRLLEGI AGLEDVFASL KPRERTTDLV LEFGEEELAN LDATGYAAEV
 IRELADSVVN GAAPEDDRDA LNLFLRLSRE V

RXA00209 (1-1491, translated) 497 residues
 MTNKYLVEGS ENELTTKTAA ELAGLIHSRE VTSREVTQAH LDRIAAYDGD IHAFHVGQE
 EALNAADDVD KRLDAGEAPA SALAGVPLAL KDVFTTTDA P TTAASKMLEG YMSPYDATVT
 RKIREAGIFI LGKTNMDEFA MGSSTENSAY GPTHNPWDLE RTAGGSGGGS SAALAAQGA P

LAIGTDTGGS IRQPAALNT VGVKPTYGTV SRYGLIACAS SLDQGGPTAR TVLDTALLHE
 VIAGHDAFDA TSVNRPVAPV VQAAREGANG DLKGVKVGUV KQFDRDGYQP GVLEAFHASV
 EQMRSQGAEI VEVDCPHFDD ALGAYYLILP CEVSSNLARF DGMRYGLRAG DDGTRSADEV
 MAYTRAQGF PEVKRRILG TYALSVGYID AYLQAQRVR TLIAQDFAKA YEQVDILVSP
 TPTTAPFKLG EKVTPPLEMY NFDLCTPLN LAGLAGMSLP SGLASDTGLP VQLQLMAPAF
 QDDRILYRGA AFEAGRK

> RXA00210 (1-297, translated) 99 residues
 VPEISRQDVA HLAKLSRLAL TEELEQFAG QIDDIVGYVS AVQNVDAAGV EPMSPHPSIA
 TTMREDVYHK TLDAAALDQ APAVEDGRFM VPQILGEGD

RXA00217 (1-1095, translated) 365 residues
 MRVLAAMSGG VDSAVAASRA VAAGHEVVGV HLALSQDPQT VRESSRGCCS LEDSAADARRV
 CDKLGIPFYV WDFSDRFKED VIDNFIDSYA IGETPNPCLR CNEKIKFAAL LERGIALGFD
 AVVTGHYARL TQPADGGDGY LRRGVDPNKK QSYVLGVLGA HEIEHCMFPV GDTIKPEIRE
 EASAAGFSVA KKPDSYDICE IPDNGTQAFI GKHGMRPGM IVDQEGTHLR EHAGVHEFTI
 GQRKGLDIKA PAADGRPRYV TDIDAKTGTV TVGTRENKLI STIHADRLKF LHPAMDGGID
 CEVQVRHGG VVSCSATIDR DADFVVLNIN EPLQGVARGQ AAVLYLPDAD GDVILSGSTI
 CTES

> RXA00227 (1-798, translated) 266 residues
 MVMQGIIGGRK LAATVLLVRD GIINGRPDVE VYIQERVSTM ANFRATVFP GGGVDSRDFA
 DGHGKEVWRG PSAAEWGVRL GVEPHVAYAL VFAAVRELPE EAGTLLAEHT DSGSLVKNAG
 QYHGVELLE THEMSTLMDL QSENLAIRSD LIVPFARWAS PEGNRQFDT FSVAVEPEG
 QCADGNTSEA SSTGYFFARL ILDGWRAGLL RLVIPTWASL FELSQFKTVE ELLESAQVD
 MSPVLDDAVD NRYAEFYQA MTERF

RXA00263 (1-1308, translated) 436 residues
 MKSTGNIIAD TICRTAELGL TITGASDAGD YTLIEADALD YTSTCEPCSQ PGVFRHHHTHR
 MLIDILPIVGF PTKLFIRLPR YRCTNPCTKQ KYQFAELSCA DHGKKVTHRV TRWILQRIAI
 DRMSVHATAC ALGLGWDLTG QALDMCREL VYNDPHHLGD VYVIGVDEHK WSHNRAKHGD
 GFVTVIDVMT GHRVDSRCPA RLLDVVPGRS ADALRSWLGS RGEQFRNQIR IVSMDFGQGY
 ATASKELIPS ARRVMDPFHV VRLAGDKLTA CRQLRQREKY QRRGLSQDPL YKNRKTLTIT
 HKWLSPPRQE SLEQLWAYDK DYGAALKLAW AYQAIIDCYQ MGNKREAKKK MRTIIDLQLRV
 HKGPNKELAQ LGRSLFKRLG DVLAYFDVGV SNGPVEAING RLEHLRGIAL GFRNLNHYIL
 RCLIHSGQLV HKINAL

> RXA00265 (1-450, translated) 150 residues
 MRSAGHPYID KFFPEPYKNM LELTKTLRKI YPDVLPSTSL IELVNVRSVQ INCGCTCLSL
 HVPARRAGV PEKKLDALAA WQMVDEFTVE EKAALQLAES LTLLESREGH LAARTACSVF
 AEEQVALEW AIIAINAFNR ISIASGHPLL

> RXA00280 (1-501, translated) 167 residues
 VDTMKGDGDD WAAAPNGGAV WGNKGAAGLL LVADKQMLMQ HRAAWTNGND TWALPGGARD
 SHETAESAL REAFETTGIL PDDVEVLDSI VTAGPFPADP ERPELAGNWT YTTVIARTKT
 GETLDTTANE ESELRLWVDI AAVDSLALMP AFAKAWPSLR KLLNTTE

> RXA00304 (1-693, translated) 231 residues
 MTAPSTQDLA TTEREVDPGS RRGQTNPNPS QDLVRVLYNG IGTALLTAE DEVELAQITIE
 VGLYAEHLK NSEPLTRAM KRDLKVLAKD GKARSHLLE ANLRVSVSLA KRYTGGMPLG
 LDLIQENGLG LIRAMEKFDY SKGFKFSTYA TWIRQAITR GMADQSRTR IRPVHLVEQVN
 KLSRIKRELY QHLGREATNE ELAEESGIEE SKIEMLLRQS RDPVSLDMPV G

> RXA00314 (1-1380, translated) 460 residues
 VTLRIFDTGT RTLRDFKPVQ PGHASVYLCG ATPQSSPHIG HRSVAFAFDI LRRWLMKAGL
 DVAFVRNVTD IDDKILTKAS ENGRPNWENV STYERETWT YNTLGVLPSS TEPRATGHVT
 QMIKYMRILI DNGFAYAVDG SVYFDVAAS KAEGSDYGS LSGNRVEDMEQ GEPPNFGKRG
 PQDFALWKAA KPGEPSWPTP WGDGRPGWHL ECSAMATYLL GEQFDIHCG LDLOFPHHEN
 EIAQAAHAGD KPFANYMMNH VWTMAGEKMS KSLGNVLAVP EMLKQVRPVE LRYLYLSAHY
 RSLVYESA LSEAAVGYRR IESFLERVGD VEVGEWTPGF EVAMDEIAPV PKALAEITHNA
 VREGNAALDK GDREAAEKLA SSVRAMTGVL GFDPVEWGS D AGADGKADKA LDVLISSLE

RRATARAENK WAWADEVDRD IADAGIEVVD TADGATWKLO

> RXA00331 (1-357, translated) 119 residues
 MVGHMSNDHP YSPAKRVGNF IFVSGALSD KDQYQVVGRR EAVDAALERM RERLATAGGE
 LKDVVKLTIFY VTDISLREEC NEQPREHFLE GRPARSFVGA SSLPYGATVE IDAIAIMIED

> RXA00333 (1-534, translated) 178 residues
 MAVPEFIVSL REKVGQDPLW LPAVTAVVIR DVPPGSPFHV VPDVLLVKRA DTGEWTPPTG
 ICDPDEQPHV TAVREVKEET GLDVSVEALL GVGAVGPVTY QNGDVASVYM TTMRCVVSGD
 SDEPHVGDDE NVDVAWFIS KMPVTNQFR MVIADAVAQL KHPQGYKPRM GYEKRNRAR

> RXA00454 (1-864, translated) 288 residues
 GDIAFPAFIP VATKATVKTL TPEQIRETGA QAILSNAYHL YLQPGPDIVD EAGGVSAFEN
 WHGPTYTDSG GFQVMSLGSQ FKKVLAMDTT NLTRNDIKAA KKERMALVDE DGVDFKSVID
 GSKHRFTPEV SMQIQHQLGA DIIFAFDELT TLVDITYDYQV ESVERTRRWA QRCLLEHERL
 TQERVVDKPLQ SLWGVVVQGAQ FEDLRRQAVK GLLDLDRQAA DEGRGRFGGG GIGGALEKEN
 LGTIIVGWCD ELPEDKPRHL LGISEPDDL FVAEAGADTF YCVAPTRL

> RXA00458 (1-228, translated) 76 residues
 MAGRYAPSPS GDLHFGNLRT ALLAWLFARS EGKFKLMRVE DIDEQRSFKE SAESQLADLS
 ALGLDWDGDV LYQSTR

> RXA00495 (1-564, translated) 188 residues
 LADTERELAD LVPQATAGDR RALORIMEII HPIVLRYARA RIGGGGRQPTA EDVAQEICLA
 VATSIRNFVD QQRPFMAFVY GIASNKVADA HRAMSRDKST PIEEVETSP DTFTPEDFAL
 VSDGSRNRVE LLDLLSEKAR DILILRVIVG LSAEETAEMV GSTPGAVRVA QHRALTTLRS
 TLEQQENK

> RXA00532 (1-585, translated) 195 residues
 AIVKSKERNP AHVTELALAA GRGDRAALTD FIRETQDDVW RLLAHLGGHE IADDLTQETY
 LRVMASALPRF AARSSARTWL LSLARRVWVD NIRHDMARPR KSIVEYEDTG ATDASNAGIW
 SEWIDVRTLI DALPPERREA LILTQVLGYT YEEAAKIADV RVGTIRSRVA RARADLIAAT
 ATGDSSAEDG KSAQG

> RXA00539 (1-477, translated) 159 residues
 MTSIHDISVT LNDGTETMTA DWAGHLLIIV NVASKCGLTP QYEGQLKLYE EYQDRGFFVI
 GVPCNQFNQD EPGTDAEVCA FAQNQYDVT FLLSKTEVNG EGHAFLYKVL KEATDGSIEE
 WNFEXPLVDA EGNITKRFAP RTEPSAAEVV EAIEENLPI

> RXA00568 (1-1347, translated) 449 residues
 VKSSVEKLSD TRSKITVEVP FSELKPEIDQ AYAALAQQVQ IPGFRKGKAP RQLIDARFGR
 GAVLEQVQVND MLPNRYAQAI EAEGIKAIQ PNEVETKIED NELVEFVAEV DVRPEFELPK
 FEDITVEVPA IKADEEAIEA ELETLRARFS TLKDNHKLK KGEFVTINIT ASIDGEEKIE
 ATTEGLSYEI DDLIDLGLD KALIGAKDE TVEFTSELAN GEHKGKEAQI SVEITATKOR
 ELPELDDEFA QLASEFDTIE ELRESTVSDV EAKQKNEQAA AIRDEVLAAA LGEADFALPO
 SIVDEQAHSQ LHQLLGE LAH DDAALNSLLE AQGTTREEDF KKNVEDAEKA VRTQLFLDTL
 SEVEEPEVSQ QELTDHILET AQSVMGDPNQ FIQGLQQSGQ IANLFSDVRR GKALAQAICR
 VNVKDSEGEN IDPKEYFGEE EVAETESEA

> RXA00588 (1-522, translated) 174 residues
 MASVDKQYIT PETKALEEE LNALIAHRPA VAAEINERRE EGDLENAGY DAAREMQDQE
 EARIKQIYEL LANSTTEREG IIEGVANVGS VHVHYVDGDE NDKETFLIGT RAGASENPD
 ETYSEQSPLG AAILGAQEGD TRQYTAPNGS VISVTVVSAE PYNSAKAATL RGKN

> RXA00677 (1-216, translated) 72 residues
 MAKEGAIEVE GRIVEPLPNA MFRVELDNHG KVLAHISGKM RQHYIRILPE DRVVVELSPY
 DLTRGRIVRY YK

> RXA00687 (1-1320, translated) 440 residues
 VSAIQAFKD ADLRKKIFFT IAMIVLYRIG AQIPSPGVYD ATISGRRLDL TQDQSSVYSL
 INLFSGGALL QLSIFAIGIM PYITASIIQV LLTVVIPHFE ELKKEGGQSGQ AKMMQYTRYL

TVALALLQSS GIVALADREQ LLGAGIRVLS ADRNFFDLIV LVITMTAGAV LVMNMGELIT
 EKGVGNGMSL LIFAGIATRL PTDGMNILGN SGGVVFAVVL ASVLILVIGV VFVEQQORRI
 PVQYAKRMVG RRQYGGSSYV LPLKVNQAGV IPVIFASSLI YMPVLITQIV NSGSLVSDN
 WWQRNIIAHL QTPSSWQYIV LYFALTIFFS YFYVSVQYDP AEQAEENMKKY GGFIPIGRRG
 RPTAEYLVGFV MNRLLFVGLS YLAVIAVLPN IMLDLGVADG SAGATPPGGT AAILILVSVAL
 TTVKQIESQL LQSNYEGLLK

> RXA00736 (1-1887, translated) 629 residues

AGLVFPKVRK HRDGAAMPLV VITETDLTGN RVGDIAGAKR RPAKRRNKVD PLALEPGDLV
 VHETHGIGRF VKMTERTISA GDETSRREYI VLEYAPSKRG QPQGDLVPM DALDMLSRV
 GGEKPTLSKM GGSQDKNAKK KARAARVEIA GELVELYAKR QSAPGHFPAP DTPWQKEMED
 NFFYVETEDQ MLAIADVED MEKSVPMDRV IIGDVGYGKT EVAVRAAFKA VQDGKGVAVL
 VPTTLAQOQH STTEFERMTG FVPTIKGLSR FTSPAESREI LSGLAAGSDV TVIGTHRLQ
 TGQVQKNLGL VIVDEEQRFG VEKHEKIKAL RTHVDVLTMS ATPIPTLELM SMAGIREMIT
 MLTPPEDRHP ILTYVGPYED KQVAASIRRE LLRDCQVFFI HNKVADIIEKK AERLDLVE
 ARVVVAHQGM SEELLEQTQV GFWDREYDVL VCTTIVETGL DISNANTLIV ENAHMGLSQ
 LHQLRGRVGR SRERGYAYFL YPKGATLTEM SYDRLATIAQ NNDLGAGMAV AMKOLEMGA
 GNVLGAEQSG HIAVGVDLY VRLVGEAVEA YRALADGKVV DGTVKGPKET RVDLPVDAHI
 PEKYINAERL RLEIYRKLAQ SESEVDRL

> RXA00737 (1-480, translated) 160 residues

HPCNPFLIVM LSRADSDQV DGMEALIPAL TDTMPVPMLE IMPENTHVLV IAPKVRRI
 ADLEATDAEF LMAGWEAAM GADGPVAAEG LDLEASSYRS YESLEVSASK SDVRRWTFAP
 PGMFEASEEA TLPLDFEAGP APRGELPKID AMMAQLLAHT

> RXA00753 (1-1422, translated) 474 residues

VVDGVGGYTE QEVATHEAI RQAQDSGAPN DELIPGEMWS DKVELPSTID KAAADEAEIA
 IAQQQSQPQA RGLAAAAACQ TFWSPYQVC GAILERYIQ GAQFGWMLL TEGQALNPGE
 QGYRQPFMNG FLYWHPSTGA HAVNNYSAQV WERNWESGW MGYPGTGEVP VSGSNIDPG
 LSGWQVTFQG GRVYRSPVLD GFQVASINGL ILDKWLELGG PDSDLGFPTA DEAVTADGVE
 RFSVPQNGVW YWHPQGHGAH ILGNIYSIR EGEASEGEF YPIDGPEKYT ENMANQVFK
 GELAAANLYPN PLEAFIEFLP FANLEEAIEY FENGLSNSRV EANSLNAKKD SIQCSQSAN
 IHRVTKSDGV GIRVPKIGFK ARMDCDLPGT VSDVYVSGWI YYDYWGRWAQ AAYAQQOFFGN
 RNSVQVTNLE AGCSGEKNTL FWGTSYFQVT YEGQPYFGQS ATNAYALPCT IDRS

> RXA00755 (1-1275, translated) 425 residues

VPGKLRVHEL AKQLGITSKE LLATLKDKGE FVKTASSTIE PPVVKRMQEH YGSSGSDKSD
 TAAKFAAAK AAPKPAASAA PKPGAPAKPA APAAKPAPAA PSAASAAPKPG AAPKPGVQAK
 PAAAKPGAP AKPAPAPAPS AAKSGSASKP AAAAKPAFSG PTPGDASKKA EPAAKPGAEA
 PRPGMPRPM GKPAKPKGAR APRVANNPFS TGGGERPAPR PGGGPRPGGG PRPGGPRFQ
 GQGRPGGQRD GQRDQGRDQG GNRGGQRQGA GAGGPRPGGG PRPGGGRSGG GGAQAQGA
 PSQRQGGGR RPSMAMPPT PGQMPAKAPG KGGRGGQAGG GAGGGPNRQG GTGGGAGRGA
 RRGGTAGAFG RPPGAPRRGR KSKRQKRNEY ESMQAPNVIG GVRLPDGKGA TIRLAGASL
 ADPAD

> RXA00758 (1-1602, translated) 534 residues

MTLKSLAVT TAAALALSLA ACSSDSSSDS SSSSSGSEGG DNYVLVNGTE PQNPLVPGNT
 NEVGGRGIRD SIFSGLVYYD VDGSPVNDVA ESIELEGDKT YRITIKDGQT FDTGTPVTAE
 SFVNAWNIVN ANSTLSSYFF ESILGYEEGV ESMELQVVD DDTFTVELTQ PESDFPLRLG
 YSAFFPLPES AFDDMDAFGE NPINGPYKL QEWNNHQDAT IVPNADYTG RQANDGVKPF
 IFYPTFDSAY ADLLSDNLVD LDAIPDSAFS SFEDELSGRS INQPSAVFQS FTTPESLEHF
 SGEEGVLRQ AISLAVNRDE ITQTIFFGTR TPATDFTSPV IDGHSDSLQ ADVLTYPDER
 AQELWQAQDE ISPWSGEFSI SYNADGGHQA WVDATANSR NLGIDAIGN EYDFDKSLRD
 DVNTRTINGA FRTGQADYP SLGNFLGPLY GTGAGSNDGD YSNPDFDAKL AEANAADVD
 ASTPLINEAQ EIILLQDLPAI PTWYSNAVGG YSTNVNDNEF QWNSQPAYYQ ITKN

> RXA00824 (1-558, translated) 186 residues

MTSSAKNSIV GVVAILAVIV ALIPQLVGGE SAEEAQGETS TSKITTRPDC VASGAAGVDL
 PCLGGANGVG NELATVNVNL AWWCEPCRAE LPIDFEFAT HPENLVNIVGH ADQNAANGAA
 LLEDLGVNLA SYQDDSNLFA GTLGLGPPVV ITIVSPDGN VDTFPQPEF TIDDLTAVA
 GALQNA

00602839.052300

> RXA00896 (1-639, translated) 213 residues
 MTFVRPIVIHG DPVLHNPTQL VTEDVSELQE LIADMYETMD VANGVGLAAN QIGVSKRIFV
 YDCPDDEGVM HGGCFINPVL ETSEIPETMP ADDGSDEEGC LSPVGEGETP GRAHNAKVTG
 LNEKGEVSVV EAEGLFARCF QHEVGHLDGF LYTDVLIGRW KRMMAKAIKA NGWTEPGLTW
 MPGEDEDFPG HDAYVFPVSA ARNLPSAIVL LHV

> RXA00927 (1-1089, translated) 363 residues
 MSDVERTFEFE IPGGIPPRRN GGQGRAADTN VDNALKPDEY DAEVTLRPKS LTFEIGQPKV
 RDQLSLVLTG AKNRGVVDPH VLLSGPPGLG KTTMAMITAQ ELGTSLRMTS GPALERAGDL
 AAMLNLMGEG DVLPIDEIHR IARPAEEMLY MAMEDFRIDV IVKGPGGATS IPLEIPPTL
 VGATTRSGML TGPLRDRFGF TAQMEFYDVP DLTKVVKRTA KILDVGDND AAVEIASRSR
 GTPRIANRLR RVRDFAEVH ADGHITMGAA NAALIVFDV EVGLDRLDRA VLDALIRGHG
 GGPVGVNTLA VAVGEEPGTV EEVCEPYLVR AGMIARTGRG RVATAAANRW LGLEPPEGTI
 GDY

> RXA00928 (1-618, translated) 206 residues
 MIASLRGTVI NIGLSSAVIE CNGVGYEVVT TPNTLSQLVR GEEALVLTTM VVREDAMKLY
 GFIDNESREM FSVLQTVSGL GPRLALACES VLSPLEISQA ITNADAKTLQ RVPVGVKKRMA
 DRLIVELKGG VAAFAAGVVD EGGEQISLPN ANIASEVVVE QVSQALVGLG FSEKQSDDAV
 SFVLAADPSL DTSALRAAL AKLSGK

> RXA00929 (1-663, translated) 221 residues
 MNHEGLRVMG IDPGLTRCGL SVVQAGRGRT VYPVSVGVVR TPPDAELAER LLRLSKAVGE
 WMDEYTPDVI AIERVFERGN VSTMNTAHA VGLVILAAE RGLPVHMYTP SEVKKAISGN
 GRADKKQMTV MISTRILGGE PPKPADADA LSLAVCHCWR APMLMRAQSQ YSEQELEKRR
 RVQQGKLGKA KTYNIAEQQA SHASDPAKAA HPSQFQRTDT N

> RXA00935 (1-651, translated) 217 residues
 SAASAWERWP KRAIALFVLI VVGVALVLL TGDRSATPKL GIDLQGGTRV TLVPQGQDPT
 QQQLNQARTI LENRVNMGV SGASVVADGN TLVITVPGEN TAQASQLGQT SQLLFRFVQG
 AGMPDMTTLM PELEEMANRW VEYGVITEEQ ANASLEEMNT AVASTTAVEG EEATEPEPVT
 VSMPTMDEPA NSIEATQRRQ EITDMLRTRD QSTDPTV

> RXA00937 (1-123, translated) 41 residues
 VYREAGTMPA PALDDLNVQV KALDMDVRR QVAEQQSGAE A

> RXA00938 (1-258, translated) 86 residues
 MRPTSGSAAG GATSDLAITA GGQTLDFYLS PKRNVAAAKR FLAKALRSNA SAGYPRVINT
 DKAPSLARAI TELKSEIGCP PTVHR

> RXA00966 (1-528, translated) 176 residues
 MTNPSGTTG LAFRYTPELA NKIEGEWQNY WTDNGTFNAP NPVGDLAPAD GKALPEDKLF
 VQDMFPYPSG AGLHVGHPLG YIATDVFAVY NRMLGKNVLH TLGYDAIFGLP AEQYAIQTGT
 HERTTTMANI ENMKRQLGAL GLGHDSRRAV ATTDPEFYKW TQWIFLQIFN SWFDAE

> RXA00968 (1-1002, translated) 334 residues
 LIDDLLELDW TEKVKSMQRN WIGRSRGAEV DFSAEGETVT VFTTRPDITF GATYVMVLAPE
 HELVDVLEK AGSYEGVDAR WTNGQASPAE AVAAYRASIA AKSDLERQEN KEKTGVFLGV
 YATNFVNGDQ ITVFIADYVL TGYGTGAIMA VPAHDERDYE FATVLGLPIK EVVAGGNIEE
 AAFTESGEAV NSANDNGLDI NGLAKDEAIA KTIWLEEK EGRGTIQYKL RDWLFAQRQY
 WGEFPFIVYD ENGGAHALPD SMLPVELPEV EDYKPVSFDP EDADSESPSP LAKAREWVEV
 ELDLGDGKKK YTRDTNVMPQ WAGSSWYQLR YVDP

> RXA00975 (1-777, translated) 259 residues
 LALFAATQEL LFRAGVEVM FEHIKSSSLHE FGTDFFVYYH ENSLFESGAV DKAVQVLKDN
 GNLVYNEGAV WLRSFTFGDD KDRVVIKSDG DAAYIAGDIA YVADKFSRGH NLNIYMLGAD
 HHGYIARLKA AAAALGYKPE GVEVLIGQM VLLRDKGKAVR MSKRAGTVVT LDDLVEATGI
 DAARYSLIRS SVDSLSIDL GLWESQSSDN PYYVQYGAH RLCSIAKAE TLGVTEEGAD
 LSLLTTHREG DLITLTGFE

> RXA00976 (1-600, translated) 200 residues
 MTPADLATLI KETAVEVLTS RELDTSVLPE QVVVERPRNE EHG DYATNIA LQVAKVGGQN
 PRDLATWLAE ALAADDADIS AEIAGPGFLN IRLAAAQGE IVAKILAQGE TFGNSDHLSH
 LDVNLFEVSA NPTGPIHLGG TRWAAVGDLS GRVLEASGAK VTREYYFNH GRQIDRFALS
 SSCSGEGRAN ARRRRLWRIH

> RXA00985 (1-495, translated) 165 residues
 VLGHVLDALL RLLHPAMPFV TEVLWQALTD RTSIVVASWF TAADTNGGVA VDADAARRIG
 DVEKLIVTEVR RFRADQGVKP SQKVPARLDF VACDLQLED SVRSLVRIEQ PEDDFAASAS
 LEIRLSQATI TVELDTSGTV DVAAERKRLE KDLANAQKEL ETTAK

> RXA00998 (1-462, translated) 154 residues
 MTSRDDQPDQ LLSLAELAAT RALTTDELEA LNNANYGLDR NLGLRYTTIE PGRVVSSELHV
 ASKHLQVVGL VNGGVYAAIA ESTGVSASMI SAPGKMVVG I NNNDTFISAV SSGVIVAEAT
 PIQLGGRTHL WQIECTHRGE VVARTTLRTM VLNK

> RXA01020 (1-747, translated) 249 residues
 MNTNLWNSVD ELPIHDSWKP VLKPVDAIR KLGVLFAEE FLPPVDDVFR AFSYPPDAVK
 VLIMQQDPYP TPGHAMGLSF STQPDVRPLP RSLNNIFKEL VSDVGSGLGDS ASEQGALDLG
 INAPGSVAGT QVALPADGDL RAWSNQGVAL FNRVLTVHP QAGSHKGKGW EAVTEQAIIKA
 LAERDQPLVA ILWKGQAQEV QKFLGDTPCI CSVHPSPLSA SRGFFGSKPF SRANEILSSL
 GATEIDWSL

> RXA01061 (1-408, translated) 136 residues
 LRVNTVVAKL IEYVNYLTKT YPDTIPAGAV LPLIVMVSP I APHIAEELWK KLGHDDTIVTY
 ERPFTEEEKW LDTDEIELPV QVNGKVRGRI TVAADASQEQ VIEAALADEK VQEIQISGNL
 IKQIVVPGRM VNLVVK

> RXA01072 (1-231, translated) 77 residues
 MATTVYTKPA CVQCNAATKA LDRAGLEYDL VDISLDEEAR EYVVALGYLQ APVVVADGSH
 WSGFRPERIR EMATAAA

> RXA01124 (1-1509, translated) 503 residues
 RWVRRAINMAC MTDVVRVFCP SPTGTPHVGL VRTALFNWAY ARHTGKGLVF RIEDTDAARD
 SEESYSAIID SLRWLGMDWD EGVEKGGPHE PYRQSQRKDI YQDVLLQLID AGEVYPAYST
 AEEVEERHKA AGRDPKLGYD NFDROLTEEQ VAAFEAERGK PVWRRLMPPEQ DWKWTDLVRG
 EVEFKSTQFP DEVVARSNGE PLYTLVNPVD DALMEVTHVL RGEDLLPSTP RQALAYEALK
 RIGVAKATPA FGHLPFVME GNKKLSKRDP QSSLFNHRDN GIIEPGMLNY LALLGWSLSA
 DQDIFGVDEL IANFDVADV L GNPARDQKK LEATINADH I RLEPKDFEAR LRAYMTEYTE
 FPADYPAEKF AIAAELVQTR IKVLSEAWDL LKFLVTADED LVFNKAARK NLKETAVEPL
 NAGIAALEAV EEWTPFNIEA ALNKALIEDL GLKPRVAFGA LRIGISGEAV SPPLFESMEL
 LGKESTLVRL KYTREQTFFV VAE

> RXA01179 (1-513, translated) 171 residues
 MHSKEELTVR KGISRVLSVA VASSIGFTV LTGTGIAAAQ DSADFYGMDP NMKNYPIDDI
 KDRPEGLSNL PYFGSKLTSW GSSYATASSG VVTSALPOYT DRYPLKGDG LPKATIDMEP
 EVLARLERFV GVDGDRIRQI NAYSFSMGR I PLVWVVPKD NTVPCPTVYA L

> RXA01199 (1-771, translated) 257 residues
 VTSPHNHVSF ATDLGEVKAR ADARQKAHEQ GPVTQGIASS LDVTMENLEN EVLRRSTQVP
 VIVLVGTFRS PDSEQLKSDL TTLAAESGRK FIFGYVNADT DADVAQVVFV GQLPSVIAVA
 AGRPLADPQG GQPADALKQW TDQVVQAVGG QLEGLPEEAT DGEQEDAPVE DPRFDAATDA
 LNRGAFDEAI AVYESILAQE PNNADAKQAP RYRKAVGPAC HRWILRWMLS LLQMLQQQTL
 IWTQATDAA VVAGDPE

> RXA01223 (1-612, translated) 204 residues
 MTSVSFSLSI QALFAPKPEL PAAKWLVLGL GNPAGKYEST RHNVMYMQD MLIDAHQQQP
 LTFATGYKAL TQLAPGVLA VRSTTFMNSH GQGVAPIAAA LGIPAEIRIV IHDELDPAG
 KYRLKKGNE NGHNGLSLT EELGTRDYLR VRIGISRPPA GMVAPDVPYLE PVDHDPQPIE
 LAEEAVDLLL AQGLSAAQNA IHSR

> RXA01226 (1-444, translated) 148 residues
 AELVLSRSFG SFSVHKRSNT DIAQLPLGLIV AKPRSFNNLS GTPIRALCDF FKISPANVIV
 VHELELDFG SVKLKQGGGD HGHNLGLSKS KSLGKTDYWK LSMGIGRPPG RMDPASFVLK
 PFGKQELADI PIMADAADL VEKHLQGS

> RXA01228 (1-216, translated) 72 residues
 VHFIKENLIF SAESNALRAQ LMLSILGSFA EFERSIIRER QAEGIAWRKR PASTRAANAP
 SPRTTSRKPG NG

> RXA01252 (1-654, translated) 218 residues
 VFEGLPLQDLI DELSRLPGVG PKSAQRIAPH LLNVDPDSIT RLQELAGGVR DGQVFCRICC
 NISREEVCR I CDSGRDGGT ICVVEEPPKI QVIERTGEFS GRYHVLGGAL DPLANIGPRE
 LNISTLQRI GGVLPDRELA DSTPENKLF DPTPVREVIL ATDPNTEGEA TASYLGRLLK
 DFPDLVISRL ASGMPGLGDL EFVDELTLRS ALSGRLQI

> RXA01264 (1-216, translated) 72 residues
 MDLAQLGHT LWRRRKNVLA SFNIGASNGP VEAINGRLEH LRGITLGFNR LNHYILRCLI
 QAGLQRKIN VL

> RXA01265 (1-150, translated) 50 residues
 MSVSATAKAL KIGWELVNQV ALDACRQLIY NDRPHLEVDE HVWKYTRKPG

> RXA01274 (1-1095, translated) 365 residues
 MKLLRRIAP AIALGIA MST IVPSTAGAA EVTPADVAGD TALSTISDSA PADEASAPRW
 RAHVNAADER VKEMWAYSFS MDRNVPLVVI TADESAGPRP VIYLLNGGD GEGAAWVMVQ
 TDVLDFYLEK NVNVVIPMEG KFSYTDWVE ENASLGKQKM WETFLVKELP GPLEEKLNTD
 GQRAIAGMSM SATSLLFPQ HFGFYDAAA SFGSCAATSS LLPWEYLKLT LDRGNATPEQ
 MWGPRGGEYN IYNDALINS D KLRGTELYVS NASGLAGEWE SVDSPPFEGL NQQVQSIAMA
 ETVTVTGGIIE AATNKCTHDL KAKLDSAGIP ADWNLRPTGT HSWGWWQDDL RGSWTTFFARA
 FELEA

> RXA01278 (1-2127, translated) 709 residues
 VAQEVLLKDLN KVRNIGIMAH IDAGKTTTTE RILFYTGIRN KVGETHDGA TTDWMEQEKE
 RGITITSAAV TCFWNNQVN IIDTPGHVDF TVEVERSLRV LDGAVAVFDG KEGVEPQSEQ
 VWRQATKYDV PRICFVNKMD KLGAIFYFTV GTIEDRLGAK PLVMQLPICA EDNFDGVIDL
 LEMKALTWRG VTPIGTEATV EEPAEALADR AAEYREKLE TVAESDEEEL EKYFGGEEELS
 IAEIKAAIRK MVVNSEIYPV YCGTAYKNKG IQPLLDVAVD FLPSPLDLGE TKGTVDKQPE
 KVLTRKPSDE EPLSALAFKI AAHPFFGKLT FVRLYSKGVE PGEQVLNSTK NKKERIGKLF
 QMHANKENPV EVAHAGNIYA FIGLKDTTGT DTLCDANAPI ILESMDFFDP VIQVAIEPKT
 KSQDEKLGV A IKLAEEDPT FTVHLDDSG QTVIGGMGEL HLDVLVDRMK REFVKVANIG
 DPQVAYRETI RKPVESLSYT HKKQTGGSGQ FAKVIITIEP YAPEADELEE GESAIYKFEN
 AVTGGVRPRE YIPSVDAIGI DAMQYFLAG YPLVNVKATL EDGAYHVDVS SEMAFKLAGS
 QAFKEAVAKA KPVLLPEIMS VEITTPPEYM GEVIGDVNSR RGQIASMDDR AGAKLVKAKV
 PLSQMGVYVG DLRSKTQGRA NYSMVFDSSA EVPANVAADV TAERNGTAS

> RXA01283 (1-1293, translated) 431 residues
 TRQGVVPVA AEVLDTAGV TGYTRHDLIE TSVSGRVLG DATNAAGEVV LAAGTDLTEL
 NIDLLVEAGI KDWKVRSLT CQPTGVCAC CYGKSMASGQ QVDIGEAVGI VAAQSIGEPG
 TQLTMRFHQ GGVGGDITGG LPRVQELFEA RVPKNCAPI SVEGVIHLED EGNFYTLTIV
 PDDGSDNVVY EKLSKRQGLA STRVAMESNA GAFIERTLE GDRVTVGQRL LRGAADPHDV
 LEILGRGVE QHLIYEVQAV YRAQCVAIHD KHIEIIRQM LRRGTVIESG STEFLPGSLV
 DLSEAKLANS EAIGAGGQPA ELRSEIMGIT KASLATESWL SAASFQETTR VLTDAAINKR
 SDKLIGLKEN VIIGKLIPAG TGISRYRNI ISKPTEAARNA AYSIPTYGES IYGGDGFGEF
 TGASVPLEA F

> RXA01284 (1-507, translated) 169 residues
 VDHGKTTTTA AITKVLADTY PELNQAFAFD SIDKAPTEE RGITINISHV EYQTEKRHYA
 HVDAPGHADY IKNMITGAQ MDGAILVVA TDPMPQTEE HVLLARQVGV PYILVALNKC
 DMVEDEEIIIE LVEMEVRLEL AEQDYDEEAP IVHISALKAL EGDEKWKGQ

> RXA01327 (1-144, translated) 48 residues

MSIAATAKAL GLGWDLTQCL ALDMCHELIY YDPHTLEIVH VIGVDEHK

> RXA01328 (1-375, translated) 125 residues
LLDVVEGRSA DALRAWLARR SPAFRHQVRY VTMDGFOGYA TTSKQLLPAA RRVMDFFHVH
LLAGDKLTRC RQRLQKEKYH RRGLEDHDPY KNRKTLTLTQ KWLSSKKQSV LMSCLALIKT
TRHCN

> RXA01329 (1-291, translated) 97 residues
MADKRRKATM MREIVDQMRL LKGQANRELA QLGRSLHKRL GDILAYFDVG INSGPVEAIN
GRLEHLRGIA LGFRNLNHYI LHCLIHSGQL THKINAL

> RXA01344 (1-2547, translated) 849 residues
VLEGPILAAS RQTKSVVDIP GAPQRYSEAK VSAPIEVPLG LDLQLDSYSW LIGTEPWRRAR
KQEEFEGEGAR VTSGLENILE ELSPIQDYSY NMSLSLSEPR FEDVKNTLE AKEKDINXAA
PLYVTAEFVN NTTGEIKSQT VFIGDFPMMT DKGTFLINGT ERVVVSQIDVR SPGVYFDQTI
DKSTERPLHA VKVIPSRGAW LEFDVDRKDS VGVVRIDRKRQ QFVTVLLKAL GWTEQITER
FGFSEIMMST LESDGVANTD EALLEIYRQK RPGEQPTROL AQSLDNSFF RAKRYDLARV
GRYKINRKLK LGGDHGLMT LTEEDIATTI EYLVRLHAGE RVMTSPNGEE IPVETDDIDH
FGNRRLRTVG ELIQNQVRVG LSRMERVVRE RMTTQDAESI TPTSLINVRP VSAIREFPG
TSQLSQFMDQ NNSLSGLTHK RRLSALGPGG LSRRERAGIE RDVHPSHYGR MSCPITYPEEG
NIGLIGSLAS YARVNPFGFI ETPYRRIIDG KLTDQIDYLT ADEEDRFVVA QANTHYDEEG
NITDETIVTR LKDDGIAMVG RNAVDYMDVS PRQMVSVGTA MIPFLEHDDA NRALMGANMQ
KQAVPLIRAG APFVGTGMEQ RAAAYDAGDVL ITPVAGVVEN VSADEFITMA DDGKRETYLL
RKFORNTQGT SYNQKPLVNL GERVEAGQVI ADGPCTFNGE MSLGRNLNLA FMWEGHNYE
DAIILNQIV EQDILTSIHI EEHEIDARDT KLGAEITRD LPNVSEEVKL DLDGRGIVRI
GADVDRGDIL VGKVTPKGET ELTPPEERLLR AIFGEKAREV RDTSMKVPHG ETGKVGIVRH
FSREDDDDL

> RXA01346 (1-1575, translated) 525 residues
MRTATKVIAT VMASTLAIGL ASCSSSSGTF DVNVYSVNGT EFORGLIPGD TNENGGGRVV
DMLYSGLVYF DEAGVAQNLD AASIDQETDT TYKTLTRDGI KFSDDGSDITA TDFVDTWNFV
VENGLLNTSF FSPKGYEEG VETLEGLNVV DDRTFTEILA QPDSEPTQRI GYGFAPMPPA
SARDLIDAFG ENPVSSGPYK LEQWHDNAEL KVVANEHYDG PRAANNGLK YVVFQNDAA
YSDLLAGNLD VLDLIPPSAY TTYEELSGR SINQPAASYL ELSIRMESEFN FEQQGQLRR
QAISMAINRE ETAEQIFAGT YTPALDFTAP VLDGWRDDLK GNDVLTFQPD KARELWDAE
ETAPFEGELQ ISYNADVPNR EWDVAVANSI SNELDVNATG NPFDFKFSR DTYRTTGLDG
AYRTAWFADY PSIGNFLGPN YTSGVASNDA KYENPEFDQL IADAAASTK EETFYQAYQA
QEMLLRDLPA ELFWYPNVVG GYSESVDNVS VNWKAIPVW AITKQ

> RXA01347 (1-2049, translated) 683 residues
MVCVTQDNNE TTSQNRADKL PKSWDPKAVE ADLYQGWDVA GYFTADPASD KPGFSIVLPP
PNVTQQLHMG HALDHTLMDA LARRKRMQGF EVLWLPGMDH AGIATQTKVE EMLKETEGKT
RYDYDREEFI AKVWEWKQY GKGIGEQMRA IGDSDVWSRE RFTLDDGLSR AVQITFKKFL
DAGLIYQANR LVNNSPVLET AVSDIEVIYK DVEGLVSR YGSLNDDPEH VIVATRVET
MGDVAVAVH PDDERYKDLV GQTLPHFFRD DLSLKVVADD YVDPEFGSGA VKITPAHDEN
DVALGLRHLN DMTPTMDKTC RIADTGTQFD GLTREARIK VREELAQQCR IVKELRPVH
SVGHSESRGE AIEPRLSLQW EVKVEELAKM SGDAVREGDT TIHPKSLEPR YFDWVDNMHD
WTISRQLWVG HRIPIWYGN DEICVGPDE QAPEGYVQPD DVLDTWFSSA LWFFSTMGP
EKTPELEKFY PTVSLVTAYD ILFFWVARM MFGTFAAKET PELLGEGKDG RPQVFETDLF
LHGLVRDEHG RKMSKSLGNG IDPMDWVNY GADALRFTLA RGNAPGVOLP VGEDSAQSSR
NFATKLFNAT KPALMNGAVS EGLFAREELT DADRWIVDLL EQVRLDVVAY LDNYQFAKAN
EELYHFAWNE FCDWYLEIAK VQI

> RXA01355 (1-786, translated) 262 residues
VTFDFSASNA DSDTQDGRPG BRAGSKSKES KPTFWYIEIP VVVVLTLLALI FVLQTFVGRM
YMPISGSMPE TLHGCEGCTG DRILLVEKVS YFTDPEPGDV VVFKGTDSDN VGFTTQRSDN
SVIRGLQNLG SYVGLVAPDE NDLVKRIAT GGQTVSCQAG DPGIMVDGKE VDDSTYLLQA
QFFPIDETSGS TECGGNYFGP ITVPGGNYFM MGDNRNTSMD SRHLGDQYQ GTIPEENIKG
KVQAILLPFS RIGGVDDPAI KG

> RXA01387 (1-369, translated) 123 residues

AILIPIFVAK FGLVGSAWAN LIAEAITASL FLGALIKHHE GSWKPSWTVM KNQLVLGRDL
IMRSMFQVA FLASAAVAAR FGTAASLAHQ VLLQLWNFIT LVLDLSLAIAA QTLTGAALGA
GTAKVARRVG NQVIKYSLIF AGGLGLVFPV LHSWIPRIFT QDADVLDATA SPFWIMVAMI
ILGGIVFAID GVLLGAADAV FLRNASILAV VVGFLPGWVI SYALDASLTG VWGCLLAFTL
IRLFAVWIRF KSMKWAR

RXA01496 (1-1728, translated) 576 residues
ADAAALVQAL FNLMGMVTAT ASVSDETLQL LGSEEMNYKVQ VVSPEDEDRE LLESFTDLQFG
EDEGGGADLA KRPPVVTVMG HVDHGKTRLL DTRKANVGS DEAGGITQGI GAYQVKVNE
DTERITTFLD TPGEHAFTAM RARGAKSTDI AVLVAADDDG VMPQTVAEIN HAKAADVPV
VAVNKDKPEF ASPEKIRGQL TEYGLIPEEY GGDITFVDIS AKQGLNIDEL LASVCLTADA
ELDLVANPEM DAQVAIEAH LDRGRGPVAT VIVQGRGLRV GDSIVAGDGY GRVRRMVRDEY
GRDVEAEGS RPVQVQGLNG VPGAGDNLV VEDDRIARQI ANQRNARKRN LAALARSKDI
SLEDLDSVLK EHSITLNLILK GDNAGSVEAL EEAALKIEMD DEVQLNIIDR GVGAVTQTNV
TLAAASDAVI IAFNVRAEGK ATEENAEAGV DVRYITIIYR AIEVEEAALK GMLKPIYEER
VIGHAEIRAI EKASSVGLIA GCMVEDGKVR RNATVRIIRD GNVAENAKI VSLRREKDDA
TEVSAGYECG MVLSPYDISV DDKIEVYEMV EVPREA

> RXA01522 (1-1578, translated) 526 residues
VTNSNPTSKN NSADLPEQLR IRREKRERIL DSGLDAYPVE VORTISISDL RSQFVVITED
LQEREQGVIT LEVGEETDVE VAIAGRVMFV RNTGKLCFAS IQEGNGTITVQ AMLSLAAVGE
ESLKAWKADV DMGDIVSVRG KVISSKRCEL SVMADSWHMA SKSLRPLPVA FADLSEDTRV
RHRYTDLMR EQARTNALTR IKVMRALRHY LEDQDFLEVE TPLMLQTHGG AARPEFETHY
NALDIDLILYR IAFELYLKRC VVGGIERFVE VNRNFRNEGV DSSHSPEEFAM LSTYEAAGDI
ETGAKILKGL VQSVQAEVFG TTLVTLADGT EYDLGGGEWK IEMYPSLINEA LARKFPGQPE
VTIDSTVEEL RELAKVIGLS VPENGGWGHG KLVEEIIWELL CEDQLYGFIF VKDFPVETFP
LTRQHRTKPG VTEKWDLYVR GFELATGYSE LIDPVIQOR FEQGARLAAD GDDEAMVLDE
DFLTAMEQGM PPTSGNGMGI DRLLMALTGL GIRETVLFPM VKPEQK

> RXA01530 (1-642, translated) 214 residues
MAFLDLIQEG NLGLIRAVEK FDYSKGYKFS TYATWWIRQA ITRAMADQAR TIRIPVHMVE
VINKLGRQQR ELLQELGREP TPQELSKEMD ISEKVLIEIQ QYAREPISLD QTIGDEGDSQ
LGDIFIDESEA VVAVDAVSFT LLQDQLQDVL ETLSEAGV VKLRFGLTDG MPRTLDEIQG
VYGVTRERIR QIESKTMASKL RHPRSQVLR DYLD

> RXA01531 (1-1017, translated) 339 residues
MVNNVNAKPT VAKKTARKTA RKAAPRVATP LGVASESPIS ATPARSIDGT STPVEAADTI
ETTAPAAKAT AKAAPAKKVA KKTARKAPAK KTVAKKATTA KAAPATAKDE NAPVDDDEEN
LAQDEQDFDG DDFVDGIEDE EDEGVEALG ESEDEDEEDG SSVWDEDESA TLRQARKDAE
LTASADSVR YLQKIGKVAL LNAEQEVSLS KRIEAGLYAT HRMEEMEEAF AAGDKDAKIT
PAYKRDRLAR ARDGRKAKNH LLEANLRLV SLAKTLHRPV HGIPGPHPRG QPRSDSCRRE
VRLQLGLQVL HLRLNLVPSG NHRPHRGREST NHPYPSPHG

> RXA01541 (1-771, translated) 257 residues
IFNSHRAPRL ASTVHIARES ADSGTLEFFI QORQSTMAYA ANAVVFPGGG VEDSDYFPM
PHRDQHMSPE HIKKHASRLH MDSETMAAHI SAARREWVEE TGVDLGNYNH ELIPIDRWIT
LPDPAFRRRY DTATEVLILS KDSTNAALQH QHOTTEATHS YWATAEELLT QWSTGHLNLL
LPTWWHINQL NHLHTLNQLY SFAQRTNHPQ HTPPTVFANW TAPADEAMQ HYGFPPDDAY
FDHATIAGRK HTLITRK

> RXA01556 (1-849, translated) 283 residues
NIRFETLNIM GPARRIHLGH VWNDRLTFFEY SRSFLGKETL SPDIARLFTD RVPTPLPAP
RKARAVQVL VSNPADQTSI EEFAGIQQVS ARTLQROFLK TGYSFSEWR AARQVCVAAS
LLAHDFSISS VANLVGFAAT SSLTRAFRRH TGATPSTFTT GQIGMGSGAG PPRIPATTTT
AEAHQDQLLV IYSGTATVTT PGYCRFMGQ GMVTIPAGTQ TRIDVAAGSI APFVPVGLDE
WGMDLTRVVA VNNQPKPLT ILEQSEWSKL SEELLNTPVP VQM

> RXA01558 (1-1209, translated) 403 residues
MTSDQTESLS TQSVKPAKKR SWFNSLYTG DGDIFTIAKT LWYWITGILL VISILFIAR
GFSLSIDFQG GTKMSMPASD YSTEQVEETF TEATGITPEI VOIVVSGDAR TLEIYSERLS
DEDVEKARLA IYEEYQPLNS EQQPSDAIG NSTYSESWG TITQRMVLAL IAFVLVIAIY

TTSARPEETK AILDYADV WDTGIAFGTL SAEKHQQIE ITTFRSDLYD GNSRNPVTF
 GDTLEGLIR RDKVNAMAV EIQADGELTF HDPVGLEDL LHTLDTPAT PEQSFNDPL
 RMLRAARFVS QLNFTLAPRV ITAMTEMAQQ ITRITVERMQ VELDKNMILGK NPEAGIDLMV
 ESGIAQIIYP EIPAMQMTQD EHMQHDKVYA HSLQVMRQAI DQEDGPDLV LRWAALLHDC
 GKPDTRDFNE EGRVSFQHE VVGAKLVRRR MRKLKYSQKM VGDVGQLVFL HMRFHGFSEG
 QWTDSAVRRY AADAGELLPR LHLVRADCT TRNKRKAARL QATYDHLER IAEIAAKEDL
 ARVRPDLGN EIMEILNIQA GPEVGKAWAF LKELRLERGP LDREVAIAEL KSWWEGENNE

> RXA01648 (1-369, translated) 123 residues
 VGFAPADHMR TSLVQEAALMM AKSQRGSQGV AVFSDHGSV YTSQAFQDTC KKLGVQRSMG
 AVGTSADNSL AESFNAALKR EVLQDSKTFA NQLVCRREV F RWCDLVQHGA QTFVLVWLGA
 CGV

> RXA01649 (1-420, translated) 140 residues
 VLKINRSSYY KWKKTALTRK KLLSDAVLG AKIKSIFTKE RGCYAKRIT AELNDGPGTT
 TPVNHKRVAR VMSSMKLVGF TKKRKVITTI PAAVKPVFFD LVKRQFNALA ANEVYVGDIT
 YLPIADGSGNM YLTTVIDCYS

> RXA01650 (1-114, translated) 38 residues
 MSEAEQIRQL KKENALLREE RDILRKAAYK FPGKRQDL

> RXA01651 (1-135, translated) 45 residues
 MPTKTYSEEF KRDAVALYEN SDGASLQQA NDLGINRVIL KNFDQ

> RXA01670 (1-612, translated) 204 residues
 HFVYHLGLIG TLOFEPAEET RGQIRLHLSD GEIAANLRGP QWCRLITDAE RTQAIGKLG
 PIRDDADPE PIRKQVRSR RSIGSLMDQ KLFAGVGNII RAETLFRLGI SPFTIGKDI
 QATFRSIWAD LVGLMKDGVV TGRIDTVRPE HTEPAMGRPP RKDDHGGVEV TYRRTGQECF
 LCATPIKEQV MEGNLFWCPR GCQR

> RXA01680 (1-411, translated) 137 residues
 MAGHTHTHR TAYKQLEALA RNHGLFTYID PPAEVDGVVVK STTNCLEGGI NAQIKALARN
 HRGMFDEHQR IAVDWLLMH TQLFGDPDEI ARQNNQWQDG LANVPDLQQ EQPHDHYGRF
 VTYDTGIDAT TTRKSK

> RXA01704 (1-816, translated) 272 residues
 DASGRAGFRK LKSNELVTEV ACSQVVPPELL EGLVGEGRARR FTFPGVEIIAA IDDAQQRHV
 ESRKAPGRRR TETVLKVLG TGEVEQKVG D YTWKFPVSSP WQAHTKAPAA YSEFIAEALT
 GLELVDVDDR GPVANDLYGG VGLFAPITTS KLQAQVHVSVE LSPGSAEAGE EALAGLPVTF
 HTGRVEGMAS QLPSPNVVVL DPPRTGAGSD VLKSIKAEAKP QLVIIHGCDP ATFARDVADN
 KNGYEMDQL AVFNAFFGTH HFETIGVFVR VS

> RXA01710 (1-408, translated) 136 residues
 MTFPKLISDT EWRERLTPOE FHVLRAGTE PPHVGEYNT TTEGVYSCRA CGEELFRSTE
 KFESHCCWPS FFSPLAGDKI IEKEDLSLGM RRVIELCANC GSHMGHVFE GEGYDTPDLR
 YCINSISLKL EEPVVS

> RXA01717 (1-282, translated) 94 residues
 PSQQMHQDIA LVVDETIPAE DVRAVVKAGA GELIETVELF HVFRSEQRGE NKKSLAFSLR
 FRAAGRITLD EEANEARLQA AELAKEKFNA EMRG

> RXA01723 (1-837, translated) 279 residues
 VDXSRVTTTA TTEPPAAPAQ SQPAEAQPAQ TQAAQQEELP VAAKESAPAT ENTQGXQGG
 AQGXQAGDEH DDXFESRSAA RRARRNRQRI IHRDGDNDAN ANTESEQNTP AQNATAQAES
 EQTAAPQAAE AAEQNQNDNS ESSENRSNRY RNNRRSRNN RNNRRYRNN ESSDAGQSS
 NDDADNNQAR SEDNDDRRS RNNRNNDRND RNDNRDRND DNDDRNRNRG RNNRRGXATT
 VTIATTEITG ITATTATMAT TTSKXEXAAG SRHPGHRGP

> RXA01724 (1-384, translated) 128 residues
 VDHNAVFVRT TGYHAAPSDV FVSNQLIRRM GLRSGDAIEG QVRMNQGGGN HNNHGRNRQK
 YNNLVRVEMV NGLPAEETR N RPEFGKLTPL YPNQRLRIET EQKILTRVI DLIMPIGKGQ

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> RXA01852 (1-1287, translated) 429 residues
VSNQKSKSEK LQSFAPKGV PDYAPPKSAA FLAVRDFAVN QAHKAGFEHI ELPFIFDTGL
FARGVGESTD VVSKEMYTFA DRGERSVTLR PEGTAGVMRA VIEHSLDRGQ LPVKLNYAGP
FFRYERFPQAG RYRQLQQVVG EAIGVDDPAL DAEIITALADR SYRSLGLQDF RLETLSLGDR
HCSPYERQKL QDDFPALPLD EETRKRAEIN PLRVLLDKRP EVQEMTADAP LMLDHLDAEC
REHFETVTGL LDDMGVPYVI NPRMVRGLDY YTKTCFEVHV DGLGAQSGIG GGGRYDGLMA
QLGGQDLSGI GYGLGVDRMT LALEAEGVTV GAERRVDVYG VPLGKDAKKA LAGIVNTLRA
AGISTDMSYG DRGLKGAMKG ADRSNALYTL VLGEQELENN TIAVKDMRAH EQHDVALDEV
VAFLOQKLI

> RXA01862 (1-1206, translated) 402 residues
MAYDFVIGMD VGKYFHHACV LDPQGRQVLS KRINQHEGSL RKLFDKFLAN DAEVLVVVDQ
PNNIGRLTVA VAQAMGADV R YLPGLAMRQL SRIHVGNSTK DVRDAYVIAH AGLNLPDALR
SVDRVEEVFL QLKVLNGIDE DLARAYTRLI NMQQSALVGT YPAFHVLRG QIHRKWILH
LLAKYGGPTK IRRVGKARLA AFARGHRARN PEPVIDAMLA AIHQQTVSIA GAEBYELGVA
MSAKDALAKL EHRKEIEGQV LELIQDIPQT EILLMPGIG PRSAAQILMT VGDMSDFPDA
AHLASVAGLS PQTNQSGTSI MSNSPNRANG KKLKNALWQS SFASIRFHER SRQFYERKRN
EGKRHHAAVV ALARRRLNVL FAMMRSGELY RDIPTAQEAA AA

> RXA01863 (1-807, translated) 269 residues
MNSNLTLFPD RYLDIAEYID VMHISHNWGT TDEFANVVGFG AMKKQPPLKA KLKLYEQMIS
NARTLSEQGM FVSAETMLNQ STLPHLRKIH QEVVHDMKCS RHEIHPMYPA DFASQLNVLIT
LAEMKFTIHD ILDFRDEDIW MLFGTLPFVP CLKDDDEQKL LSLRLNARNN TRNDPDGRS
RLNVNVFTGN VIIVTFGDET GTISNIQKDK LTDVPDKWLS SDLAKSLNCH CSEFSCLGPN
VLVKNMYYPN MDFKDNERNH HKQPQIIQF

> RXA01864 (1-471, translated) 157 residues
NERYWTGPRP ETHGPNDPGG VDLVGGVEH AVLHLLYARF WHKVLFDLGH VSSKEPYRRL
YNGQYIQAFA YLDSRGVYVP ADDVEEKDGK FFYQGEENVG EYKMGKSLK NAVAPDDICN
NFGADFLRVY EMAMGFLDRI RPWATKDVVG AQRLSVN

> RXA01872 (1-765, translated) 255 residues
MGNDGGDLRI DDLRSFISVA QSGHLTETAQ RLIGIPQPTLS RRISRVEKHA GTPLFDRAGR
KLVLNQRGHA FLNHAISAIVA EFNSAATEIK RLMDPEKGTI RLDFMHSLSGT WMVPELIRTF
RAEHPNVEFQ LHQAAMLLV DRVLADETDL ALVGPKPAEV GTSLGWAPLL RQRILALAVEA
DHRLASFSGQ GELPLITAAE EPFVAMRAGF GTRLLMDALA EAGFVFNVV FESMELTTVA
GLVSAGLVG VVPM

> RXA01878 (1-879, translated) 293 residues
MEEPGSAQLL GPVEIRALAE KLDVPTTKKL GQNFVHDPTN VRRIVAAEEL TPNDHVVEVG
PGLGSLTIAL VESAASVTAV EIDPRLAAEL PETFWORAPA LAHKLISVLK DALKVQOSDM
AVOFTALVAN LPYNVSVPVL LHMMEEFPTI NKVLVMVQAE VADRLAADPG SKIYGVPSVK
ASFYGVETRA GSGIKNVFWP APKIESGLVK IVREDTAWKQ DDETRKKVWE IIDAFLQRR
KTLRAALSGH YSGSQAAEEA LRAADIDPTL RGEKLDVTDY VRLAGVLQOK DEK

> RXA01913 (1-825, translated) 275 residues
MANYTAADV KLELTGSGM LDCKKALEES AGDFDKAVEI LRVKGAKDVG KRAERNATEG
LVAVSGNTMV EVNSETDFVA KNSDFKEFAA KVADAAAAAK ANSQEELAAV DVDGQTADAA
LQEFSAKTGE KLELRRRAVL EGDKTAVYLH QRSADLPPAV GVLVAFTGEG EAAEAAARQA
AMQIAALKAS YLTREDVPAE IIEKERSIAE QITREEGKPE QAIPIKIVEGR LNGFYKENVL
LEQSSVADSK KTVKALLDEA GTVTVSFAF EVGQA

> RXA01926 (1-672, translated) 224 residues
LRSFYTPQQA IEREGDVWKA ATEEAELLAA DGAVHDQELF LNCTTSPLIF ASAMLNFGVH
QILDITLCQLA PSAPGRDADP KALEAATSAM DDHRTTDDF SGVVFVKVQAG MDKNHRDTIA
FMRVVSSEFD RMQQVTHSQS GRSESTKYAL TVFGTRSTRV ETAFPGDIVG LVNAGALAPG
DTIFEGRKIQ YPFMPKFAPE HFRIILRAKSL GKYKQFRKAL EQLD

> RXA01938 (1-915, translated) 305 residues
LDESAYKHRA AYQRIFDRLG LEYATCQATS GAMGGSASEE FLAVSENGED TFVRSTSGNY

AANVEAVVQ PGVERDIEGL PEPVYETPV SETIDALVDW ANSIDVQIEG REVTAADDTLK
 CIVVVKVREPG AEAEALTGIL LPGDREVDK RLEASLEPAE VELAVESDFA DNPFLVKGV
 GPVGLAKNGV KVLADPRVVT GTSWITGADE KERHVVGLVA GRDFTPDGFI EAAEIKEGDP
 APAGEGTLTL ARGIEIGISS SAAASTPKPS TSKSWTKTAS APSQPWALRA RCHFPARRPG
 RTAPR

> RXA01953 (1-381, translated) 127 residues
 MIAAYREKDR SLGRAAMEAL IDAVSQDVPA GLDELRLKGR TLKARATDVL AYFERPGTSM
 GPTFAINGRL EHLRGSALGF RNLNTYIARS LLEFRRIQTS TTPSSVKS RFHPSSSRTTM
 NDVPTH

> RXA01954 (1-840, translated) 280 residues
 VLADDVVVVA EFRDRIYPGL VETGRVERGG DKPFHTVVNA ENYHALEMLT YTHRHSDAI
 YIDPPYNTGA RDWKYDNDYV ASDDDYRHSK WLAFMERRLK ICRELMRSDA TLVAPIDEHE
 VNRLGVLLDQ LFPESTRQLV TIVNNPKGVT QGYLSRVVEEY AFFVFGPDAR IGSVDODLLT
 HRDMADAEGE LQRPFWKGLL RSGDDSLRAD RKDMFYVPWF DESTGRLSHA GEALPLDET
 DFPSPQDLTP IWPFRDMKE GPTRAAPRRS ILDYALHPLH

> RXA01975 (1-1896, translated) 632 residues
 LSHHTHLNNY ITSLSDNADL REKVTATVDA FRHTVMDDFD YISDQVLLY GDVQSGKTS
 MLGIIADCLD STEHTIVILT SPNTRLVQQT YDRVAQAFPD TLVCDRDGYN DFRANQKSLT
 PRKSIYVVGK IPAVLGNWLR VFNDSGALSG HPVLIIDDEA DATSLNTKVN QSDVSTINHQ
 LTSIRDLATG CIYLQVTGTP QAVLLQSDDS NWAAEHLHF APGESYIGGO LFFSELNNPY
 LRLFANTQFD EDSRFSDAIY TYLLTAALFK LRGESLCTML IHPSTASSH RDAFAEARLQ
 LTFAFERFYE PMIQNHFORA YEQLAQTDNS LPFLRKILNI LGGMEDDFSI HIVNSONPTV
 EEDWADGINS FMVGNLGRG LTFNNLQTVF YVRESKRPQA DTLWQHARME GYKRHKDTMR
 VFMPATIAQT FQEVYLGNEA IKNLQDLGTH INDIRVILGD GVAPTRANVL DKRKVGNLSG
 GVNYFAADPR IKNEVALDKK LLAYLDKHGE DSTIGMRAII TILNAFTVDF NDLDLATFKA
 ALLDFERNQP HLTARMVLR NRKVNQGTGA LLSPTDQALS RAEVAHPLLI LYRIEGVND
 AAGRGEPWTS SDFIWPVNIK LPGQRQFCW DG

> RXA01998 (1-708, translated) 236 residues
 MGIFSGROFP REIILWAVRW YCRYGVSYRD LEEMMTERGV PVDHTTIYRW VQKYAPELDK
 KTRWYQVDP WQARSWRVDE TYIRVGGKWC YLYRAITAGS QTLDFYLSPK RNVAARAKRL
 AKTLRSNKSA GYPRVISTDK APSLARAISE LKAEVGPST VEHRRVKYLN NVIEGDHGR
 KRILGPKGAF KNRTSAYRTL KGMEAMHSLR KQGTMFAYG HNPDAVIVS RVFETA

> RXA02002 (1-378, translated) 126 residues
 MSNANPDTTA AEAHRRRTFA VIAHPDAGKS TLTEALALHA HIISEAGATH KGAKRKATVS
 DWMMEKDRG ISIASSALQF EYAEPEGHAGE PFMINLVDT GHADFSEDYI RVLMAVDAAV
 MLMHSV

> RXA02015 (1-519, translated) 173 residues
 VLKFSNLLED DIRPRAMSRD IDWGIPIPV GWQDNNAKLL YVWFDAVVGY LSASIEWAYR
 SGDPFAWRTF WNDPETHSYF FMGKDNITFH SQIWPFAELLG YAGKSGRGGE IGDGLVNLN
 TEVVSSEFLT MSGSKFSSSK GVVIYVKDFL KEFGPDALRY FIAARPNND TDF

> RXA02025 (1-651, translated) 217 residues
 MAWFFAPEPV MVTADALKG GRHPVLENPA PHTVLGTPVT GPWKEGQRI WIGLGCFGV
 EQMYWQMDGV EGTSGVYAGG FTPNPTYREV CSGRTGTHEI VEVVYDPSKI SLEQLVARGL
 EAHDPQCFGR QGNDVGTQYR SAYYTENEED AARVKAVDDA YGTELQKHGF GETITIGIVI
 SPSDYFLAED YHQYQLDKNP DGYCFHHSTG IFCGVEA

> RXA02047 (1-192, translated) 64 residues
 WDDRVHPAHA RLFAQALLDA GQAVDYENT EGGHAGAADN KQTAFFVESLI YTWIEKTLQD
 QGSI

> RXA02065 (1-648, translated) 216 residues
 MTYMKKSKSD DAFVVIETVQ AEHAEELTGT AAFDAGQADM PTWGEVLAEH ADSVRYLAYR
 LSGNQDAED LTQETFMRFV RSLKSYQPGT FEGWLHRTT NLFDMVRHR GKIRMEALPE
 DYERVPNDI TPEQAYTEAN LDPALQAALD ELSPDFRFAV ILCDVVGMSY DETAETLGVK

00250-0002060

FDTSHQEGGL RGHVINPVWE PLTEDTQTGK EGCLSIPDVS AETTRYETVR LSGQDRDGNP
VGFVANGLLA RCIQHETDHL DGVFLFKRLD PAERKAAMGV IRASAWFNK

> RXA02243 (1-945, translated) 315 residues
MRLVFAQTPE PAVVALQKLI DSDHEVVAVL TQPDARRGRG RTLHPSAAVE LAQOHGIEVL
KPTSLKADTE DQQAIRQRLA ELAPDCLPVV AYQGLITKDL LDVAPHGWNV LHESLLPAWR
GAAPVQASIR EGDQITGATT FRIDEGLDTG VILSTIEDTI QPTDTADDLL TRLAYSGGDL
LVETMTGLEQ GTITPRAQEG EATYASKITT QDAQIDWSKP AEVIDRHRA HTPGPGAWTT
LVDARLKVGP ISHSGEVEVA ADLAPGAILA QKNSVVVGTG TTPIVLGNIG PPFGKMMNAA
DWARGVQLDQ EAKFQ

RXA02251 (1-300, translated) 100 residues
VADPTTYRPA PGTIPEPGV YKFRDENRRV IYVGKAKNLR SRLSNFYQDV TQLHPRTQRM
VFAASSVEWT VVSSEVEALQ LEYTWIKRFD PRFKRKIPRR

> RXA02252 (1-1824, translated) 608 residues
LIRGSNVKRY DDKTYPMNAV STGERFPRAF FFRGPRKGV RYFGPYSHAW AVRETLDLLT
RVFPMTCTSK GVFNHRESLG RPELLGYIDK CAAPCVGRVS EEEHREIVDG FTSFMAGHTD
KVTRKLNADM MAAAEELDFE RAARLRDDLE AIDKVMKEQA VVLGDGTDAD IIAFATDQLE
AAVQVFNIRG GRIRGQGWV VEKPGDYAGL LVDATTQPEG DAPETDPALP FLMQDFLVPQ
YGDVERAET EAKEDAAVIE RRGVDKHSFE EAAPVTRASV VPREILVQVA PNEAEQTLKV
LEELRGAGVD ARVPQRGDKR ALMETVERNA KELLKQHKLK RVGDLTARSA ALQELQEAAL
MEQALRIEC TDISHIQGTD VVASLVFED GLPKSDYRR YRVKEAAGG HSNDVASIAE
ITRRFLRHQ KQIKLAVPEAE EFDGSTFSD KVEEMSTDAR RFAYPPQIFI VDGGAPOVAA
AQEVFDELGI VDVVLIGLAK RLEETIWLPGD PDPVILPRNS QALFLQQIR DEAHRAFIATY
HQQRSKRMK VSELSIKGL QQSRRTELVK HFGSVAKLKE ASVEDISQVK GFGPKLAEAV
YEGHLASK

> RXA02260 (1-231, translated) 77 residues
MALTLQIILV VASLLMTVFV LLHKGKGGGL SSLFGGCVQS NLSGSTVVEK NLDNRVTILVA
VIWIVCIVAL NLIQTYS

> RXA02290 (1-399, translated) 133 residues
VDLNLAFEIL TLNVVQFQVGT WHAVLSKREG FRQAPAFQDV AKVAAFNEDD VERLLDDLQI
FRNRKINAA ITNAKALLE NDETGTFSI IADHSTDATA MVKHLKALGF THIGLTSLSI
LQQAIGVTEL KAA

> RXA02291 (1-654, translated) 218 residues
VVHLPNFLGL AEQKALVAQA RDLAREVVGT PLAMVRPKLK SGQMSVHMLH LGKYWASNPF
RYVDVVDGFP VPPLPDSFVD LAHRALLSAG SLNSLQDAS EAYRAEALV NYSPDASMG
MHQDANESE APVISLSIGD TGIFRLGGTL NRNKPWTDRG LMSGDLIVFG GANRQAFHGI
PSIEANTAPA GCGLKEGEST SRSANLHYKT PGRGMSRG

> RXA02323 (1-924, translated) 308 residues
MSSHDLVDVV VVGAGAAGLA AVALGRSLR SVIVIDAGQP RNSYAHAAHN VLQEGGIAPA
ELLEKRAEA RSYGTIAPG RVAKVERTGS TFAITLDDAS LLHSRIILA HGAVDLPEV
EGLSDFWGK VLHCAYCHGF EARDSEIVVV GTSPMAAHQA LMFSQLSKTV SLVGTLDIDE
QTSESLDSAG VKVLGTNAVR VSAEGDGLSV ELSBGHLSL DNIVVASRPL VDGTLTYQLG
QMEENPMGR FIPFGQTGR TPIEGVWAAGN AQAPMAMVYG SAAQGVAMGA EINFDLILED
ISVASAQ

> RXA02385 (1-771, translated) 257 residues
MIEVRLVPA AVMMMAVAAL IINGSWVLVS GIVGIAIIAA CVFKHWQAV VIAALGVAV
VMAALRISSA KAFEAPQTWV GTAETIKFLD SGDQLIGLRV EGYPAPIPV YSGSDTIEKA
SLIAYSGRIK PDSFGVGD L TISTEDIDL EPTTGYSAWV NQVRDGFSA VEETVGESSR
GLIPGMVLGD TRLQGSIEAQ TYIDTGLSHL SAVSGSNVAI VVSSVVVLSY FLTAGPRIRV
VASLLSLGIF VSLVGFE

> RXA02386 (1-405, translated) 135 residues
VSVVGHVAKP GLVTIAEGSR VADALATAGA LPDADLTALN LAQLLVDTGQ IHVLAIGEVO
PISVDAAATS ASGLISLNTA TVADLVLP GVEKTAQAI DFRESNGGS TVEDLLQVKG

IGPSKFEQIS GLVSP

> RXA02388 (1-846, translated) 282 residues
 AIINSSRMPE MHGSLSLVC LLYFDSNLAV HYGFLLSCAA TAGIVMLQPL LYRAIGPPLA
 VMKVPDIIVR AFAYVIAADL VTIPIIALMA RQISLVAVLA NVLVELAVPP IYLLGLIAVL
 ASLLPWPVEY PLLKIIEFFT WWHIHWAKWC QQLPNSTLEI SAGWAGIAWA CMAAVVVVVI
 IYKGYVRTLA VCCVCFFLFG AWWNRLPAQI DPTELRFVII ADDSELTDVP EHAELIIVED
 PHGMSMDRPI VTREGIPVLY PYRDGEVSLH IDGTQHAADG RF

> RXA02413 (1-492, translated) 164 residues
 MTSSENSQSD IWLTDQQDV WLDVWMTMRIG LPARLDLQKL EAAGVSHFEY FTMAQISMAMP
 EHRVMSLELA ELSDMTLSHL SRVVTRLEKA GWVKRVPDDP DGRATVAVLIT DSGWEKVKAT
 APGHVKEVRK LVFDDLTPEE LKVMGTAMKK IVNRLDMSNR LPRV

> RXA02416 (1-2640, translated) 880 residues
 DKPVDVLDIG LSPAVSIDQK STNRNPRSTV GTITEVYDYL RLLYARAGTA HCPVCDARVE
 RQTPQQMVQD ILGMEELKLF QILAPVVRTR KGEFVDLFDL LASQGSYRVR VDGEVHQSLD
 PPKEKQIKH DIDVVVDRLQ VKASQKQRLT DSMETALRLA DGVAVLEFVG LEEDDPNRLR
 RFSEKMSCPN GHALTVDLE PRAFSFSNPY GACFACDGLG VRTEVDIDLI IPDPAAPATK
 AVQPWNSSPN HSYFEKLIEG LAKALGFDPE TPYSELTAQ KKALVYGSKE EVSVRYKNRY
 GRVRSVTAFF EGVMGYFDRK LEQTDSETQK DRLLGYTREV PCPTCKGARL KPEILAVRLD
 SGSGHSLAIA GLTALSVEHA FEFLDNLTLG KREEMTAGAV LKEIHARLKF LLDVGLSYLT
 LDRAGATFLSG GEAQRIRLAT QIGSGLAGVL YVLDEPSLIG HQRDNRQRLIT TLEHRLDIGN
 TILIVHEHED TIRRADWLVD IGPRAGEFVG EVVYQGEPKG ILDCEESLTG AYLSGRRITG
 VPDTRREIDK ERQLKVVVGAR ENNLQGIDVK IPLGLVCITG GVSGSGKSTL VNQILAKVLA
 NKLNRARQVP GRAKRVEGLE HLDKLVQVDQ SPIGRTPERSN PATYTGVDK VRNLEAFETE
 AKRVGYKPPR EFSNKGGRG EACQGDGTLK IEMNPLPDVY VPCEVCDGQR YNRETLEVKY
 KGKNIAEVLG MPISAEADFF EPITSIHRYL ATLVDVGLGY VRLGQAATTL SGGEAQRVKL
 AAELQKRSNG RTVYILDEPT TGLHFFEDIRK LMMVIEGLVD KGNVSIIEH NLDVIKADWD
 IVDMGPEGGG GGGTVVAEGT PEQVAEVAGS YTGQFLKELL

> RXA02418 (1-567, translated) 189 residues
 VVRVYKFSRT ANRGVHISAE ARINERIRVP EVRLVGPNGE QVGIVRIEDA RKLAFDADLD
 LVEVAPNAKP PVCKIMDYGK FKYEAAQAKR ESRKNQQQTV VKEQKLRPKI DDHDYETKKK
 NVIRFLEKGS KVKVTIMFRG REQARPELGY RLLERLANDV VDFGIVETRA KQDGRNMTMV
 LGPVRKGKK

> RXA02429 (1-2289, translated) 763 residues
 VAGFDWFWKA LGGKSGRNQK RSVAVINQVE NHAAELDLDL DVALAQRKAD LASGGRIDNH
 AEFLLAILGVA SQRTLGLKPY PVQSQAVLRL IEGDVVHMAT GEGKTLVGAM AATGLGLMGK
 RVHSITVNDY LAVRDAEWMR PLVEFFGLSV ASISEKMDAG ERRQAYKAAI VYGPVNEIGF
 DVLRDQLIR REDAVQHGD VAIIDEADSV LVDEALVPLV LAGNQPGHAP RGKITDVVRS
 LKENDYITID DDRNVFLTD KGAAKLEQQL GISSLYDDEH VGSTLYQVNL ALHAQALLIR
 DHYIVRDSK VLLIDASGRG VADLQRWPDG LQAAVEAKEG LAVSEGGKIL DTITLQALIG
 RYPMACMGMT TAVEATDQLR TFYDLHVSVI ERNHPLKREF EADRIYATMA EKNRAIIDEI
 ALLHSTQGPV LVGTHDVAES EELATALREL NIEVSVLNAK NDAAEQIIIA EAGDIGRTVY
 STQMAGRGTD IRLGGADEAD YDEVVLKGLG AVIGTARHRS QRLDNQLRGR AGRCQDGPGLS
 LFFVSLDDDD VVSGGGRRESV SAQPDATGLI DSDRIRDWVG HCQRVTEGQL LEIHSQSWNY
 NKLADQRVI IDERRERLID TALAAWEELQ HAPARAEELE DLDQSVREQA ARDIMLYHLD
 YNWSEHLAM DDVRESIHLR AIARETFLDE YHRIAVREFK DLAQRAVDDA VSTFKSVTID
 HEGAHLDEEG LARPSATWTY MVSNDPLAGS GNSVISGIGN IFR

> RXA02436 (1-561, translated) 187 residues
 VVGISLDVVM MGVMTSKTAT AILHTNRGDI TIDLFGNHAP ETVANFVGLA QGTDKYQSAN
 AQGDSGPFY NGSVFHRVID GFMIQGEDPT TGRGGPGYTT FADEFHPELR DRDIMLYHLD
 NAGPGTNGSQ FFITVTPTPH LNNHAITIFE VTDAESQKVV DAIATTATDR YDRPADAVVI
 ESVEITA

> RXA02445 (1-1689, translated) 563 residues
 VEPFELEKDL ERLKRNKDD ETVEVKSNGR LPLSKGSKSF WESLSAFANT NGGYILLGLS
 EPDFTPVVEG DSQASIQFIR AGLNPQDRDA QKVEVPVHHE IHMTVDGAE VVLVSVSPLS

VNGPCYYLPV GIINGSFKRV GDEDRKLSHL EIYELQNRV QTKTDRNPVP DSSIDDLNNO
 LAASFQRLI ESNRSRLGTD DNWLLRKNIT TSKGELTIAG LLAGLSYPOQ FFRPRVIDVA
 VHPGLHKSPI GTSIRFEDRK ICEGNLEMV QEAMSAIKRN LRVRRVVEGL SGKDVLEIPE
 EVLRREALANA VLHRYSELA QNEAIHVDIY KDRVEITSPG GLPNKGKRPES ILDGSEPEPN
 RVLRLMLMDI PWTHEVQVGL AESNGTGVPF MFNLMRAGL PVPNFKIDTS SVTVLDSRRH
 LLDAQTSWL VEKLGSDFSN TQGIALLAK ELGAVTSRDL RNTQGHDSED MRSLLDALVD
 RGVNLQNLQN QYQLATSSVN VTQSEQEVLD AINKTTPVTI REIATKTGKT ASSRLPLLRG
 LVEAGLVVAT APFSSRNRAY LKA

> RXA02456 (1-618, translated) 206 residues
 MAENRTGTVD GDALAAFEE EALPLLDQLY GGALRMTRNP ADAEDLVQDT YIKAYQAFAS
 FKPGTNLKAW LYRIMTNTYI NMYRKKQRP QTSADEITD YQLVESQSH TGLGSAEVE
 ALKNLPDGKI GDMNQQLSPE YRMVYVYADV EDLAYKEIAE IMDVPLGTVM SRLHRGRKQL
 RGMLKEVAKE QGIGLEHPDM KKNSEA

> RXA02462 (1-915, translated) 305 residues
 EAGGLVLGT ERHESRRIDN QLRGRSARQG DPGSTRFYLS MRDDLNVRFV GPTMENMMNR
 LNVPPDDVPIE SKVTNSIKG AQAQVENQNF EMRKNVLKYD EVMNEQKRYI YSEREILES
 ADISRYIQNM IEETVSAYVD GATANGYVED WDLKDLWAL EALYDPSINW TDLVEGSEYG
 KPGELSAEDL RTALVNDHAH EYAKLEEAVS AIGGEAQIRN IERMVLMPIV DTKWREHLVE
 MDYLKEGIGL RAMAQRDPLV EYQKEGGDMF NGMKDGIKEE TVRQLFLSAS SSSSKTRKSL
 TNSEP

> RXA02476 (1-879, translated) 293 residues
 MSFTAFQAL LVWFRANARD LAWRDPNTSA WGILLSEVMS QQTVPARVEP IWREWEKWP
 TPEDFANAST DEILRSWGKL GYPRRALRLK ECAEVIVEKH AGEVPTDVEA LLALPGIGDY
 TARAVAAHFQ GQRVPVVDIN VRRVQRAVA GRYLAGPAKK QELIDVSLLL PNTHAPEFSA
 AIMELGALIC TATSPKCDTC PLLDQCQWQK LGCPSPSEEE LASAKKRVQV FVGTDQRVGR
 LIMDVLRNAT APVPLSAIEDV VWPDAAQRSR ALFSLIEDGL AEQNEAGYFH LPR

> RXA02502 (1-1392, translated) 464 residues
 MVSVLVGVMS HRSAPVSLLE RLSMDDSVRG ETTQALLGRA SLSEALIVST CNRLVEYTVT
 SSVFTGVNDG VLVHEASGV DIETLRGLY VRYADAAAEH MLVVTSGLDS MVLGEQOIIIG
 QVRTAYQAN EYGSVGPALH STQTALHTG KRHVSETAID DAGASMVSFA VDRALVQMLG
 DSEAEAPLGS KATLVLGAGA MSSLAATHLG RAGISNLIMA NRTLERAERL AEHSLEAGVP
 AEVVEYDQRA SAYNRVDLVV SATGADDETV KPEDIPEGAS LMLVDLSMPR DIDDACADLP
 GVDLVNIERL HKASREGGSG MAPSEEEALA IVREELDSFT SEQIRDIV AVSALARQAA
 SVGSDELDRL RQRAPGISEV EWGEVEKTGR RVVDKLLHEP TVRVKELAAE SSGISYDSAL
 QELFGLESIA STAAPATTSV NASELPDAGI VAFVNPASAT QIRE

> RXA02509 (1-1971, translated) 657 residues
 DLPNKGPFAI VCAKDAEGQL KDLSHVPETT ATFTAPVANT DDGRAVIRHS CAHVLAQAVQ
 AEFFPGKLGI GPAIENGFIY DFDAEFPFT EDLKTIEKRM KKIIKTQKQF ERRVYESAEA
 AAELLNKPEY KRLVIQDKN VDPNSDEATE VGAGELTAYD VNNPRTSEVE WSDLCRGPHI
 PTRYIYPAFA LTRSSAAYWR GDQDNAGLQR IYGTAWEDKE SLDAYQTMLA EAEKRDRHRL
 GTELDLSFPP DDLGSLPVF HPNGGIVRNE MEDHSRRRHI AAGYSFVNTLP HITKQDLFER
 SGHLGFYKDG MFPMPQVDAE FDEGDNVTKP GQEYLLKPMN CPMHNLIFDS RGRSRYELPL
 RLFEFGNVYR YEKSGVHGL TRARGFTQDD AHYCTEDQL EAELTSVLDF ILSLLRDYGL
 DDYFYLELST DPKKSVGSD EWERSTEILN RVATNSGLEL VDPPEGAIFY GPKTSVQARD
 AIRGTWQMSV VQLDNPMPER FNLEYTSSDG SKQQPIMHR ALFGSIERFF GVLLHYAGA
 FPAALPHQV MGIPVADDCI PHELTITACL REKGRADVD TSDDRMQKKI RNHTTGKLVF
 MLAGARDE ANAVSERFLD GTQVNGVPVD EIAVIVSSWI GDRINDQPSE DSIAARR

> RXA02523 (1-819, translated) 273 residues
 VTIFPEYLPD LRHALLGKAI EDGILEVGVH DLNRNATGGH KAVDDTPYGG GPGMVMKPEV
 WGPALDDVAA GRVSGAELDS ASLHLKNNVRH DELGGVEKRA YVVEEDRDLP LLLVPTPAGK
 PFTQADAQAV SNEEHIVFAC GRYEGIDQRV IDDAANRYRV REVSIQDYLVI ICGEVAIVLVI
 AEAVVRLIPG VLGNRRSHEE DSFSDGLLEG FSYTKPRTW RGLDPEVLFES GNHAKVDRWR
 RDQALRLTQA IRPELIDASL LDSTDLKVLG LDK

> RXA02557 (1-588, translated) 196 residues

MSSLIVGTGDS LSRPSSWAAQD PLMRDYYDTE WGMPIRDEQG LFERVSLEAF QSGLSWATIL
MKRDSFRAAF SQFDPKELVAK FTDADIERLM EDAGIVRNKR KILATINNAK ATLQLEKRG
LVEFVWGFKP IDTPQPETLE EIPTQSPESV ALSKALKKEG FSFVGPTTMTF ALMEAIIGIVD
THLVGSHRRG SSGVWA

> RXA02563 (1-732, translated) 244 residues
MMPYITDIAA LEHVGVAAAQ TEKVPFRVL REKRMLDFRA PITVITGENG VGKSTLLEAI
AINAGFDTAG GEHTGKFKPS DNFLQTVAKA HKGKEPMRGY FLRAETHFNV ASGYRDEAGG
WVNLHHMSHG ESMVHIVQNA FVGKGLYLM DPEAGLSFIR QMAILAEALF LAESGAQIII
VTSPVLMAI PGAEIWEFSA SGELHRGFDF EVTTAFRALR DFFEDPEETA EYMMDMVMMDN
KGES

> RXA02590 (1-936, translated) 312 residues
MGISLLSLL KIHGFPPVAD FFFALAVVVA IVIIGGWLIV RSPSFKTEVM PAWAMLSMGL
IALGTASPVV LGDDLWGFME VCVSIGTAVG LVAYSLEYITA ILRSKAGTPT FAWGLPLVPT
MVASTSAAQL HEHFELPAML WVSFGLLELLT LASAPAVETR VYFYFPGPKA QGIFLMATPT
SWIPLGMVGQ STAAAQLIGA SFGSKTATM GIYGIIMGI FTIPLGAIAH VFYFRAVFGK
ATYSPTWAS STFPVGTLSLG AHFLSQSTGV EWFNYFSLYL IALMLFHVIV STIAGTIAVM
RRIVGKLKSK LA

> RXA02607 (1-219, translated) 73 residues
MRDTAFRSIK AKQAQKRSL WIAAGAVPTA IALTMSLAPM ASAQSSNLS DAVIGSIAQG
VTDGLTDYLK PRV

> RXA02608 (1-1695, translated) 565 residues
VRVISAEWAT SKHVILTIQS AAMPERPIKV QLLLPDRWYS SPNREFFETW ALDGLRAIEE
QSGWTIETNI EQYADKNAI VVLPVGGESS FYSWDEGPNN GKNYQWETFL TQELAPILDK
GFRSNTDRAI TGISMGGTAA VNIATHHPDM KFEVGSFSGY LDTSAGMPT AISALADAG
GYDANAMWGP VGSERWQEND PKSNVDKLGK KTIYVSSNG ADDFGKEGVS AIGPANAAGV
GLEVISRMTS QTFVDRASQA GVEVVASFRP SGVHSWEYQ FEMTQAFPHI ANALGMSTED
RGVECAPVGA IADAVADGAM GTCLTNEYDV TGGKAQDFAN GRAYVSNANTG AFLGLVGRINA
RYSELGGPAS WLGYPTSSSEL KTPDGRGRFV TFEHGSYIWT ATTGPWEIIP DMLAAWGTQD
YEKSLGYPT GAAYEYNGGL RQFEGGYVF RTSNNQSYWV RGEISKKYAE DGIFAQQLGF
TGNEKLINGG AFQEFKNGNI YWSASTGAHV ILHGDIFDAW GAKGWEQGEY GFPTSDQTAI
TAGGQTIDFQ NGTIRQVNGR IESR

> RXA02625 (1-786, translated) 262 residues
MTAAFYDLMD FDEVLEKYDP VMGLEVHVEL GTETKMFAS SAHFGEFNS NVDPVSLGLP
GALPVVNAKG VEWAIKIGLA LNCSTAESR FARKNYFYDP QPKNYQISQY DEPIAYDGYL
DVVLEDGTWEV RVEIERAHME EDTGKLTHLG GTSGRIGHAT ASLVDNCRAG VPLIEVVTKP
IEGAGARAPE IAKAYVSALR DLVKALGVSD GRLDQGSMRV DANLSLRPIG QEEFGTRTET
KNINSLKSV E QASTFEMRQ AQ

> RXA02671 (1-579, translated) 193 residues
MKSCGCFEVS DGIKEVPDPS GLFLSHRGST PDGTAVTVAM DGVRPLLAEV QSLLVDPASK
NPRRVYGLD ANRVPMVLAV LSARAGROTQ GKDAYVATVG GMKVGEFATD LAVALATAGA
LAKKPLPKDT VVLGEVGLAG EIRRVFNVD RLAEEARLGY EKAVIPGGSG IKQTSRLVIE
ASTLAELAA VSL

> RXA02686 (1-1137, translated) 379 residues
MSVAQLANRL AQLSPAHEGF AWFDEPITAG HGVQPLHGMV IPAKDLNDVA GMPTAFGNAS
RRKVATDTPD FIQNLIDRGA IAGTKTQSE LGMTAYCEPI DMDAPSNPVL PGHTPGGSSG
GAAVAVARSL VDAHASDGG GSIRVPAAAC GLVGFKAHD SSGGNPSTQG FITRDVATQV
RLHALQFTRR RLRIQVLAEP IHANSLVDAP FLSILESTA LLEKAGHEIV SVPLPYGAWA
FLDAYTEVFM KSAGLNLGS PITRNLSEQG RSLSPSDRQS SVKAFDSVAE TVHGAWDIDV
LLTPTLAYAP PKIGYFSSMP FEEDFLAQTK WTPWATLFNM TCGAAISVPV EGVGIHLGGI
RVRDDELGL AAFVERAVA

> RXA02692 (1-1266, translated) 422 residues
MIDLKFLRN PDVVRASQIT RGEDPALVDE LISADESRRE AIKAADDLRA EQKAFGKKIG
QASPEDRPL LEGSNELKAK VKDAEAAQEA AEAKVNLQM KLSNVVSGAP AGGEDDFVVL

ETIGEPRTFD FEPKDHLELG ESLGLIDMKR GTKVSGARFY YLTGDBGMLQ LGLMLMLAAQK
 AREAGFSMMI PPVLVRPEIM AGTGFLGDHS EEIYYLERDD MYLVGTSEVA LAGYHKDEII
 DLNEGFPVKYA GWSSCFRREA GSYGKDTGT LRVHQFDKVE MFVYCKPDEA EDVHQQLGLM
 EKEMLAATEV PYRVLDVAGG DLGASAAKFK TTEAWVPTQD TYRELTSSTN CTTTQARRLQ
 TRYRDENGKP QIAATLNGTL ATTRWLVAIL ENNQADGGSV VVPEALRPFV GKVDLKPVKQ
 AG

> RXA02726 (1-2934, translated) 978 residues

LPLATRPCRG YRVPRVFSWD THGLPAELEA EKQLGIKDKG EIEAMGLAKF NEYCATSVLQ
 YTKEWEEYVT RQARWVDFEN GYKTMDSLSM ESWIAFKEL YDKGLIYQGF RVLPPYSWAEH
 TPLSNQETRL DDSYKLQDDP TLTVTFFVTG VVEGSSANAG LVGALALAWT TTPWTLPNSL
 ALAVNPVITY ALVEVAEDGE AEFVGRVLL AKDLVGSYAK ELGAEAVIYS EHPGSELVGL
 TYEPIYGFYR DHANGFQILG AEYVTTEDGT GIVHQAPAFG EDDMTCNAA GIEPVIPIVDI
 DGKFTGLVPE YQGQLVFDAN KDIIKDLKAA GRUVRHQJTE HSYPHSWRSQ EPLIYMALPS
 WFNVNTEIRD RMVEVYNQDIE WMPAHIRDGQ FGKWLLEGARD WNISRSRYNG SPIPAWVSDN
 DEYPRVDVYG SLDELEADFG VRPKSLHRPD IDELTRPNPD DPTGKSTMRN VTDVLDVWVF
 SSGSMFPAQVH YPFENKEWFD THAPADFIVE YIGQTRGWFY LLHVLSTALF VDRPAFKVVA
 HGIVLGGDDL KMSKSGKNYP NVNEVFDRDG SDAMRWFLMS SPILRGNGLI VTEKGIREGV
 RQAQLPMWNA YSFLQLYTSK NATWSVDSTD VLDRIYLAKL HDLVAETQAA LDGTDIKAC
 DLVRNFCDAL TNWYVRRSRD RFWAGDEAHP EAFNTLYTLV ETLTRVAAPL LPMTEVILWR
 GLTGERSVHL TDFPSAESFP ADADLVRTMD EIRGVCSSAS SVRKAHKLNR RLPLPLGTLVA
 LPDSARLADG ASIIIRDEVNV KNVDLTSDVD SVGTFEVVVN AKVAGPRLGK DVQRVIAKVK
 AGNRYREGDV VVADGIELNE GEFTERLVAA NPDSTAQIDG VDGLVVLDME VTELEAEAGV
 AADAIRGLQD ARKNSGFEVS DRISVVVSVP EDKKEWITTH ADHIAAEVLA TSFEIVTDAL
 DGETHDIVAG VTAKEVTKN

> RXA02731 (1-2097, translated) 699 residues

MAFAAEHPVL SHSEHRPVGE IERSDDKFVV VSEFEPAGDQ PAATKELDER LDRGERDVVL
 MGATGTGKSA TAAWLIEKQQ RPALVMAPNK TLAAQLANEL RQLLPNNAVE YFVSYYDYQ
 PEAYIAQTDI YIEKDSSINE DVERLRHSAT SLLSRDVRV VVSSVSCIY LGTPQSYLDLH
 SVVLNVGEEI DRDRFLRLV QIYERNDVGT FTRGAFFVKQ GTVDIIPAYE ELAVRIEFFG
 DEIDLALYIH PLTGDTIRQV NEIRIFPATH YVAGPERMKE AVADIKAELE VRLADLENRG
 KLELAQRILR RTEYDLEMIE QVGFCSGLEN YSRHIDGRGE GTAPATLIID YPEDFLIHD
 ESHVTPVQIG GMFEGDMSRK RNLVEFGFRL PSAMDNRLPT WEEFDERRGQ TVFMSATPGK
 FEIAAADGEF VEQVIRPTGL VDPKVTVKPT KGQIDDLIHE IRQRTDKDGR VLVTTITKKM
 AEDLTDYLL E NGIRVRYLHS DIDLTLQVREL RLQRLGLEVD VLVGINLLRE GLDLPEVSLV
 AILDADKEGF LRSTTSLIQT IGRAARNVSG EVIMYADKTI DSMQYAEET DRREKQVAY
 NKEHGIDPQ LKKIADILD QYVDNSADGA GPSASGDAAV VAKPDVSSMP AKEVQKLIDD
 LSQAAMAAAR ELKFELAGRL RDEIFELKKE LRGIKDAGI

> RXA02742 (1-2349, translated) 783 residues

MSEQRDLQLE RRLSELEREI AAIRQEIQRQ RLVLPEPEPV KVDTVIATEA TGVNASSGPE
 AKIALEMERF SGRHDVYARR WTSRKTGKSG WSPATRGQFY SKDTPPKDYI PFTVDTVNAH
 LRGGGDHGL YVMVIDTCK LLACDFDDGT WKODAAAFVS ACTDHGIDAL AEISRSDDGD
 PVWIFDPTPI SAMLARRLGF AMLRQAMNSR PMDMSSYDR FFPAQDTIAT RANGSARLGN
 LIALPLNGDC RARNTVAFAD SETWVFEDP FALAATILPT ATEKIEQIIA TQEKFGPEP
 EHTKRPTRA E LKQVKANGET IKLTITNELS VPTERLPAAV TAEIKHRAVI PNPEFYRROA
 QRSTFGVPR IVIRFAQAEQ RLLPLRGLVD DTLRLTLTAG YKVSVIWPRQ TRKTDISAFE
 GELRSMQOEG IDSLLGQRTG VLVAPPAGAG TVMACALINR RKIPTAVIYN RAEILSQWRD
 RLQAQLSLDA DSIQIGIAGR RKTGTGIDLI TVQSLSRKDS DPKILEQYQ IIVDECHNIA
 APGAEAALN VKAPYWLGLT ATPFRSDHMD EIITMQCGPV RHRMEVATDN EQRILIHET
 SFDSEETTEE QDLYNELAVD SARNAQITAE VHKALEAGDR CLVLVNRRIA LEALTSITE
 SGDHTVLVMH GRQTQEEVRH LRAQLASLSE KQDPFVLVAM NKVAGEGLDI PSINTFLAA
 PVSFKGLVIQ QIGRVTRATG DQNAAPPVTAT VHDVFDSKIP TLKRMHGRL RAMQKEGFV
 SEP

> RXA02748 (1-1641, translated) 547 residues

VFESLSDRIN SALSLGRKGG KLTEADINAT TREIRLALLE ADVSLTVVRA FINRIKERA
 GAELVQALNP AQQVQIKVNE ELVQILGGET RRLSLAKNPP TVIMLAGLQG AGKTTLAGKL
 SKHLVQKQHT PMLVACDLQR PGAVQQLQIV GERAGVITFA PDGTSIDSL EHEMGTHSGH
 PVEVARAGIE EAKRTQHDI V VDTAGRLGI DETLMTQARN IREAINPDEV LFVIDSMIGQ

DAVDTAEEAFR DGVDFGTGVVL TKLDGDGARG AALSIREVTG KPIMFASTGE KLDDFDVFP
 ERMASRIILGM GDVLSLIEQA EAVMDQEKAE VAAQKLGSGE LTLEDFLDQM LMIRRMGP
 NIKMLPGGK QMSQAMMDV EKQLDRICAI IRGMTPAERD NPKILNASRR KRANGSGVT
 VSEVNLKVER FFEARKMMGQ MAGQFGMGPG SRSATKKQAK GRKGNGKRR PAKKGTPQK
 MPMGGMFGMP GMPGGMGAGM PDLAELQKQL GGAGGGMGGL GGGPLGMPKP PKGMENIDL
 NLDFGKK

> RXA02788 (1-2664, translated) 888 residues

VQTHEIRERF TNHFVNAGHQ AVPSASLILD DPNLLFVNAG MVFPKPYFLG QQTPTPFENG
 ATSIQKCVRT LDIEEVGITT RHNTFFQMAG NFSGQGYFKE GAIHAWGLL TGSVADGGFG
 LDPERLWUTV YLDDDEAAEI WEKKIGVPSE RIQRLGMADN YWSMGVPGPC GPCSEIYYDR
 GEKYGKEGGP VADDNRYMEI WNLVFMKEKER GGGIGKDNFD ILGDLPKKNI DTGMGVERVA
 CILQDVENVY ETDLRLPVID VAETLTGTGY GSDNTSDIRF RVIADHSRTG MMLILDGVPT
 GNEGRGYILR RLLRRIIRSA RLLGATGETM EQFMNTIMDT MTPSYPEIAD NRERIMRVAV
 TEERAFKLTL VSGTHLFEEA ATSIKAAGST KVAGAQAFAH HDTYGFFIDL TLEMAAEAGL
 EVDVEGFDLS MAEQSRRAKA DSQAKKHGHT DLSIYREWVD NNPTVFTGFE ELDSQSKVLG
 LLLSDGAKISE ATEGQVEEVI LDQSPLYAES GGQLGDRGQI LLGDTVLVDH DVQIKGKLLW
 VHKAIVANGG LAVGDEVVAS VDKQWRHAAR QAHTATHLH AALRQVLGPT ALQAGSMNKP
 GYLRFDFNYT EQLTPAQVEQ IQAITNEAVD TDWAVNTVET SLEEAKAMGA MALPGENYGS
 TVRVVEIGGP FSEMELCGGTH VAHSSQIGPV ALLGESSIGS GVRRIEAYS G LNSENYLSKE
 RALAEGLASS LKAPSEELPE RVAQLVDKLK AAEKEIEALH RQQLMAQTAD LLNNAQEIGG
 VTTLLLRVKD NTNAGDLRTI ATTLKDKLGD REGVLVTASD NAGKVPFVVA ATKAAVARGA
 HSGNLVKLVG SYIDGRGGGK ADLAQGSGAN IAGLESFAGA VRAETIAL

> RXA02822 (1-570, translated) 190 residues

GTEVSHPAHG AWSQPKFEGG VHRVQRVPEVT ESQGRQITSA AGVLVYPEPD EVENVEIDEK
 DIRVDYRRSS KGKGGQVNTT DSAVRITHLP TGLVVTQKE RSQIQNRARA MQVLAARLQA
 MKEEEAABEA ATGRAAQIRT MDRSERIRTY NWPENRISDH RIGFKANNLD SVLDGELDDL
 FTALQAEARA

> RXA02837 (1-174, translated) 58 residues

MNTKLHAYVD ATGRPIRFFM TAGKVSDYIG AMALLGSLPK AGWLLADRGY DADWFRDA

RXA02860 (1-438, translated) 146 residues

DLQNPFAKMS KSGDNPKGII NLLDDPKVST KRIKSAVTDN DGVIAYPDEN KPGVSNLLVI
 QSALTGTSID SLVDGYQGAG YGALKGDTAD ALEAFTTFLK AKYDEYMND R GELERVLAI
 AERATEVANE TLADVDYKIG FLASRR

> RXA02866 (1-480, translated) 160 residues

MTTQDKDLTA QTSASVLSGI QPTADSYHLG NYLGAHVQWI DLQDSYDAFY FIPDLHAITV
 DQEPPEELNR TISGAQAALL LGIDPERSTL FVQSHVPAHA ELSWLVLTCLT GFGEASRMTO
 FKDKSKRGGA DRTSAGLFTY PMLMAADILL YRPHLVVPE

> RXA02886 (1-831, translated) 277 residues

MKLFSPKAAGV IAAALLVAGG IAPVAQGGAS QVVTPEQDA YVQQFHHEGN TPPVVDGVGG
 YTEQEIAIEH EATRQAQESG APNEELIPGE MNSDKVELPV TIDKAAADEA EIAIAQQSQO
 PQRGLAARAA ACQTFWPSPH QVCGAILERY IQGGAQFGWM LFPSEGQTLN PDGGQGYRQR
 MNGFVYWRPT TGAHAVNNYS AQVWERNGWE SGWMMGYPTG EVPVNGSNPI DGELSGWVQT
 FQGRGVHSEF VLDGVPQVASI NGLILDKWLK LGGPDSD

> RXA02890 (1-1083, translated) 361 residues

MHEGRYRSAP HTFGTKGEAQ EFLASERTAI INGTWMDFEM RERFEQAQRE AEERMETTF
 SYASRWIETR TNAQGGKLSQ GVKDDYFRYI KSDRLSYWAD YALCEITVAD VREWYSDTIQ
 DGKLTSMARS YSMKMSVMEI AVEDGIIPMN PCKVRGGGNT KTGKKVDVPT DAELEAIIGA
 LPSKYFCLAI VAAAGALRFG EIVALRTTDV DVFDRSGFV DCVRIIRISRS IHRTRYHGRV
 EGPPKTEAGV RSLYIYGKDA AETAKHVDTI DVGRLRLWSSM RDPDEPMFYH TFKHNWDRAR
 ESVHSKATVH SMRHYSGTGY AQVGATLKEV MARLGHSTPS AALRYQHSGE RDEELAKRMA
 R

> RXA02894 (1-786, translated) 262 residues

FLMHLEPEPL EAAIGADGQR SIVGMSMSGG SVLNFATHDP NFYSSVGSFS GCAETNSWMG

RRGIAATAYN GNVVPEQIFG EVDSDYSRYN DPLLNAAKLE EQDNLYIFAG SGVSELDVI
GDNAPIDEDA FKNRVLVGF EAMSN'TCTH NLKAATDQMG IDNIN'DERP TGTHAWDYWN
EALHRRFFPLM MQGFGLDGGP IPVYNPNGVS SSSSSSELSS DVSLGTVIGS VAGSSGSSE
SSVREFLAGSS SGSSQSTGSF YE

> RXA02904 (1-675, translated) 225 residues
TDPRIYLGKD DLPKATIDME PEALARLERF VGVVDGRIRQ INAYSPSMGR TIPLVWVVPE
DN'TVPGPTVY ALGGGDDGGQ GQNWVTRTDL DELTSENIN LIMPMLGSSF FYADWAGESE
SMGGAQWET FILMHELPEPL EAAIGADGQR SIVGMSMSG SVLN'FATHDP N'FYSSVGSFS
GCAETNSWMG RRGIAATAYN GNVVPEQIFG EVDSDYSRYN DPSIL

>RXN00046 TRANSLATE of: rxn00046.seq check: 4489 from: 1 to: 696
MDLNTQRSKLYAQLQGQLIVSVQAPDGHAMRDTHLT'HVAAACVDGGAPAIRCGGYGGLLE
DIRSISNRVDVPVFGITKEGSEGYITPTRDSVRAVAESGATVVCADATFRPRPDGSTFA
ELVTVAHDSGILIMADCATPEEVL'SAHKAGADFVSTTLAGYTEHREKTVGDFDCLREAR
ELVPDAFLIGEGRFSPADVAHGR'LGANAIIVGTATIDPGFITQG'FASLLH

>RXN00083 TRANSLATE of: rxn00083.seq check: 5101 from: 1 to: 300
VTLFSSIIDPLWCQFAALIPPVTDTHPLRCHRPRIPDRIIDFKLIQVLVLGASYAKIAD
TTCSATTLTRRDEWITAGIEFQLEQICLEFYDRIVGLDL

>RXN00127 TRANSLATE of: rxn00127.seq check: 8871 from: 1 to: 465
WVTLSPYDGGHRNVIALKEHGRADLVAFVGVAVGASISYLA'AQGEIEHDI'LVVAPATRA
TSRRRRGDPVERVCNASRLSTFPCLQISSRTPD'PSVGQTAQQRRLNMRV'ELVQPRGSVL
IIDDVVTTGATISASANVLAAGVQVRGALTYCQA

>RXN00172 TRANSLATE of: rxn00172.seq check: 1609 from: 1 to: 612
MFGSSFEQTTNPRSQRVSYLRVSSTDQNLARQEA'VNHSCHIDREFTDLSGGAKSHRP
GLEDCINYLREDDVLVVASIDRLARSLVDL'RVIIDRITDKGASVIFLKENLT'FAAGRDP
RANLMLGILGSGFAEFERSIIRERQAGIALAKKACKYAGRPKALDKEQIQEAKDMAIQAQE
TKSAVAKHFGNRRSTLYEYLNKPD

>RXN00211 TRANSLATE of: rxn00211.seq check: 7693 from: 1 to: 663
MSFLIRVLLSDTPGSLALLAEALGIVEANIQSV'DVVERFNGTVMDDLVISIPRDVMA'DT
IITAAEEVDGVEIDSIIRPFSGTVDRRGQIQMLAAVAHQRRDITAAMEEMVDV'IPRTMTSG
WALVIDLKGPI'TRIAGSLAEPDDCTV'PENIVLKEARMLNPENDF'WIPESWTL'DSSLA'I
APIGKHGLALIIGRPGGPDFLASEVEHLGQV'GDIIGAMLQK

>RXN00380 TRANSLATE of: rxn00380.seq check: 9027 from: 1 to: 621
VRITKLAATIGCVTL'SGLALVACSSDSTAGTDAVAVGGTTFQFHSPDGKMEIFYDEADRQQ
LPD'IGDGSIMEEGTQINLSDFENQV'VILNAWGQWACPRSESDDLQI'HEELQAAGNGDT
PGGT'VLGINVRDYSRDIAQDFVTDNGLD'YPSYDPPFMTAASLGGVPASVIPTTIVLDKQ
HRPAAVFLREVTSKDVLDVALPLVDEA

>RXN00454 TRANSLATE of: rxn00454.seq check: 9628 from: 1 to: 1293
MCGEAGCTLDLAFMSDLSFTLNNKLADAPGKHGR'TGVIHTPHGDIATPAFIPVATKATV
KTLTPEQI'RETGAQAILSNAYHLYLQCPD'IVDEAGGVSAFENWHGFTYTTDSGGFQVMSL
GSGFKVKLAMDTNLTNRNDIKAAKKERMALV'DEDGVDFKSVIDGSKHRTPEVSMQIQHQ
LGADII'FAFDLTTLVDTYDYQVESVERTRRWAQRC'CLEHERLTQERVDKPLQSLWG'VVQ
GAQFEDLRQAVKGLLDLDRQAAD'EGRRGFGFGIGGALEKENLGTIVGW'WCDLPEDKP
RHL'LGISEPDDLFAVEAGADTFDCVAPTRLGR'RGVYTL'DGRMNLTGARF'KRFDFKGI
EVGQYASENYSRAYIHLLKAKEFLAGT'LTCTMNRNLFHMTIVDKIRASID'GTYYEFKEE
FLGRYYASVS

>RXN00458 TRANSLATE of: rxn00458.seq check: 4019 from: 1 to: 636
MAGRYAPSPSGDLHFGNLTALLAWL'FARSEGGKFLMRVEDIDEQRSSKSAESQ'LAIDL
ALG'DWDGDVLYQSTRYDAYRAALEKLD'TYECYCSRRIQASRA'PHVAPGVYPGTCRGL
KEEERVEKRATLAAQNRHPAIRLRAQVTSFDFHDLRGPQ'GTGPVDDFILLRGGQEP'CWAY
NLTVVVVDDAYQGVQVQVVRGDDLLEFGARQATL

>RXN00484 TRANSLATE of: rxn00484.seq check: 6349 from: 1 to: 1080

VDA TLKKNLRDKGIEVHSHPGFLLTEPWEVSTATGTPIYKVTFPSKAAWEVARVHAYETV
KNNVPVPSHLTGPEDVELPILEMEQFWSSTLVKECAPGEKNASEKLFDFLEHLQDYPQA
RDSLARSATSKLSAHLRFGEISIHVWAETAADISEGTEFLFKELLWRDFAWHRLYALPH
MDTQNVRMQFNRFEGSWDPEKDKLNTPSTPLIPTKADQFHEDLAARAGKTGIPLVDA
MRELWATGSMHNRVMVASFLLTKNLQIHWHRHGEWFWETLVDA DPASNAFNWQWAGSG
DDASPYFRIFNVPVTKAKKFDPEYIIRWVPEYGTSPYDPDIVDLKESRQIALDAYSAIK

>RXN00493 TRANSLATE of: rxn00493.seq check: 4601 from: 1 to: 1614
MAKLIAPDQDAREGILRGVDALANAVKTLGPRGRNVVLDKAFGGPLVNDGVTTIARDID
LEDPFENLGAQLVKSVAVKTNIDAGDGTATLALQALIAEGLRNVAAAGANPEMLNKGIS
AAAEKLEELKARATEVSDTKEIANVATVSSRDEVVGEIVAAAMEKVKGDKGVVTVVEESQS
INTELEVTEGIESFDDKGYLSPYFINDNDTQQAVLNDPAVLLVRNKISSLPDFLPLEKVVVE
SIRALLI IADVEGEPLQTLVNSIRKTIKVAVKSPYFGDRKAFMDDLAIATVKTATVVD
PEVGINLNEAGEEVFGTARRITVSKDETIIVDGAGSAEDVEARRQGIIRREIAGTSTWDR
EKAERLAKLSGGIAVIRVGAATETEVNDRKLVRDAINAARAAAQEGVIAAGGGSALVQI
AETLKAYAEFEGDQKGVGRALATALGKPAYWIASNAGLDGSGVVVARTALPNGGGFNA
TLEYGNLINDGVDPVKVTHSAVNVATSVARMVLTTASVVEKPAEEAADAHAGHHH

>RXN00669 TRANSLATE of: rxn00669.seq check: 6043 from: 1 to: 882
MDNSTVRIRLDLAYDGTDFHGWAKQGTSDLRITVQKVEDNLSMVLRETVELTVAGRTDAG
VHAAGQVAHFEDI PAHALEQRSIDGDP SKLVRRLGRLLPDDIRVHGVRFAEPGDFARFSAM
RRHYVYRITHTHPAGALPTRRHDTAQWPKPELERMQLAADALLGLHDFVAFCKAKPHATT
VRELQKFAWKDVSTDI EPQVYEAHVADAFCSMVRSVLVSGCMVAGEGRGSGFTAEALLD
ASERSPMVPVAPAKGLSLVGVDYPSADKLQERALETRAVREFPDASASLKLDDE

>RXN00737 TRANSLATE of: rxn00737.seq check: 824 from: 1 to: 993
MKVSDIRQFSVADQRTIPEITIKSIEIFPARELLITEEVSARAESLISKHPGNPTLVEML
SRIADSQVDGMEALIPALTDPTMVPMLLEMPENTHVLVIAPEKVRRIADLEATDAEFL
MAGWEEAAMAGADGPVAAEGLDLEASSYRSYESASKSVDYRWWTFAPGMEFAESAEF
LPLDEAGAPAPRGELPKIDAMMAQLLAHTTGGGAAFIAPTQGAIKRMVDRFAEKGIPT
VATPGWEPTPGQVTLHYALSHAGLVFPKVRKHRDGAAMPLVVI TETDLTGNRVGDIAGR
VDLQNAARTWILMRWSQGIWFMKPTALVVL

>RXN00833 TRANSLATE of: rxn00833.seq check: 7757 from: 1 to: 495
MAKTHFQGNETATSGELPQVGDNLAEFNLVNTLGEVSSKDFQGRKLVNLNIPSVDTGVC
ATSVRKFEAAASLENTTVLCISKDLFPALGRFCSAEGIENTVPVSAFRSTFGEDNGIVL
EGSPLKGLLARSIVVDENGKVAYTQLVDEIFTEFDYDAALAGLN

>RXN00937 TRANSLATE of: rxn00937.seq check: 2481 from: 1 to: 372
MATIDVTEETESTVTGDI VLDVAWSWCGPCRQFAPTYEKVSETHDTATFAKLDTEAN
QGLAAALQIQSIPTLMVFRDGMVYREAGTMPAPALDDLQNVQKALMDMDVRRQVAEQGQ
SAEA

>RXN00966 TRANSLATE of: rxn00966.seq check: 3319 from: 1 to: 540
MTNPFEGTTPPLAFRYTELPANKIEGEQNYWTDNGTFNAPNPVGLDAPADGKALPEDKLF
VQDMFFYPGAGLHVHGHPGLGIATDVFARYNRMKGNVHLTGLYDAFLPAEQYATQTGT
HPRTTMANIENMKRQLGALGLGHDSRAVATTDPEFYKWTQWIFLQIFNSWFDAAEQQKA

>RXN00975 TRANSLATE of: rxn00975.seq check: 760 from: 1 to: 1650
MTPADLATLIKETA VEVLTSRELDTSVLEQVQVVERPRNPEHGDIATNIALQVAKVVGON
PRDLATWLAELAAADDAISAEIAGPGFLNIRLAAAQGEIVAKILAQGETFGNSDHLSH
LDVNLFEFVSANPTGPIHLGGTRWAAVGDLSGRVLEASSAKVTREYFFNDHGRQIDRFALS
LLAAAKGEPTPEDGYGGEYIKEIAEATVEKHPEALALEPAATQELFRAEGVEVMFEHKS
SLHEFTGDFDYYHENSLEFSGAVDKAVQVLDKONGNLYENEGAWLRSSTEGDDKDRVVI
KSDGDAAIYAGDIAYVADKFSRGNHNLNIYMLGADHHGYIARLKAAAALGYKPGVEVLI
GQMVNLRDGDKAVRMSKRACTVVTLLDLEAIGIDAARYSLIRSSVDSLSLIDLGWESQ
SSDNPVYVYQGHARLCSARKAETLVTEEGADLSLTHDREGDLIRLTLEGEFAVVKAA
ADDERPHRIAYAEELAGTFHFRFYDSCHLLPKVDEDTAPIHTARLALAAATRQTLANALH
LVGVSAPPEKM

>RXN00985 TRANSLATE of: rxn00985.seq check: 4212 from: 1 to: 2709

MVCVTQDNNETTSQNRADKLPSWDPKAVEADLYQGWVDAGYFTADPASDKPGFISVLPFP
PNVTQGLHMGHALDHTLMDALARRKRMQGFVEMVLWLPMDHAGIATQTKVEEMLKETEGKT
RYPDYDREEFIKAWWENKQYEGGKIGEMQRAIGDSVDSRERFTLDGLSRVAVTIFKKLF
DAGLIYQANRLVNVNSVPLETAVSDIEVIYKDVGEGLVSIYRGLNDDEPHVIVATRVET
MLGDVAVAVHPDDERYKDLVGQTLPHFPRDLDLSLVVADDYVDFEFGSGAVKTI PAHPDN
DYLGLRLHNLDMPTIMDKTGRADTGTQFDGLTKEEARIKVREELAAQGRIVREKIPVYH
SVGHSESRGEAIEPRLSLQWVFKVEELAKMSGDAVREGDTHIPKSLPRYFDFWVNDMMD
WTISRQLWNGHRIPIWYGPNDEIICVGPDEQAPEGYVQDPDVLDTWFSALWPFSTMGWP
EKTPELEKFPYRSLVLTAYDILFFWVARMMPFGTFAAKETPELLGEGKDRGPQVPTDLP
LHGLVRDEHGKMSKSLNGIDPMDWVENYGADALRFTLARGANPGVDLPVGEDSAQSSR
NFAATKLFNATKFAALMNGAVSEGLPAREELTDADRWI VDLLEQVRLDVAIDLNYQFAKAN
EELYHFANNEFCDWYLEIAKVQIPREGTSAQGENTQKVLGHVLDALLRLHLPAMPFVTEV
LWQALTDRTSIVVASWPTAADTNGGVAVDADAARRIGDVEKLVTEVRRFRADQGVKPSQK
VPARLDFVACLDQLEDVSRLVRIEQPEDDFAASASLEIRLSQATITVELDTSGTVDVA
AERKLEKDLANAQKELETTAKKLGNEAFLSKAPDAVVDKIRGRAQIAQEEVERINKRLE
ELA

>RXN01061 TRANSLATE of: rxn01061.seq check: 5052 from: 1 to: 1038
ISRYREQFCNIENERYWTGPRPETHGPNDPGGVDLYVGGVEHAVLHLLYARFHHKVLFDL
GHVSSKEPYRRLYNQYIQAFAYTDSRGVYVPADDDVEEKDGFYQGEENVNQEYKMGKS
LKNVAPODDICNNFGADTLRVYEMAMGPLETDRPWATKDVVGAQRFLQRLWRLVVDENTG
EVLTRDEVLTDDDNKQLHRTIAGVRDDYTNLRVNTVVAKLIEVYNYLTPTYPTIPAGAV
LPLIVMVSFIAPIHAEELWKKLGHDDTVTYEPFPTFEKWLTDDEIELPQVNGVKVRGRI
TVAADASQEQVIEAALDAEKVQEQISKNKLIKQIVVPGRMVNLVVK

>RXN01284 TRANSLATE of: rxn01284.seq check: 2030 from: 1 to: 567
VAKAFERTKPHVNIPTIGHVDHGKTTTAAITKVLADTYPELNEAFADSDIKAPEEKE
RGITINISHEVYQTEKKRYAHVADAPGHADYIKNMITGAAQMDGAILVVAATDGPMPQTR
HVLLARQGVGPYIILVALNKCDMVEDEEIELVEMEVRELLAEQDYDEEAPIVHISALKAL
EGDEKWKQKQ

>RXN01345 TRANSLATE of: rxn01345.seq check: 9398 from: 1 to: 1452
MRFGDLGTTTITIAAAGVDRGNYPITVVEDSLGDTHTDFIPSVVALKADRI VAGWDAIEVQ
DHPSFVRSFKRLLESPNVTEATPVYLGDVHPLGAVLEAFAENVVLTALRAFQTLQDGTSP
IEVVIGVPAHNSHSAQRLLTMSAFSATGITVVLVNEPSAAAFYTHRHARTLNSKQIAIV
VYDLGGGTDPSSLRIDGTHHEVVSSIGISRLGGDDFDELLQCALKAAGQHDHAPGKRA
KNLLDESRAKEALVPQSRRLVLEIGDDITVPVFNKFEAAATPLVEKSLNMEFLIGVD
DLKDSDIAGIYLVGGGSSLPVLSRLRERFGRVHRSFPFSGSTAVGLAIAADPSSGFHL
RDRVARGIGVFREHDSGRAVSFDPLIAPDTSATVAKRCYKAVHNGWFRFVEYTSVSD
GSPGDLSLSLEIKIPFDSITDVTATEISRFDPGEVEETITVNDNGVASISIKLGGVTV
EHTI

>RXN01404 TRANSLATE of: rxn01404.seq check: 9645 from: 1 to: 999
QKMTSRPTIYDVAKAAGVSKSLVSLVLRGSPNVSKSEAAVKTAIKLNLQPNRAASDL
AAKRTQLIAVLIDDYSNPFIDLIQSLSDVLT PKGYRLSVIIDLSTSQAGTDPIISALSMR
PDGIIIAQIDPFTVPDLSPPFVIAGTRITQASTHDSVANDFERGAETIAKHLIDLGHTH
IAHLRVGSGAGLRRFESFEATMRHGLEPLSNDYDPAVEHAGYTTETLALKKEHPEVTAI
FSSNDITAI GALGAARELGRVPELDSIIIGYDNTPLAQTRLINLTITIDNSIGVGYNAAL
LLLSMLDPEAPHPEIMHTLQPSLIERGTCAPRG

>RXN01490 TRANSLATE of: rxn01490.seq check: 1933 from: 1 to: 891
MNAAPKPKGLVIVDKPAGMTHDVVSKLRRASFTRKVGAGHTLDPMATGVLVVGIERGTR
FLAHMVASTKAYDATIRLGAATSTDDAEGEVISTTDSAGLDHSTILAEI VNLTDGDMQKP
TKVSAIKIDGKRAHERVDRGEEVDIPARPVTVSVFVDLVYHVGFEYDLVVRVHCSSGY
IRALARDLGNALQVGGHLLTALRRTVEGFFTLNDATPLSKLQENPELSLNLQALTRSYVP
LDITEDEGVDLSMGKWLEPRGLKGVHAAVTPSGKAVALIEEKGRRLATVFAHENTL

>RXN01496 TRANSLATE of: rxn01496.seq check: 8990 from: 1 to: 3012
VPGKLRVHELAKQLGITSKELLATLKDKGEFVKTASSTIEPPVVKRMQEHYGSSGSDKSD
TAAKPAAPAKPAAPKPAASAPKPGAPAKPAAPAAKPAAPASAAKPAAPKPAAPKPGVQAK
PAAAKPGAPAKPAAPKPAASAKSGASKPAAPAAKPAFSGPTPGDASKKAEPAAPKPAAGAE

PRPGGMPRPMGKPAKPGARAPRVANNPSTGGGERPAPRPGGGPRPGGGPRPGGGPRPQ
 QGGRPGQGRDQGRDQGRDQGRNRGQGRQAGAGGPRPQGGPRPQGGSRPQGGSSAQGAQGA
 PSQERQGGGRPS PAMPEPTPGMPAKAPGKGRGQAGGAGGGNRRGGGTGGGARGGG
 RRGGTAGAFGRPGGAPRRGRKSKRQKRNEYESMQAPNVIGVRLPDCKGATIRLAGASL
 ADFADKTGADAAALVQALFNLGEMVTATASVSBETLQLLGEEMNYKVQVVSPEDERELL
 ESFDLQFGEDEGGEADLAKRPPVVTVMGHVDHGKTRLLDTRKANVGSDEAGGITQGIGA
 YQVKVNVEDERTITFLDTGHEAFTAMRARGAKSTDI AVLVAADGVMPQTVAEINHA
 KAADVPVVAVNKIDKPEASPEKIRGQLTEYGLIPEEYGGDTIFVDISAKQLGNIDELLA
 SVCLTADAELDLVANPEMDAQGVAIEAHLDRGRGPVATVIVQRTGLRVGDSIVAGDTYGR
 VRRMVDYEGRDVEEAGPSRPVQVQGLNVGPVAGDNLLVVEDDRIARQIANQRNARKNARL
 AARSKRKVSLEDLDSVLKEHSTLNLILKGDNAGSVEALEEALKEIMDEVEQLNII DRG
 GAVTQTEVNTVLAASDAVIAFNVRAEGKATEEANAEGVDVRYTIIYRAIEVEEAALKGM
 LKPIEERVIIHAEIRAIKASSVGLIAGCMVEDGKVRNATVRIIRDGNVIAEKIVS
 LRREKDDATEVSAGYECGMVLSYFDSVDDKIEVYEMVEVPREA

>RXN01541 TRANSLATE of: rxn01541.seq check: 7782 from: 1 to: 777
 MTPPHSHRAPLASTVIIARESADSGTLEFFIQQRQSTMAYANAVVFPGGGVDSYFP
 MLPHRDQHMSPHIIKHASRLHMDSETMAAHISAAARVEEETGVDLGNYNHELIPIDRW
 ITFPIPAFRRRYDTATFVLILSKDSTNAALQHQTTEATHSYWATAEELLTQWSTGHLN
 LLLPTWWHINQLNHLHTLNQLYSFAQRTNHPQTPPTVFANWNTAPADEAAMQHYGFPDPD
 AYFDHATAGKHHTLITRK

>RXN01559 TRANSLATE of: rxn01559.seq check: 3150 from: 1 to: 1842
 VLIVVGVVALVLITGDRSATPKLGIDLGQGTTRVLVPQGDPTQDOLNQARTILENRVNG
 MGVSGASVADGNTLVITVPGENTAAQASLGQTSQLLFRFPVQAGMPDMTTLMPLEEMA
 NRWVEYGVITEEQANASLEEMNTAVASTAVEGEATEPEPVTVSATFMEPANSIETAQ
 RRQETDMLRTDRQSTDPTVQIAASSLMQCTTDEMDFLAGTDDPRPLVACDPVAGGVYV
 LDPAFLINGETDEENGARLTGNEIDNRPITGGFNAQSGQMEISFAFKSGDGEESGATWS
 SLTSQYLQOQIAITLDSQVISAPVQISATPVGSATISITGDTQTEAQDLANNRLRYGALP
 SFAGENERGEGGTTTTPVPSLGAASLAKGLIAGVIGIALVAIFVFAYYRVGFVSFLTFLFA
 AGVLYVGLLVLLGRWIGYSLDLAGIAGLIIGITGADSFVYPERIKDETREGRSFRAV
 PRAWESAKRTIVTGNMVTLLGAIVIYLLAVGEVKGFAFTLGLTTFVFLVTVFLITAPLVI
 LASRNPFFAKSVNMGCRMVLMVEERRANGELDEPEYLKKIHAKNAADKASTDNSSTDN
 SEAPGTDINQEEK

>RXN01583 TRANSLATE of: rxn01583.seq check: 2692 from: 1 to: 2343
 VETIEELTEFFKPIRHCHVNVGDANGTGLQSVICGARNFEKGDVVVSLPGAVLPQDFA
 ISARETYGRMSAGMICSASELGLADKQNSGIITLDPYSGEPGEDARQALGLEDTVFDVNV
 TPDGRYALSARGLTRELASAFSLTFTDPAIEPAVAGIEVKVPAVEGSLINVELREETKAI
 RFRGLRVKSGIDPAEASEPFWMQRELMLSGQRPNVNAATDVNTVMYMLLQGPMPHDAKVTG
 DLVVRNATAGEKFETLDHVKRTLNEEDVVIITDDNGIQLSAGVMGLTSEISDITTDVYFE
 AATWDTITVARTSRRHKLSSASRRFRFEGVDPAIVEIALDIAATLLVEIAGTVDAGRTVL
 VGDVPAMQPTIMKVTREPSELAGVDYSATVIAELEEVGCTVAVSGDTLEVTPTVRGLDT
 MSYDLVEEVRLLEGLEAIPITIIPTAPAGRGLTDAQKRRRAVGHALAYAGYAEIIPSPFMD
 PEVFDVWGLAADDERKRTVSVINPLEAERNVLSTSLPLSMLDAVKRNVARGHNDLSFLGL
 QQVAFEHGSGVSPMPSVASRPEESVVAELVDSLNPQLHVATVGTGNIEFEGPWGKGRAY
 TFDAALIESARAVARAAGVTLELANADALPWHPGRCALLIDGTFVGYAGELHPQILEKAG
 LPARTCAMELDLSALPLVENLPAPVLSFPALHQIALVVDTEITPAEDVRVAVEACAGEL
 IETVELFHVFRSEQRGENKKSALFSLRFRAAGRTLDEANEARLQAELAKEKFAEMER
 G

>RXN01670 TRANSLATE of: rxn01670.seq check: 7045 from: 1 to: 807
 MPEGHVIRLAGELTKNFGDTILDATSPQGRFTSEAAIINGHRIAVAEAYGKHLFVEFDA
 DHEPHILYIHLGLTGLQFPAEETRGOIRLHLSDGELIAANLRGFPQWCRLLTDAERTQAI
 KGLGADPTRDADPEPIRIKQVRSGRSISGLLMDQKLFAGVGNIYRAETLRLGISPFTI
 GKDITTAQFRSIWADLVGLMKDGVVTVGRITVTRPHTPEAMGRPPRKDDHGGEVYTYRT
 GQECFLCATPIKEQVMEGRNLFWCPCGQR

>RXN01671 TRANSLATE of: rxn01671.seq check: 7692 from: 1 to: 1149
 MNHVNFASHLEDAALKQAEATATMPTIYPHVALMDPAHFGLGSSVGTVFGTKGAIIPAA
 VGVDIGCGMIGVCTNYTASDLEGRDLVTLRDYIERVPLSPGNYNSTTLKETAKVVAEL

>RXN01784 TRANSLATE of: rxn01784.seq check: 6464 from: 1 to: 582
 MMTERGVPVDHTTIYRWVQKALELDKQTRWYQVPDQWASSRWVDETYIRVGGTWCYLY
 RAITAGGQTLEFYLSPRKNVAAAKRFLAKTRLSNTTAGSPRVINTDKAPALAKAISLKA
 EGICPQTVHEHRQVKYLNNVIEGDHGRLLKRLGPKGAFKNRISAYRTLKGMEMHSLRKGQ
 GTMFDLTGTRTQTR

>RXN01795 TRANSLATE of: rxn01795.seq check: 439 from: 1 to: 597
 VLVIGIRRDQTFDFKHPAPTHGPRGDMPYKTAGEALKGVKDVPTNNHMKIMPRTVEVLK
 RIPEGENETAIPKDDDPYVKGMISSHVYRRLHRDEFSKTLIAGGGGGTGWGYHIEKNRALT
 RERARIQSFPDDFEFLGSNTEVRRQIGNAVPPVGMHAGVERLMNLYTGNYPDVLDEEQHA
 YLQTLISIKERLALADQAD

>RXN01837 TRANSLATE of: rxn01837.seq check: 8888 from: 1 to: 777
 VSTNKERRQQALSQLEKEIKSRDRKEKTKPLTVVFASLAVILVVGGIYAAATSTEDEV
 ITADETSTTAETPDYQPLALTRTTALGDSVTCYEPDAGEASKDVSKPATENVPATGTVTV
 NLTTAQGNIMELDRSVSPCTVNAVEHMASEGYNDTVCHRITTSIGIYVLQCGDPSSTGA
 GPGGFSFANEYPTDEATDLTTPVIYERGTIAMANAGADTNGLFVLPQLRGFPPTGTEHLHL
 RPDHRRRRCNPRRHRSSWH

>RXN01863 TRANSLATE of: rxn01863.seq check: 1675 from: 1 to: 1149
 MNSVKKLQKQPSIYNDPWESYNDVKEHQGLTSLNIEFTTTLNLCMRCSCHAVGYTLQTVDP
 EPLDMDLIYRRLDEIPNLRMTSITGGEGPMFSKKSIKRVNVKPLLYAHHRGIYTQMNSNLT
 LPQDRYLOIAEYIDVMHISHNWGTTDEFANVGFEGAMKKQPPLKAKLKYEQMISNARTLS
 EQQGMFVSAETMLNQSTLPHLRKIHQEVVHDMKCSRHEIHPMYPADFASQLNVLTLAEMKK
 TIHIDLDRFDEIWMFLGTLVFFCLKDDDEQKLLSRLSRNANNVTRNDPDGRSRLNVNV
 FTGNVITVDGDEGTITISNIQDKLTDVDFKWLSSDLAKSLNCHCSEFSCLPNVVLKMN
 YYPNMDFKDNERHMHKQPIIQF

>RXN01872 TRANSLATE of: rxn01872.seq check: 8549 from: 1 to: 828
 MNDGGDLRIDDLRSFISVAQSGHLTETAQRLGIPQPTLSRRISRVEKHAGTPLFDRAGR
 KLVNLQGHAFNLHASAIAVEFNSAATEIKRLMDPEKGTIRLDFMHSGLTMMVPELIRTF
 RAEPNVEFPLHQAAAMLRLVDRVLADETDLALVGPKEPAEYVTSGLWAPLLRQLRALAVPA
 DHRLASFSCQCELPLITAAEEFPVAMRAGFGTRLMLDALAEAGFVPNVVFESMELTTVA
 GLVSAGLVGVVPMDDPYLSTVGIVQRPLSPPAYRE

>RXN01926 TRANSLATE of: rxn01926.seq check: 2379 from: 1 to: 741
 LRSFYTPQEAIEREGDVWKAATEEAELLAADGAVHDQELFLNCITTSPLIFASAMLNFGVH
 QILDTLCLQAPSPAGRADAPKALEAATSAMDHRDRTDDFSGVVFVKVQAGMDKNHRDTLA
 FMRVVSSEFDRGMQVTHSQSGRSFSTKYALTVEGRTSTVETAFPGDIVGLVNAGALAPG
 DTIFEGRKQIYPPMPKFAPEHFRILRAKSLGKYKQFRKALEQLDSEGVVQILKNDLRGDA
 NPGHGRC

>RXN01938 TRANSLATE of: rxn01938.seq check: 4407 from: 1 to: 1428
 MITRLSTLPLRLTREDPADAEPVPSHKLVLVRAGYIRRVAPGIYSWPLPLGLRAVRNIEAVVR
 EEMDAIGGQELLFPTLLPREPYETTRQWTEYGDLSFLRKLDRKGADYLLGPTHEEMFAATV
 KDLVNSYKDFPVTLYQIQTKYRDERPRAGVLRGRFVMDKDSYSFDISDAGLDSYAKHR
 AAYQRIFLRGLLEYAICQATSGAMGGSASEEFLAVSENGEDTFVRSTSGNVAANVEAVVT
 PQGVVERDIEGLPEPVTYETFPVSETIDALVDWANSIDVGIEGREVTADDTLKCIVVKVREP
 GAEEAELTGILLPGDREVDMKRLASLEPAEVELAVESDFADNPFLVKGYGVGPVGLAKNG
 VKVLADPFRVYTGTSWITGADEKERHVVGLVAGRDFTPDGFI EAAEIKEGDPAAPAGEGLT
 LARGIEIGTSSSSAASTPKPSTSKSWTKTASAPSQFWALRARCHPPARRPGRTAPR

>RXN01969 TRANSLATE of: rxn01969.seq check: 287 from: 1 to: 366
 LWAYDKAYGALKLAWLAYQAIIDCYQMKNKREAKKMTIIDQLRVLKGPKNKELAQGRS
 LFKRLGDVLAYFDYGVSNPGVEAINGRLEHLRGIAGLGRNMLNHYILRCLIHSGQLVHKIN
 AL

>RXN02002 TRANSLATE of: rxn02002.seq check: 9539 from: 1 to: 378
 MSNANSDDTAAEAHRRRTFAVIAHPDACKSTLLEALALHAHIISEAGATHGKAGRKATVS
 DWEMEMKDRGISIASLQFEYAPEGHAGEFFMINLVDPGHADFSEDTYRVLMMAVDAAV

MLMHSV

>RXN02004 TRANSLATE of: rxn02004.seq check: 647 from: 1 to: 207
RVGRLMRQNGILIIIRSRKFKRTTGSDFTHFIAPNFLQQDFMASRPNQKWAGDITYVWTRE
GLGLSGRHS

>RXN02267 TRANSLATE of: rxn02267.seq check: 5927 from: 1 to: 873
VQKWGLSFVERIVIVNNVQQFHRFFDDSAVYYPCEVPLDRAIGHFDRQNKPMRSRFIGTL
ILPLAKLEEAAQYTGDEVLRVSAVISTDGLADLRDRDFYELPNIDIASVEIKLVGAALNT
VLGKGDVEKLIQOHRNTFVWVEIPTALVTADIVRKLRRHMGAGLKYRTGGDREELFFSPQDL
VTVLRTAIDAAPLFFKLTAGLHRLALRYRDEKTRGLHFGFLNIAAAVATLRAGKGAEAEALKI
LEGDDAAPLIHALQSGENWRDSFRSFSTCNVVEPLNTLIDLDVLAEGDVHP

>RXN02280 TRANSLATE of: rxn02280.seq check: 171 from: 1 to: 1824
MQESSRDNFQVDLGGVVDLSRHHYSGPRVYVRELLQNAVDACTARSEQGEEGYEPSIRI
RPVTKDRATFSLVDNGTGLTAQEAARELLATVGRTSKRDEFGLQREGRLGGQFGIGLLSCFM
VADEITMVSHAEGASAIIRWTGHADGTFNLEILGDDATDVPVGTTVHLTPRPDERTLLTE
NSVVTIASNYGRYLPPIPIVVQGEKNTTITTSPVFAKTDQOHRLYAGRERLGKTPFDVID
LTGPGIEGVAYVLEPAQAPHMRRHSIYVNRMLVSDGPGSTVLPNNAFFVECEINSTDLEP
TASREALMDDTAFATREHIGECIKSWLINLMTKPHRVREFTAIDHLALRELQCSDADD
AETMLGLLTETSGRGISIGETITLSTEDVSLQLATLDDFRQLNTIARPDTLIINGGY
IHDSDLARLIPVHYPLTVSTADLRESMDLMELPPLQDIEKAKALDAQVTESLKDFQIKG
ATRVFEPADVPVAVIISKAAQASDRNETQSATTDRAWADILATVDNTLSRQTANIPQQDG
LSALCLNWNLSVRKLASTDDTAVVSRTVRLLYVQALLSSKRPLRVKERALLNDSLADLV
SLSLSSDI

>RXN02287 TRANSLATE of: rxn02287.seq check: 4446 from: 1 to: 552
VYSISETIARTLMPRTDHFVFLMGNGNAWFVDALERLGRGITVPTVETVAAADTYHRV
TRRPVATTTYGAGFTNTMTTLADVALSRIPLLLVVGTAPSAGPRCDFIDRQGLARAVGV
ETFTVHADDDVAATLQAWNNTPENTHVIIEIPYDLAAATADTDTVTYLLRPGFQKLPMS
PTLS

>RXN02291 TRANSLATE of: rxn02291.seq check: 8232 from: 1 to: 654
VVLHPNPLGLAEQKALVAQARDLAREVVGTPLAMVRPKLKSGQMSVHMLHLGKYWASNPY
RYVDVVDGFPVPPLPDSFVDLAHRALLSAGSLNSLQSWSEAYRAEALVNYISPDASMG
MHQDANESEAPVISLSIGDTGIFRLGGTLNRNKWTDIPLMSGDLIVFGGANRQAFHGI
PSIEANTAPAGCGLKEGESTSRSANLHYKTPGRGMSRG

>RXN02325 TRANSLATE of: rxn02325.seq check: 7224 from: 1 to: 867
MDHAHSDSCPTLRRDLEVTGQLQPEKAVDLAAPHEGKVANITKVTSNMEHTITQASKAK
EVVVLIGHSLPFTQDLKEDI LHFQAGNKGGRFSVAIVDPDRSADVVARFPKQIPVAVV
KDGSAIEFNSLNKEPVAQWLDHFVSRETIPNEKEGDVQKIDPRLWRAEALVNYISPDASMG
ALALYEQLPQDATVKRAHAASVILARMSVADRGDPIEKSRDDPDVKNKALAAADMYVLM
NQPDTLAHLAALLPKPEAARRIVELLNLFDPDLVDLAELTRAQVGNAMS

>RXN02386 TRANSLATE of: rxn02386.seq check: 6167 from: 1 to: 459
MAALAENYQTPAPSSQVVSVGVHAKPGLVTLAEGSRVADALAIAGALPDADLTALNLA
QLLVDTQIHLVAIGEVQIPISVDAATSASGLISLNTATVADLVLPVGVGEKTAQAIIDF
RESNGFSTVEDLLQVKGIGPSKFEQISGLVSP

>RXN02388 TRANSLATE of: rxn02388.seq check: 380 from: 1 to: 1662
MIEVRLVPVAAVMMMAAALIINGSWVLSVGVIGIAIIAACVFKHGWQAVVIAALGVGVA
VMAALRISSAKAFAPQTWGTAETIKFLDSGDQIGLGRVEGYPAIPVYSGSDSTIEKA
SLIIVASGRITKPSFPFGDLTISTEDIDQLEPTTGYSAWNVQVRDGFSGAVEETVGESSR
GLIPGMVLGDTRLQGSIEAQTYIDTGLSHLSAVSGSNVAIVVSSVVLSYFLTAGPRIV
VASLLSLVIFVSLVGFEPSVLRASVTGIVGLLAIINSSRMEPMHGLSLSVICLLFYDSNL
AVHGYFLLSCAATAGIVMLQPLLYRAIGPPLAVWVKPDIVVRAFAVSIADLVTPPIAL
MARQISLVAVLANVLAVPPIITLLGLIAVLASLLPWPVEYPLLKIEEFTWNIHHVAK
WQOCLNSTLEISAGWAGIAWACMAAVVVVVIYKGYVRTLAVCCVCFLLFGAWNRLPA
QIDPTELREVIIDSSSELTDVPEHAELIIVDPHGSMSDRPIVTRREGIPVLYPYRDGEVS
LHIDGTQHAADGRF

00602379.06.27.00

>RXN02416 TRANSLATE of: rxn02416.seq check: 4089 from: 1 to: 2829
 VRGAREHNKGVGVDILPRDSMVVFTGLSGSGKSSLAFDTIFAEQORRYVESLSSYARMLF
 GQMDKPPVDLIDGLSPAVSIDQKSTNRNPRSTVGTITEVYDYLRLLYARAGTAHCPVDA
 RVEROTPCQMVQDILGMEEGLKFQIILAPVVRTRKGEFVDFADLASQGSYSRVRVGEVHQ
 LSDPFPKLEKQIKHDDIVVDRLOVKASQKRLTDSMETALRLADGVAVLEFVGLEEDDPN
 RLRRSESEKSPCNHGHALTVDELEFRAFSFNSPYGACPACDGLGVRTVEVDILLIPDPAP
 ATKAVQPWNSSPNHSYFEKLIIEGLAKALGFDPETPYSELTAQKKALVYGSKEEVSRYK
 NRYGVRWSWTAPFEGVMGYFDRKLEQTDSETQKDRLLRGLTREVPCPTCKGARLKEPILAV
 RLDSGSGHGLSISAGLTALSVHEAFELDNLTGLKREEMTAGAVLKEIHARLFELLDVGLS
 YLTLDRAAGTLSGGAEQIRLATQIGSGLAGVLYVLDEPSIGLHQDNQRLITTLLEHRD
 IGNTLIVVHEDEDITIRRADWLVDIGPRAGEFGGEVYVQGEKPGILDCEEELTGAYLSGRR
 TLGVDPDRREHIDKERQLKVGARENNLQIGDVKIPLGLVLCCTIGVSGSGKSTLVLNQILAK
 VLANKLNRRARQVPGRAKRVGLEHLDKLVQVDQSPIGRTPRSNPATYTGVDKVRNLFAE
 TTEAKVRGYEKGPRFSFNKIGGRCEACQGDGTLKIEMNLFDPVYVPEVCDGQQRNRETLE
 VKYKGKNIAGVLGMPISEAADFEFPITSIHRYLATLVVDVGLGYVRLGQAATLSSGGEAQR
 VKLAELQKRSNGRTVYILDEPTTGLHFEDIRKLMVMVIEGLVDKGNVSIIIEHNLDVIAK
 ADWIVDMGPEGSGGGGTVAEGTPEQVAEVAAGSYTGQFLKELL

>RXN02431 TRANSLATE of: rxn02431.seq check: 2412 from: 1 to: 876
 DPLPVGALWGVGPVTGSKLASMGVETIGDLAALTQKEVEISLGATIGISLWNLARGIDDR
 PVEPRAEAKQISQEHTEYKDLLTRQQVDAIIRSAEGAHRRLKDGRCARTVSKLARM
 FRIESRSTLSYATDDYATLEATAFRLARYPGEVGPRLVGVFSGLGEESRQDILFELD
 QQIIVFPAPDRTDYEVGVQSSSSSESTQVEAPQDVALSMWCATQDVYHPEYGHGWVGAGH
 GVVSVRFETRSTTKGRKTSFSMDPDLTPADPLDSLWDADWFAENGETGDDE

>RXN02462 TRANSLATE of: rxn02462.seq check: 3189 from: 1 to: 1818
 MTKDVHVEVDERKRTVGVKEEGVEYVEDQLGIDNLIYAPHSQVLSYLNNAIKAQELFTRD
 KDYIVRNGEVMIVDGTGRVLGRRYNEGMMHQAIEAKERVEIKENQTLATVTLQNYFRL
 YTKLAGMTGTAEAEALNQIYKLDVIAIPTNRNPNQREDITDLVYKTQEAFAAVVDDIA
 ERTEKQPVVLVGTVSVERSEYLSQLLTKRGIKHNVLNAKHHEQEAQIVAAQGLPAGVTV
 RNMAGRGTDIVLGNPEIILLIKLRERGLDPFEDEESYQEAWDALPAMKQRCEREGDKV
 REAGGLYVLGTERHESRRIDNQLRGRSARQGDGSTRFYLSMRDDLVRVFGPTMENMMN
 RLNVPPDDVPIESKTVTNSIKGAQAQVENQNFEMRKNVLKYDEVMNEQRKVYSERIEILE
 SADISRYIQNMIEETVSAYVDGATANGYVEDWDLKLNLALEALYDPSINWTLDLVGESEY
 GKPGELSAEDLRTALVNDAAHEAYAKLEEAVSAIGGEAQIRNIERMVLPVITDKWREHLY
 EMDYLKEGIGLRAAQRDPLVEYQKEGGDMFNGMKDGIKEETVRQLFLSASSSSSKTRKS
 LTNSEP

>RXN02543 TRANSLATE of: rxn02543.seq check: 6877 from: 1 to: 1854
 MGRAVIGDLGTTNSVSVLEGGEPVIVANAEGSRTPPSVAFAKNEGVLVQSAKNAQVAT
 NVDRTTIRSVKRHIGTDWSVAIDDKNYTSQEIARTLMKLKRADEAYLGEDVTPAVITVA
 YFEDSQRQRTKAGQIAGLNVLIRVNEPTAAALAYLEKGEQEQITILVFDLGGGTFDVSL
 LEIGDGVVEVRSTSGDNLGGDDWDQRIVDWLVEKFQSSNGIDLTDKMALKRLREAAEK
 AKTIELSSSSANINLPYITVDADKNFLFDELTSRAEFQRTITQDLLARTKTPFNQVVKDA
 GVSSEVDHVLVVGSTRMFAVTELVKELTGGREPKNGVNPDEVVAVGAALQAGVLRGEV
 KDVLLEDVTPSLSGIETKGGVMTKLIERNTTIPTKRSETFTTAEQNPQSVQIQVFGGERE
 IATANKLLGSFELGGIAPAFRGVPQIEVTFDIDANGIVHVTAKDKGTGKENTITIQDGG
 LSQDEIDRMIKDAEHAHEDDKKREEQEVNRNNAESLVYQTRKFEVENSEKVEDLKAKEVE
 EAAKGVEEALKGDELEAKAAVEKLNTESEMQMKAIYEADAAGATQADAGAEGAADDNV
 VDAEVVEDDAADNGEDK

>RXN02651 TRANSLATE of: rxn02651.seq check: 4052 from: 1 to: 930
 MNNRQSRITLPVPEGLAGMRVDAALSKLLGISRTVAELATAGDVSDGAVVGKSERLVAD
 SMLDVLPEPAPLPKKEIIVPGLDILYSDDDVIAVNPVGVAHPTVGVGEGPTVVGGLA
 AAGFRISTSGPPEPKGIVQRLDVGTSGVMVVAASERGYTVLKRAFRDRITVKTYHALVQG
 HPDPLTGTIEAPIGRHPSAGWRFAVTEGKHAVHTYETLEAFQEAATLLKIHLETGRTHQI
 RVHFSALHHFPCCGDPMYGSDPALSERLGLNRQWLHVASLGFNHPADGRWMEIVSPYPTDL
 QHALDVLREQ

>RXN02732 TRANSLATE of: rxn02732.seq check: 432 from: 1 to: 441

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MSENYKIVVGTGDSKSSLLAVERAARIAAAFDATLIIGCAYYESKEDASETLRQDSVTI
LGDDPARENLDKAADAARAVGATSIEETVTRTGPVEALMAIVNDHQADLLVVGNGRGINYL
TGRLLSVFPADVARGSDCDVMIVHTVS

>RXN02736 TRANSLATE of: rxn02736.seq check: 2617 from: 1 to: 957
MIFELPDTTQQISKTLRLRESGTQVTTGRVILTLIVVTDSESDVAAVTESTNEASREHP
SRVITLVVGDKTAENKVDAEVRIGGDAGASEMIIMHLNGFVADKLQYVVTFLLLPDTPIV
AWWPGESEPKNSQDPIGRIAQRITDALYDRDDALEDRVENYHFGDPTDMTWARLTQWRGL
VASSLDHPHSEITSVRLTGASGSTVDLAAGWLARRLKVFIREVDTAFTVPTDEFQTP
LLAIQRLEIVRTGSIIITIDAHTLQVEMPESGNAPLSVAITGRRESDCSEELRHMDP
DLGYQHALLSGLSVKLETV

>RXN02827 TRANSLATE of: rxn02827.seq check: 5045 from: 1 to: 423
MYEQQKILNEVSEKRLQAIKDFTELGSFGKIAMRDLISIRGAGNLLGAQQHGFIDAVGFDM
YSQMLSEAVXRKQCKNSQVEKXVEIDXGVDAYLPEYTVADRXRQKIEIYKRIRELDSEQEM
LDELEDDLDRFGEKPEEVAH

>RXN02915 TRANSLATE of: rxn02915.seq check: 8269 from: 1 to: 378
MPKPLPPETRRKIIDDFPAPNSPSIEEFCSRKLISRFSFYINRNYQQDANAALHSHSS
APITARRTYDESITSTLLSIRARLKAQGWEGYPTISIRFEGIFTRELTAIPSVSTIARLL
RAAGAV

>RXN02919 TRANSLATE of: rxn02919.seq check: 2536 from: 1 to: 534
VPVDHTTYRWQKYAPELDKQTRWYRQVPDQWASSWRVDETYIRVGGTWCYLYRAITAG
GQILEFYLSPKRNVAAAKRFLAKTLRSNTTAGSPRVINTOKAPALAKAISLKAEGICPQ
TVEHRQVKYLMNVIEGDHGRLLKRILGPKGAFKNRISAYRTLKGMAMHSLRKSGSNDV

>RXN02938 TRANSLATE of: rxn02938.seq check: 1933 from: 1 to: 741
LMNYPDLPHDFPQNTLETPAKAPVWMHRLDLRHTGRMANPLDGAETLGDTSEKRAAV
LMLFSGSETSFDLNDASVLLTHRTPTMRSHAGQIAFPGGRIIDPTDINAVDCAFREAWEE
TGLDRRTATPLAQLNEVHIRATGYVPVYPLGHWHTPSFPVAVASPHETDEVLDAPLYDLID
PKNRLMVGWREWHGPAFRINDYIIVGFTGGLLSAILDTAGWATEWDTDRIFDLNLTLS
RNNRMER

>RXN02949 TRANSLATE of: rxn02949.seq check: 1467 from: 1 to: 333
VSDEQNSGVGGTSRPTGKRQLSGASTTSSSYEAKQVSTQKSSGSDSKPCGGVISFLPE
VVGVEKVIWPTARQMVITYTLVVLGFLIVLTALVSGVDFTLAGLGVEKILTP

>RXN02963 TRANSLATE of: rxn02963.seq check: 2332 from: 1 to: 1308
MKSTGNIIADTICTRAELGLTITGASDAGDYTLIEADALDYTSTCEPCSQPGVFRHHTHR
MLIDLPIVGTGTFKLFIPLRYRCTNPCTCKQYFQAEELSCADHGKVTIHRVTRWILQRLAI
DRMSVHATAKALGLGWDLTQQLALDMCRELVYNDPHHLDGVYVIGVDEHKWSHNRAKHGD
GFVTIVVDMTHRYDRCRPARLLDVVPGRSADALRSWLGSRGQFRNQIRIVSMDFGQGY
ATASKELIPSAARRVMDFFHVRLAGDKLTACRQRLQREKYQRRGLSQDPLKYNKRTLLTT
HKWLSFRQESLEQLWAYDKDYALKLAWLAYQAIIDCYQMGNKREAKKMRNTI IDQLRV
LKGPENKLAQLGRSLFKRLGDVLAIFYDVGVSNGPVEAINRLEHLRGIALGFRNLNHYIL
RCLIHSGQLVHKINL

>RXN02985 TRANSLATE of: rxn02985.seq check: 7956 from: 1 to: 333
MRLESYAMKVDTSNATPALALLTERQIPFELDVHDVDPKSSKGFALDASEVMGVEPEV
VFETLMADIDGHEVVAIVPASRTNLKQLAKAGKGGKHAMMDSRAQVVTG

>RXN02986 TRANSLATE of: rxn02986.seq check: 1309 from: 1 to: 138
VFLDESAILQERIYVSAGRRGWSLIIAPDDVLLATDGVYADIADHS

>RXN02988 TRANSLATE of: rxn02988.seq check: 6478 from: 1 to: 606
MSTKPTIVSTFSGCGGLDLGLQEVGFDPFIWANDFSEEAQTYKHNIHGDHIVHGDITEIDP
FTDDTIPDGLDVTGGFPQDQFSMIWKRPGLDGKRGTLYQNRDFVAAKKPKAFIAENVKG
LLTANQHKAIKTIKTSKLLSLATSSSLACTTSLNTVSHNSANVCSLLFAVTPALISST

QLLPMALAVTCRIRLPAKRSKA

>RXN02989 TRANSLATE of: rxn02989.seq check: 5945 from: 1 to: 1140
MAPKKTATKATAAKGNDRQKALDAALALIEKDFGKGAVMRLGDNRPPIQTITSSNGTAID
IALGIGGFPRGRIVEVYGPESSGKTTVALHATAQAQKAGGIAAFIDAHAHLDPEYARKLG
VDTDALLVSPQDTGEQALEIADMLVRSGAIDIIIVDSVAALTPKAEIEGEMGDSHVGLQA
RLMSQALRKMTGALYNSGTTAI FINQLREKIGVMFGSPETTTGGKALKFYASVRCDIRRI
QTLKDGQDAIGNRTLRLKVVKNKVSPPFKIAEFDIMYGEGISRESSVIDLAVDNGIVKKS
SWFTTEGEQLGQGGKVKRLSLKENPELTDELEDKIFKKLVGKGYAAASDELTDDEPVELVP
NVDFDDEADTEADTEADAED

>RXN03033 TRANSLATE of: rxn03033.seq check: 9071 from: 1 to: 1158
VDEQRAFDQGLKEENTLITDLTTCARLSHNKALRLIKLSKSTAYYRNKPRPRAPKPVQ
AVPAPTAPGVEPTPEPWQCKEPAVSSVRQALAEHERQFIVDAITAYPQLSVSGVFNMLFN
KGIYRASLRWVRVAKQHLLHKDRVSALSPGKRSPTPRVKPRLEATQPGQVVCWDTVFL
PSLVRGKTYALHLAIDLFSRKIVGAKVAPTENTSTAVELLTQVLADNPGVVTVHSDNGSA
MTSTRVRLRLADHGVALLSIRPRVSDDNFAVESVHTLKYRPFYKVFASMDQARVWVEE
FVVYNTVHPHSGVAGHTPQSVFDGSWRAAHLRVQALDAHRYQFPQRYVGRPVVQEVAG
VVRNLGARDGSGQERVGGVALLSA

>RXN03035 TRANSLATE of: rxn03035.seq check: 9071 from: 1 to: 1158
VDEQRAFDQGLKEENTLITDLTTCARLSHNKALRLIKLSKSTAYYRNKPRPRAPKPVQ
AVPAPTAPGVEPTPEPWQCKEPAVSSVRQALAEHERQFIVDAITAYPQLSVSGVFNMLFN
KGIYRASLRWVRVAKQHLLHKDRVSALSPGKRSPTPRVKPRLEATQPGQVVCWDTVFL
PSLVRGKTYALHLAIDLFSRKIVGAKVAPTENTSTAVELLTQVLADNPGVVTVHSDNGSA
MTSTRVRLRLADHGVALLSIRPRVSDDNFAVESVHTLKYRPFYKVFASMDQARVWVEE
FVVYNTVHPHSGVAGHTPQSVFDGSWRAAHLRVQALDAHRYQFPQRYVGRPVVQEVAG
VVRNLGARDGSGQERVGGVALLSA

>RXN03038 TRANSLATE of: rxn03038.seq check: 812 from: 1 to: 726
MHGKEELTVRKGISRVLSVAVASSIGFVTLTGTAIAAQDSAFDYGMDPNMNYNEIDDI
KDRPEGLSNLPYFGSKLTSWSSYATASSGVVTSALPOYTDPYPLGKDDLPKATIDMEP
EVLRLAFVGVGDGDIRIQINAYSPSMGRTIPLVVVVPEDNTVPGPTVYALGGGDDGGQ
QNVVTRTDLEELTSDNNINLIMPLMGFSFSFYSDWARESQSMGCAQWETLLMHLEPEPLV
AA

>RXN03039 TRANSLATE of: rxn03039.seq check: 1469 from: 1 to: 630
ALPQYTDPRYPLGKDDLPKATIDMEPEALARLERFVGVDGDIRIQINAYSPSMGRTIPLV
WVVPEDNTVPGPTVYALGGGDDGGQGNVWTRTDLEELTSDNNINLIMPLMGFSFYADW
AGESESMGGAQWETFLMHLEPELEAAIADGQRSIVGMSMGGSVLNFATHPNFIYS
VGFSGCAETNSWMGRWRHRSCLQRQCR

>RXN03040 TRANSLATE of: rxn03040.seq check: 6898 from: 1 to: 309
MSXGDNAPIDEDAFKNRVLVGFEIAMSNTCTHNLKAATDQMGIDNINYDFRPTGTHAWD
YWNELHRRFFLMQGGFGLDGGPIPIYNPGVTSSESSXRTVF

>RXN03049 TRANSLATE of: rxn03049.seq check: 1664 from: 1 to: 942
MVHMFVGDMMNTDRAAQAYIIIVITIVMVVLFVIVLRYSLADRARAQRFTASITEIGRKI
FLNLRPRMSRQNTYTDKDISQFHWNTGLPPTDDESPWIAARDNEWEGYITLGGDDPN
TEKTIITLDDLRELQTSYVAVHTCMQGSATARTWGVRRLDVLCHDLVHTLDDLHHRHSR
LLTIEIIPKPLPETRCKIIDFDLFPNPSPIEEFCSRLKISRRSFYINRNRYPQDASAA
LHPSSAQITSRRTYDESITILLSAIRAPPESPRMGXRXDLXIRRHXRGTCTDTSIRL
NRYLLVTRCRSSRK

>RXN03051 TRANSLATE of: rxn03051.seq check: 1794 from: 1 to: 735
MRSDVIELPEGVSKEKADQLEVAEARLNEGARLMATTGCEVMWETGFSVCGRILDTYRVQ
GGQLSWLGPFPKSNELTNPDGVGKRSEFFGGAIYHPPTGAYAVTLTGRLQWGTINWESGP
LGYPYTGPMDTNYPLTORQTFQGGDNYNPLTGGAVWGDIKQRYEELGGSNHAIGIPITN
ELPSGTIEFYNNFNSGTISWRNRDQTRFMYLATQVWVWALGRGTGRLGFPPEADETPEVSG
LFHVA

MLIDLPIVGFPTKLFIRLPYRCTNPCTCKQYFQAEISCADHGKKVTRHVRTRWILQRLAI
DRMSVHATAKALGLGWDLTCLQALDMCRELVYNDPHLDGVYVIGVDEHKWSHNRAKHGD
GFVTYIVDMTHGRYDSRCARLLDVVPGRSADALRSWLGSRGQEFRNQIRIVSMDFGQY
ATASKELIPSARRVMDPFHVLRAGDKLTACRQLRQREKYQRRGLSQDPLYKKNRKTLLTT
HKWLSRQOESLEQLWYAKDYGALKLAWLAYQAIIDCYQMGNKREAKKKMRTIIDQLRV
LKGPNKELAQLGRSLFRKGLDVLAYFDVGVSNQVEAINGRLEHLRGIALGFRNLNHYIL
RCLIHSGQLVHKINAL

>RXN03161 TRANSLATE of: rxn03161.seq check: 570 from: 1 to: 384
MGIFSGRQFPPEIILWAVRWYCRYGVSYRDLDEEMTERGVVPDHTTIYRWVQKYAPELDK
KTRWYRQVPDWQARSWRVDETYIRVGGKWCYLYRAITAGSQTLDFYLSPKRNVAACKRFL
AKTLRSNN

>RXN03165 TRANSLATE of: rxn03165.seq check: 3775 from: 1 to: 321
MGNLPQALRHSFTWDQGVQMAEHARLSVVTKCPVFCDPHSPWQRGSNENTNGLVRDFFP
KGTNFAKVSDEEVQRAQDMLNYPKRMHGFSAKTQVYIEIIVVGASTD

>RXN03168 TRANSLATE of: rxn03168.seq check: 4805 from: 1 to: 1083
MSTRTPQDRTYDEYIERVKNDEPGLVDKLRDKHDWFDHLMNRERFGAGGNQLSAGI
TYFSVLISIFPIAMLVFGIAGVILAGNPEVLTDIQRINDALEGEIGNTVNGIIDSIAIQR
GAVLGGQVTALWSGLGWMANLRFVSRMWAIDPTEGNFIQKLTDLVALIIVLLAMGVA
FKGTALGASGILTKNLLDFVLGEIPGISYITVWVAALVGLANFLVFMWILFSLPRTKVP
MKPGLOQALLGAIGFEVVKQVGSLSNALSNPAGAAFGPIIGIMVVLVILWRILMYCSA
WAATSEALRLATVPAPEPAIRVRHEIDPCEEVSQARKVGVIGVAVGAATAGAFALLRK
K

>RXN03169 TRANSLATE of: rxn03169.seq check: 5370 from: 1 to: 438
DLQNPATKMSKSGDNPKGIINLLDDPKVSTKRISAVTDNDGVIAYPDENKPGVSNLLVI
QSALTGTSIDSLVDGYQGAGYALKGDTADALEAFTPLKAKYDEYMNDRGELERVLAIG
AERATEVANETLADVYDKIGFLASRR

>RXS00061 TRANSLATE of: RXS00061.seq check: 8093 from: 1 to: 2667
VTEKTDQTLMLIDGHSMARFAFFALPAENFSTSGGOATNAVYGFLSMLSTLLKDEQPTHVAVAFDVGRK
TFRTDMFPAYKQREATPEFKGQVEILKEVLSTLGITTIEKIDFEADDVIATLSVAAKPLGFKTLIVT
GDRDSQFLVNDTTTVLYPMKGVSVLHREFTEAVEEYKGLTRQYQPEFAALRGDPSNLPNIPGVGEKTA
TKWIAQYETLBNLLDHADIEKGVKVASLRERIEQVRMNRKLTEMVKDLELPLGPDDEFMKPVQAEVAA
KFDDLEFGTNLREVRVLAUVKAGSAAPEVEAEQVVVDQSLAQWLPARAGQALALAGVAKPAAGD
TYALAIADTKRHAVLVDVADISAEDEKALATWLASEDPKMLHGAKAAHYHMLAGRGFELHGVVHDFAIAA
YLLRPGQRTYELADVYQRHLRQLSTNDNGGQLTLDDAADQSLVDVVIALLSEELTKQLQEIQAFE
LYHDLIEPLSGILARMEATIGIAVDVATLEEQLKTFIGQVAQEEEAARELADEPTLLNKKPLQQLVLF
TFGMPKTKTKTYGTSAAAEIEALAIKNHPFLDHLHLAHRQYQMKMTLEGLIREVAPDGRHITTFNQT
VASTGRLSSTDPNLQNPVRTEAGRKIRSGFVVGEGYETLLTADYSQIEMRVMMAHLSQDPGLIEAYREG
EDLHNYVGSKVNPVIDGVTPELRRQVKAMSYGLVYGLSAFGLSQQLSPAGEAKQIMESYFERFEGGVQ
RYLREIVEEARKAGYETLEFGRRRYLPELTSNDRVARENAERAAALNAPIQGTAADIKIVAMIRVDRSLK
EAAVKSRLVQLVHDELVEVAAAGELEQVREILEREMDNAIKLSVPLEVSAGDGVNWDAAAH

>RXS00076 TRANSLATE of: RXS00076.seq check: 5232 from: 1 to: 1371
MTEPLRVAIVAGAGPAGIYASDLLIRNEEREVFVDLFEQMAPFGLIRYGVAPDHPRIKGIKVSLSHNVL
KPRILRLGNIEIGKDIITVEELRDYDAVVFSTGAVADRDLNIPGIEAGSGFAGEFVGYDGNPFERS
WDLASQSVAVIEGVNGLDVARILAKTGDELKVTIESDNVDSLKENKATEVHVFGRRGPAQVVKFT
LKELDHSPTINVVDPEIDYDGASEARRASKSQDLVCQLLEQYAIPEPKDAPHTLQIHLFENPVEVL
QKDGKVVGLRTELSLNGGVNGTGEFKDWPVQAVYRAVGYKS DPI DGVVPFDENKHVILPNDGKHVLT
PGAEVPVGLYATGWI KRGPIGLIGNTKSDAKETTDILIKDAVAGVLEAPKHQGEAEIIELLDSRNIPT
TWEGWYKLDAAERLAGEAERERKKTIVDWEEMVRQAREAPAV

>RXS00170 TRANSLATE of: RXS00170.seq check: 511 from: 1 to: 1854
MLLAIGVASPVAAQVEDQFELVKEISDEQFADDGVYVPPNRNAPTVEKQLEDDESAAHEPVVIEYHEHV
NDSKDNVEELPLPKRIDYAVEGMSDVIELPEGVSKDEADQYVAEARLNEGARLMAATGCEAMWPTGFS
VCGRIILDAYRQGGQLSWLGGPKSNELTNDGVGRKSEFVGGAIYWHPTD GAYATVLDGLRQWGLTWNE
SGPLGYPTSGPMDTNYPLTQRQTFQGGDNYYNPLTGAVAGWDIKQRYEELGGSNHAIGIPITNELPSGT

EYFYNNFFNGTISWRNDRQTRFMYLATQRVWDALGRETGRLGPFPEADETEVSGSLFHVVNFAERGVIAM
 NGILGARELYGDVVSJLWLYQNTDTPLGWPIPSLTSLNESLEQEFTRGVVLGSGGDALTWIPDDEERSLE
 DFLPIGSSGSSSSSQEMTLFSQRAQYVDCKNLPDLDEQRTENNIEKNGGPIKKEYSSRGFPTEFRFVV
 RKGHYDRYRNEGWGLKNYCKHNFANHAMAEAVVDKAVI DYGSSPGTSYYKFEKTYVFLDCRTRYTFNKN
 SGCKEMHAPQWVTIYINPHFTTGANSNRPKGVISAWCNSSTPPGGIEHEPEISQCPDHVNLNKLRI

>RXS00212 TRANSLATE of: RXS00212.seq check: 8164 from: 1 to: 1560
 MNILCLLCKWFAVRCSSSLNRISQEVNAQRIADGGKPFANPRNAAAGSLRQKNIEDVKRRRLMRNLSHGIG
 TEGFSPASQHDAYLALAAWGLPTSPYTEAVDTPEDVVKVSVYADHRHDALHEMGOGLVIVKDDIASQR
 ALGTSRAPRPAIAAYKYPPEEVTTKLLDIQVGVGRTRGVTPFAVMEPVLVAGSTVSMATLHNQSEVKRK
 GVLIGDTVVIKKAGEVIVPEVLGPVVELRDGTEREYI FPTLCEPCGTRLAPAKADDVDWRCNNMQSCPGQ
 LSTRLYTLAAGRGAFDIEALGEKGAEDLIRTGILLDESGFLDLTEDDLLSSNNVITNAGVNASGKKLLD
 NLQSKQTDLRVILRMLSLSRHVGPATAARALAGRYHSIQALIDAPLEELSETDVGVTIIAQSFKDWFDEVD
 WHKAVIDKWAAGVTMEEEVGEVAEQTLEGLTIVVTGGLEGFTRDSVKEAIISRGKGASGVSXKKTIDYV
 VIGENAGSKATKAELGLRILDEAGFVRLINTGSADE

>RXS00213 TRANSLATE of: RXS00213.seq check: 5673 from: 1 to: 573
 VTEDNAQLRRTWDLAEKVRYHRDRYNEQPEIPDADFDALFKQLQLEEDHPELAVPDSPTMVVGAPV
 AEQSSFDNVHELMRLSDNVDFEQELRDWLGRTPAKQYLTCLKIDGLSIDLYVRNGQLERAATRGDGR
 VGEDITANARVIEDI PHQJQDGTDEYFVPAVLEIRGEVFITVEDFPFGGQRAAHC

>RXS00671 TRANSLATE of: RXS00671.seq check: 9925 from: 1 to: 1014
 MLISQRTPIETEEFYNNARSRFVIEPLEPGFGYTLGNSLRRTLLSSIPGAAVTSVKIDGVLHEFTTISGV
 KEDVSDIILNKGLVLSSDSDEPVMQVLKVEGPGVVTAGDIQPPAGVIEHNPDLHATINETAKEIEEL
 IVERGRGYVPATVATATGELIGRIPVDQIYSPVLKVSIVKEATVEGORTDFOKLIVDETKNISITARAL
 ASAGKTLVELFGLARELNLAAEGIEIGSPQETEYIAAYSMPTIEDLDFSVRSYNCLRKEDHITVGLAE
 RASGDLDIRNFQKGSINEVKIKLAGLGLTKDAPEDFPTSTLEGYDAETGGYIDVEAEDSE

>RXS00724 TRANSLATE of: RXS00724.seq check: 5366 from: 1 to: 1977
 VVGIDATEGDLVTIVGGVAFKQSYTQSGKMLYKVTVLTERIGISFFGAKHILPRLLPEGTALFTGK
 VKFRFNEPQLSHPEFIVIPDPSGRRRLATGGMKSLAAYGDVEVALRLVDREYIPIYAGTATMTTWRI
 MAAVQVRVLETFMEVIEKPLSVVPEGMPFSFDEAIRGHDHPGHESTPTFINRLKYNALSLATVMAIRRAAT
 KNRKAPMPRALKGQHMLIDALNFQLTVGQKVIREISADIEQRPVMSRLQLQEVGSGKTLVLSIAML
 QAIIDSGRCQACMLAPTEVLATQHARSLSKTLDDAGLDINVLLTGSMPTGAKKEALLEISGDAIVVGT
 HALIQDTVEFFDLGLVVVEQHRFGVEQRDLRTKGREGLPHLLVMTATPIPTIAMTVFGDLAVSTL
 RELPGGRRPIQTSVIPDHKPGWVKRGWERIGEEVLGAQYAVVCPRIEGEGGVLEIHAYLESEQVYPLGN
 VGMHLGRMDTDLKDSVMQFEAQGEIDILVATTVIEVGIDVANATVMLIREARFQVSVQIHLQLRGRVGRG
 QHDSCLLHTTFDEDSFQGRLLAAISTTDDGFLSELDLQVNEGDLVLTQSGSDTLKRLHLSFISDQK
 IIERALIDATELVAASRSALVELVSDITAMINQYELEKS

>RXS00823 TRANSLATE of: RXS00823.seq check: 2648 from: 1 to: 780
 MGSITPQKRPVVGSHIANGQETDIGRKRARRINRLTVAYPDAHCELDFTNPLELTATILSAQCTD
 VRVNGVTPALFKRYPTATDYANADRTLEEFTIRPTGFYRNKATSLIGLGEALISLHDGGVPGTLEQLVE
 LFGVGRKRTANVVLNAGFVPGITVDTHFGLRVRLKLTDEEDPVKVEKVMNLEIEKPENTMFHSHRLIFH
 GRRICHSRAACGACMLAADCPSEGLGEGSDPPEAQKLIKSDREHLKLMAGM

>RXS00898 TRANSLATE of: RXS00898.seq check: 9031 from: 1 to: 789
 MRVINWNNVNSARTVRDMVDLRLHDDVVLAVQETCKCKDEQFPTERTFEIGYEVAFHGLNQWNGVAIIS
 RVGIENVEVTPAQPGFNKDITKEQSEIARAIGARGCVQWLSLYVPNGREIADPHDYKLRWFLSLRN
 YVIDTLEYRPEEKLVLLGDFNIAPTDDVWDIAAFEGKTHVTEPERAAFDGLIEAGLKETTPEGPGTYTY
 WDYKGARFLKGEGRMIDFLASPALAATAGETFDVDEERSSTGASDHAPVIVDYKV
 RXS00898 - 5'-Region

>RXS01066 TRANSLATE of: RXS01066.seq check: 7389 from: 1 to: 726
 MRSDFRDLRVKTYTDFGEADRIIVLLTRDHGIVRGVAKGVRRSKSRFGSRLQLGVFLDVLQVYPRKGL
 STISGADTVGYASGIIEDFTFRYSCASAILIATHIAGLENDPHLFETTRALKNKIQSDSPPIINLDEF
 MLRAMNHAGWAPSLFDCAACGRPGPHNAFHPGVGGAVCLYCRPPGSAEVPPEALHMMWLAVANGQAARIP
 REHEPQQTTHIQLTTHALHQLWHIERKLPTLAVLDQA

>RXS01277 TRANSLATE of: RXS01277.seq check: 992 from: 1 to: 2004

MSDENINEFEQDEDLNFGASFSDFAADDFFDAEADVEADAAEASALEAEQDLEETLDAPEEAAEEAP
 AAASEAPVEDEEADSLAQAALGDTDEQDADAIEYKARLRKFTRELKKQPGVWYIIQCYSGYENKVK
 ANLDMRAQLEVEDDIFEVVVPTEQVTEIRDGKRKLVRKRLPGYVLVRMDMNDRVWSVVRDTPGVTSF
 VGNEGNATPVKHRDVAKFLMPQEQAVVTGEAAAAAEGEQVAMPTDTKKPQVAVDFTVGEAVTILTGA
 FASVSATISSIDPELQKLEVLVSIFGRETFVDLSFDQVEKVS

>RXS02830 TRANSLATE of: RXS02830.seq check: 565 from: 1 to: 648
 RRLEDSLGVSLFERAGRGLALTGAGDQLLSQARRLIALNDEVYARLNAGAYEGEVTLVGPQDVIYFVIP
 RVLQQFARDFPRVQIHLISNFTLMLKEQFRGEIDVMLTTEDELGEGGETLAQRELIWVGAPGSSAWTR
 RFLPLAFERACIFRSFVQRRLDANSIDWQMVVSSESTRITIEATVSADLAVHTYIEGAEPALHERIATTA
 PCRNYPVQFH

>RXS02990 TRANSLATE of: RXS02990.seq check: 3521 from: 1 to: 597
 MDIQAIEKLEKRLKALDNFERAHARGESDFDHEKEEKKANVRRRALLLNQRARSVNELSTRLKALEFE
 EDIINEVIGDLTRSKLLDDEVFATEWVRQRAARRGKSSRALDRELQEKGVQDKTRAALAEQIDQADERD
 TARAVAVKKARSETKIPQDRADYKALRRVVGALARRGFPAGMSSMDLAREALDARIEDLN
 RXS02990 - 5'-Region
 GAAGACTAAGCACCAAGTTTAAACAAAGCAGGACAATCCACACACTTAAACCATGATGTGGCTTGTTC
 TGCTTTTTTCGTCACGAAGGCGAACACGCG

>RXS03098 TRANSLATE of: RXS03098.seq check: 3946 from: 1 to: 624
 MPTTDFVFNVRVLALEPLADPARATGMASYMRDQFSFLGIPSTPRKEACKFVLSALKELDTDFVSDCFGA
 AEREYQYVACDHINRVGITDLGFAKALVQTKSWWDTVDSLAKPIGAKHDDMLKMTWALDEDFVRRIRAI
 IHQLGRKKNTDAALLAWTIEQNLGSSEFFINKATIGWALRDFARHDPFSWVRAFDATDLSPLSRREALKN
 I

>RXS03175 TRANSLATE of: RXS03175.seq check: 2273 from: 1 to: 783
 VRASEKDTATALQPALDNGWHYIGAPAAKGRAGVGLSRHELEDVNI GFSGFLDSGRYIEATIKDTTL
 DVPVTVASLYLPSSAGTQDKQDEKYRFLDEFEGLDQRAKERSHMVIGGDWNICHRREDLKNWKTNQKK
 SGFLPDERAFMDSVFGTFPDEATQVAGAGDFFGAVDYEGTRRREATTDPAPWDFVARRLQPEGDGPTW
 TYRGKAFDTGAWRVDYQAATAMLERAERSWVWKAAAYDLRWSDHSLPVIYIS

>RXS03207 TRANSLATE of: RXS03207.seq check: 2273 from: 1 to: 783
 MTPASTQDLATTEREVDPGSRRGQTNDNPSQDLVRVYLNIGIKTALLTAEDEVELAQTIIEVGLYAEHLL
 KNSEEPFLTRAMKRDVLAKDGKKARSHLEANLRLVLSLAKRYTGRGMPLLDLILQENGLIRAMEKF
 DYSKGFKESTYATWIRQAITRGMADQSRITRLPVHIVEQVKNLSRIKRELYQHLGREATNEELAEESG
 IEESKIMLLRQSRDPSLDMFVGADEEAPLGDFIEDSEATDAESAVVMSRHSDIRAVLNTLEPREQD
 VIRLRYGLDDGVPRITLDIQIRRFGLSRERVQIEREVMKSLRDRGERASRLREYAQ

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